

# 3500/3500xL Genetic Analyzer

## USER GUIDE

3500 Series Data Collection Software v3.3

Windows™ 10 Operating System

**Catalog Numbers** 4405186, 4405186R, 4405187, 4405187R

**Publication Number** 100079380

**Revision** E



For Research Use Only. Not for use in diagnostic procedures.



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Legal manufacturer of these products:

- Applied Biosystems™ 3500 Genetic Analyzer
- Applied Biosystems™ 3500xL Genetic Analyzer



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Legal manufacturer of these products:

- Applied Biosystems™ 3500 Genetic Analyzer (refurbished)
- Applied Biosystems™ 3500xL Genetic Analyzer (refurbished)

Revision history: 100079380 E (English)

Revision	Date	Description
E	1 December 2023	<ul style="list-style-type: none"> <li>• Refurbished instruments were added to the list of supported instruments (4405186R and 4405187R).</li> <li>• Connect cloud-based platform was updated to Thermo Fisher™ Connect Platform.</li> <li>• The instructions to install the Cathode Buffer Container (CBC) septa were updated for clarification.</li> <li>• The environmental design standards were updated to include Commission Delegated Directive 2015/863.</li> </ul>
D	3 November 2021	<ul style="list-style-type: none"> <li>• The IMPORTANT text instructing the user to log in to the computer with the same Windows™ Administrator account was added in “Start the computer and instrument” on page 33 and “Restart the instrument and the computer” on page 279.</li> <li>• The following figures were updated: pump image in “Check for leaks and spills” on page 38; capillary to plate mapping image in “Capillary-to-plate mapping” on page 67.</li> <li>• The 384-well plate mapping image figure was updated to indicate the plates are for use supported on 24-capillary instruments.</li> <li>• The CRL definition was updated to the latest approved wording in “Review sequence quality” on page 104, “Pass/fail criteria for the sequencing install check” on page 150, and “Basecalling protocol—QV settings” on page 205.</li> <li>• Dye set Z was added to “Condition Number” on page 136.</li> <li>• The information for AnyDye was updated by request from Tech Support, “Create a new dye set using the AnyDye template” on page 195.</li> <li>• The RFID read/write unit model and manufacturer was updated in “Specifications” on page 327</li> <li>• The safety compliance standards for 60825 were updated to 2014 in “Safety (compliance)” on page 338.</li> <li>• Radio compliance information was added in “Radio compliance” on page 340.</li> </ul>
C	4 May 2020	<ul style="list-style-type: none"> <li>• Product information: Add new status for blinking amber front panel indicator. Add network configuration and security information. Update formamide storage conditions. Update information for antivirus software.</li> <li>• Spectral calibration: Add information to spectral calibration and the grayed out <b>Cancel</b> button. Add example spectral calibration result for dye set E</li> <li>• Install check fragment only: Change from POP-6™ to POP-7™ Polymer. Update capillary failure information to indicate that you can deselect 1 failed capillary for 8-capillary instruments or 2 failed capillaries for 24-capillary instruments.</li> <li>• Instrument specifications: Add note about using computers that have been validated by Thermo Fisher Scientific.</li> <li>• Change CutePDF to PDF printer.</li> <li>• Troubleshooting: Add camera error to Error message and Run troubleshooting.</li> <li>• View and print an install check report. Add note: The Date Performed field reflects the date that the install check was accepted, not the date it was run.</li> <li>• Restart instrument and computer: Update the list of reasons to use the procedure, add information about using only one Windows™ administrator account to log in to Windows™ on the instrument computer.</li> <li>• Environmental requirements: Add Electromagnetic interference to update information for CISPR 11 Class B TO A. Update electrical ratings. Add warnings.</li> <li>• Run modules: Update fragment analysis long run modules. Update FragmentAnalysis50_POP7: 40 to 45; Update LongFragAnalysis50_POP7 125 to 130; To run times for these modules, add fn to runtime - Throughput is an estimate extrapolated from average run time.</li> <li>• RFID appendix: Update distances to 10 cm.</li> </ul>

Revision	Date	Description
C (continued)	4 May 2020	<ul style="list-style-type: none"> <li>• RFID Specifications: Table 12 Minimum separation distance of the instrument from external RFID read/write units: Change 3 feet to 10 cm; Add row: "Minimum separation distance of the instrument from other lab equipment (e.g. centrifuge, thermal cycler)" - "1 m"</li> <li>• Safety: Update safety labels on the instrument.</li> <li>• Safety compliance: Update EU Directive standard.</li> <li>• EMC Compliance: Update standards.</li> <li>• Connect cloud-based platform: <ul style="list-style-type: none"> <li>– For non-UI elements, changed name from 'Thermo Fisher Connect'.</li> <li>– Updated website from <a href="https://thermofisher.com/cloud">thermofisher.com/cloud</a> to <a href="https://thermofisher.com/connect">thermofisher.com/connect</a>.</li> </ul> </li> </ul>
B	29 January 2019	Fix minor errors. In Chapter 3, change "Disconnect individual users" to "Unlink individual users" and update information.
A	30 October 2018	<p>New document for v3.3 features.</p> <ul style="list-style-type: none"> <li>• Preferences for reagent to run past on-instrument time and expiry.</li> <li>• Signal optimization in Spatial Calibration.</li> <li>• Size Standard Normalization Factor and Avg Normalization PH displayed in results.</li> <li>• Export Consumables log.</li> <li>• EPT plots available for terminated runs if plate is still linked. Flexible plate loading – pause a run, load a plate, then run new plate.</li> <li>• Export injection list</li> <li>• Connect cloud-based platform function.</li> <li>• Remove license manager.</li> </ul>

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# 1

## Instrument and software description

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### Instrument and software description

#### Overview

The Applied Biosystems™ 3500 Genetic Analyzer and 3500xL Genetic Analyzer are fluorescence-based DNA analysis instruments using capillary electrophoresis technology with 8 or 24 capillaries.

The 8-capillary model (Cat. No. 4405186 and Cat. No. 4405186R) and the 24-capillary model (Cat. No. 4405187 and Cat. No. 4405187R) include the following components:

- 8-capillary or 24-capillary array and POP™ polymer
- Reagents and consumables for your application and for system qualification
- Computer workstation and monitor
- Integrated software for instrument control, data collection, quality control, basecalling, and sizecalling of samples





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**IMPORTANT!** The protection provided by the equipment may be impaired if the instrument is operated outside the environment and use specifications, the user provides inadequate maintenance, or the equipment is used in a manner not specified by the manufacturer (Thermo Fisher Scientific).

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**IMPORTANT!** Observe current good laboratory practices when using this instrument.

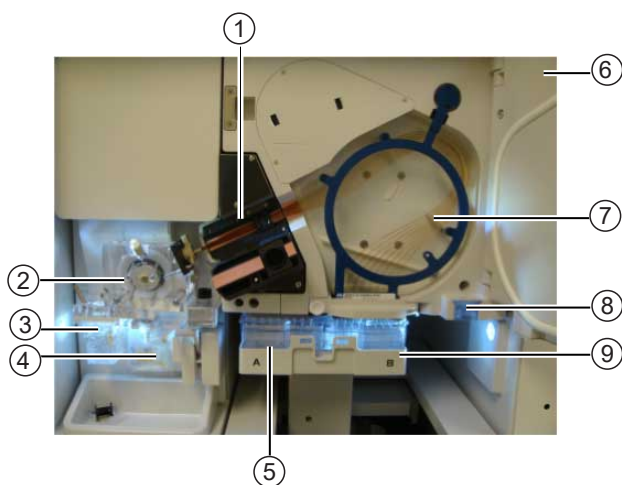
---

## Precautions for use



**WARNING!** Radio frequency identification (RFID) could possibly disrupt the operation of patient-worn and/or implanted active medical devices. To minimize such effects, do not come within 10 cm of this instrument if you have a patient-worn and/or implanted active medical device.

## Instrument interior components



**Figure 1** Instrument interior

- ① Detection cell heater block
- ② Polymer delivery pump (PDP)
- ③ Anode buffer container (ABC)
- ④ Polymer or conditioning pouch
- ⑤ Cathode buffer container (CBC)
- ⑥ Oven door
- ⑦ Capillary array
- ⑧ Oven condensation reservoir
- ⑨ Autosampler

## Instrument parts and functions

Part	Function
Anode buffer container (ABC)	Contains 1X running buffer to support all electrophoresis applications on the instrument. Has a built-in overflow chamber to maintain constant fluid height.
Autosampler	Holds the sample plates and cathode buffer container (CBC) and moves to align the plates and CBC with the capillaries.
Capillary array	Enables the separation of the fluorescent-labeled DNA fragments by electrophoresis. It is a replaceable unit composed of 8 or 24 capillaries.
Cathode buffer container (CBC)	Contains 1X running buffer to support all electrophoresis applications on the instrument.
Detection cell heater block	Holds the detection cell in place for laser detection and maintains the detection cell temperature of 50°C.
Oven/oven door	Maintains uniform capillary array temperature.
Oven condensation reservoir	Collects condensation from the oven.
Polymer delivery pump (PDP)	Pumps polymer into the array and allows for automated maintenance procedures. Includes the displacement pump chamber, polymer chambers, piston water seal, capillary array port, check valve fitting, water trap waste container, buffer valve, anode electrode, buffer gasket, and holds the anode buffer container.
Polymer pouch or conditioning reagent pouch	<ul style="list-style-type: none"> <li>• <b>Polymer pouch</b>—Supplies polymer to the polymer delivery pump.</li> <li>• <b>Conditioning reagent pouch</b>—Used for priming the polymer pump, washing the polymer pump between polymer type changes, and during instrument shut down. Has adequate volume for a one-time use.</li> </ul>
Radio frequency identification (RFID) (for more information, see Appendix F, “Radio Frequency Identification (RFID) technology”).	<p>RFID tags on the following primary instrument consumable labels are detected by read/write units in the instrument interior:</p> <ul style="list-style-type: none"> <li>• Capillary array</li> <li>• Cathode buffer container (CBC)</li> <li>• POP™ polymer</li> <li>• Anode buffer container (ABC)</li> </ul> <p>The instrument reads and tracks the following information:</p> <ul style="list-style-type: none"> <li>• Lot numbers</li> <li>• Serial numbers</li> <li>• Dates (expiration)</li> <li>• Capacity (usage)</li> </ul> <p>RFID tags are read and written in response to a user action (for example, running a wizard or starting a run). All dashboard values are updated when RFID tags are read and written. The days on Instrument is also updated automatically every 6 minutes.</p>

## Instrument front panel indicators

Indicator	Status
All lights off	Instrument off
Green light	Idle
Green light (blinking)	Run is in progress <b>Note:</b> You can only abort an injection when the green light is flashing, not when it is solid green.
Amber light (blinking)	Power-up self-test is in progress
	Instrument has paused. If the door is open, close it. If the amber light is still blinking, restart the instrument and computer (see “Restart the instrument and the computer” on page 279).
	Communication issue between instrument and software. Restart the instrument and computer (see “Restart the instrument and the computer” on page 279).
Amber light	Standby
Red light	Self-test failed or instrument failure. Restart the instrument and computer (see “Restart the instrument and the computer” on page 279).

## Instrument and computer requirements

---

**IMPORTANT!** Do not modify the instrument hardware or software without notifying Thermo Fisher Scientific. Any modifications must be made by Thermo Fisher Scientific under change control.

---

For minimum computer requirements, see “Instrument specifications” on page 315.

### Windows™ software requirements

3500 Series Data Collection Software v3.3 runs on the Windows™ 10, 64-bit operating system (IOT Enterprise).

The computer provided with the instrument contains validated software and settings.

Do not update the Windows™ operating system or firewall settings.

## Antivirus software requirements

The computer provided with the instrument does not include antivirus software because customer preferences and network requirements vary.

The 3500 Series Data Collection Software v3.3 has been tested with these antivirus software applications:

- Symantec Endpoint Protection 12
- McAfee Endpoint Security version 10.5

---

**IMPORTANT!** McAfee Endpoint Security can block services that are needed to start the Data Collection software. If you observe this issue, disable the firewall from McAfee Endpoint Security Settings or create a rule to allow traffic for the IP address 192.168.0.1 on the local network.

---

## Other software



**CAUTION!** Do not install additional software on the computer other than antivirus software. Changes to the configured software could void the instrument warranty and cause the instrument software to be non-operational.

---

**IMPORTANT!** Do not rename the computer after the software is installed. The instrument computer has been assigned a unique name. Changing the name may cause the software to malfunction.

---

## Instrument firmware

Instrument firmware is to be updated only by a Thermo Fisher Scientific representative.

# Theory of operation

## Preparing samples

When DNA samples are prepared for sequencing and fragment analysis on the instrument, fluorescent dyes are attached to the DNA.

## Preparing the instrument

Two calibrations are required to prepare the instrument for sample runs:

- **Spatial calibration**—Determines the position of the image from each capillary on the CCD array. For more information, refer to [page 125](#).
- **Spectral calibration**—Generates a matrix for each capillary that compensates for dye overlap and is used to convert the 20-bin data into 4-, 5-, or 6-dye data. For more information, refer to “Perform a spectral calibration” on [page 133](#).

## During a run

During a run, the instrument:

- Prepares the capillaries by pumping fresh polymer solution under high pressure from the polymer delivery pump to the waste position in the cathode buffer container (CBC).
- Electrokinetically injects the sample into the capillaries by briefly applying a low voltage.
- Washes the capillary tips in the rinse position of the CBC, then returns the capillary to the buffer position of the CBC.
- Ramps the voltage up to a constant level.

A high electric field is created between the ground end of the anode buffer container (ABC) and the negative voltage applied to the load header of the capillary array. This field pulls the negatively charged DNA through the separation polymer. The smaller fragments migrate faster than the larger fragments and reach the detector first.

To ensure optimal separation and maintain denaturation of the DNA, the capillaries are thermally controlled in the oven and in the detection cell. The oven has a Peltier heat unit and fan-circulated air.

In the detection cell, the dyes attached to DNA are excited by a narrow beam of laser light. The laser light is directed into the plane of the capillaries from both the bottom and top. A small amount of laser light is absorbed by the dyes and emitted as longer wavelength light in all directions.

- Captures the fluorescent light on the instrument optics while blocking the laser light. The light passes through a transmission grating, which spreads the light out. The light is imaged onto a cooled CCD array. For each capillary, 20 zones on the CCD are collected to provide 20-bin data for each capillary.
- Converts the 20-bin data into multi-dye data for the entire run. For sequencing applications, 4 different dyes are used to determine the 4 bases A, G, C and T. For fragment analysis applications, up to 6 dyes can be used in a single run for higher throughput.

## Results

The software generates an electropherogram (intensity plot) for each dye based on the migration of DNA fragments over the run and generates primary analysis results:

- For sequencing applications, the electropherogram is adjusted to compensate for slight mobility differences due to the dyes, then basecalling is performed and quality values are assigned.
- For fragment and Human Identification (HID) analysis, the software uses the internal size standard to assign a fragment size and a sizing quality value to each peak.

## Materials for routine operation

All materials for routine operation are provided when the instrument is installed. For more information:

- See Appendix D, “Catalog numbers”
- Contact your Thermo Fisher Scientific representative

## Instrument consumables handling, usage limits, and expiration

**IMPORTANT!** Before handling chemicals, read and understand all applicable Safety Data Sheets (SDSs) and use appropriate personal protective equipment (gloves, gowns, eye protection, etc). To obtain SDSs, see Appendix I, “Documentation and support”.

Containers and pouches are ready-to-use. Labels include a radio frequency identification (RFID) tag that the instrument uses to track usage and expiration date.

### Buffers

Cat. No.	Description	Storage
4393927	Anode Buffer Container (ABC) 1X running buffer, 4 containers	2–8°C  The 1X running buffer has been qualified to ship at ambient conditions.
4408256	Cathode Buffer Container (CBC) 1X running buffer, 4 containers	See the expiration date on the label. Do not use expired product.

Instrument	On-instrument supported limits  Lower of:	Guidelines
8-capillary	14 days, 240 injections, or expiry date	The buffer has been verified for use for up to 14 days on the instrument.  The software displays a warning message when a usage limit is met and allows you to continue running. Before doing so, see “Important notice regarding use of consumables that exceed supported limits” on page 25.
24-capillary	14 days, 100 injections, or expiry date	

### Polymer

Cat. No.	Description	Storage
A26070	POP-4™ Polymer (96-sample) <sup>[1]</sup>	2–8°C
4393715	POP-4™ Polymer (384-sample) <sup>[1]</sup>	
4393710	POP-4™ Polymer (960-sample) <sup>[1]</sup>	
A26071	POP-6™ Polymer (96-sample)	
4393717	POP-6™ Polymer (384-sample)	
4393712	POP-6™ Polymer (960-sample)	
A26073	POP-7™ Polymer (96-sample)	

(continued)

Cat. No.	Description	Storage
<a href="#">4393708</a>	POP-7™ (384) Performance Optimized Polymer	2–8°C
<a href="#">4393714</a>	POP-7™ (960) Performance Optimized Polymer	

<sup>[1]</sup> The polymer has been validated for HID applications.

**IMPORTANT!** For the POP-4™ Polymer and POP-7™ Polymer (Cat. Nos. [A26070](#), [4393715](#), [4393710](#), [A26073](#), [4393708](#), and [4393714](#)), the on-instrument supported limit is 14 days only when the instrument operating temperature is 15–25°C. When the instrument operating temperature is > 25°C, the supported limit is 7 days.

For the POP-6™ Polymer (Cat. Nos. [A26071](#), [4393717](#), and [4393712](#)), the on-instrument supported limit is 14 days when the instrument operating temperature is 15–30°C.

Pouch size	Instrument	On-instrument supported limits <sup>[1]</sup> Lower of:	Guidelines
96 samples	8-capillary	14 days, 96 samples, 12 injections, or expiry date	The polymer has been verified for use for up to 14 days on the instrument.  The software displays a warning message when a usage limit is met and allows you to continue running. Before doing so, see “Important notice regarding use of consumables that exceed supported limits” on page 25.
	24-capillary	14 days, 96 samples, 5 injections, or expiry date	
384 samples	8-capillary	14 days, 384 samples, 60 injections, or expiry date	
	24-capillary	14 days, 384 samples, 20 injections, or expiry date	
960 samples	8-capillary	14 days, 960 samples, 120 injections, or expiry date	
	24-capillary	14 days, 960 samples, 50 injections, or expiry date	

<sup>[1]</sup> The pouch has adequate polymer to support the stated number of samples or injections, plus additional volume to accommodate installation and wizard operations. Multiple pouch installations and/or excessive use of wizards reduce the number of remaining samples and injections. For example, if you run the total bubble remove option in the Remove Bubbles wizard more than four times, the number of remaining samples and injections is reduced.

## Conditioning reagent

Cat. No.	Description	Storage
4393718	Conditioning reagent , 1 pouch	2–8°C After removing from storage, use the pouch within 24 hours.

On-instrument supported limits	Guidelines
After it is installed on the instrument, the pouch is good for a one-time use.	See the expiration date on the label. See “Important notice regarding use of consumables that exceed supported limits” on page 25.

## Capillary arrays



**WARNING! SHARP.** The electrodes on the load-end of the capillary array have small, blunt ends that can lead to piercing injury.

Cat. No.	Description	Storage
4404685	8-Capillary, 50 cm	Room temperature
4404689	24-Capillary, 50 cm	
4404683	8-Capillary, 36 cm	
4404687	24-Capillary, 36 cm	

On-instrument limits	Guidelines
160 injections when used with Thermo Fisher Scientific reagents, or expiration date listed on packaging and RFID label	Capillary arrays have been verified for use for 160 injections when used with Thermo Fisher Scientific reagents. The software displays a warning message when a usage limit is met and allows you to continue running. Before doing so, see “Important notice regarding use of consumables that exceed supported limits” on page 25. Store capillary arrays with the loading-end of the capillary array in distilled water to prevent the polymer from drying in the capillaries.



## Hi-Di™ Formamide

Formamide is used to prepare samples, it is not installed on the instrument as are the other consumables listed in this section. It does not include an RFID tag on the label.

Material	Cat. No.	Storage
Hi-Di™ Formamide (4 × 5-mL bottles)	4440753	-25°C to -15°C  If frequent sampling is required, dispense and freeze small aliquots of Hi-Di™ Formamide into smaller tubes. Minimize freeze-thaw cycles and exposure to air and room temperature because the quality of the material may decrease when exposed to air.
Hi-Di™ Formamide (25-mL bottle)	4311320	air.

## Important notice regarding use of consumables that exceed supported limits

**BEFORE DISMISSING THE WARNING THAT THE CONSUMABLES HAVE REACHED SUPPORTED LIMITS AND CONTINUING WITH OPERATION OF THE INSTRUMENT, PLEASE READ AND UNDERSTAND THE FOLLOWING IMPORTANT NOTICE AND INFORMATION:**

Thermo Fisher Scientific does not recommend the use of consumables that exceed supported limits. The recommended limits are designed to promote the production of high-quality data and minimize instrument downtime. Reagent and consumable lifetime minimum performance are based on testing and studies that use reagents and consumables that have not exceeded supported limits.

The use of consumables beyond the supported limits may impact data quality or cause damage to the instrument or capillary array. The cost of repairing such damage is *NOT* covered by any Thermo Fisher Scientific product warranty or service plan. Customer use of expired consumables is at customer's own risk and without recourse to Thermo Fisher Scientific. For example, product warranties do not apply to defects resulting from or repairs required due to misuse, neglect, or accident including, without limitation, operation outside of the environmental or use specifications or not in conformance with Thermo Fisher Scientific instructions for the instrument system, software, or accessories.

Please see your specific service contract or limited product warranty for exact language regarding coverage and ask your Thermo Fisher Scientific representative if you have further questions.

# Overview of the software

## About the software

During a run, the software:

- Controls the instrument and generates sample data files:
  - Sequencing (AB1)
  - Fragment analysis (FSA)
  - HID analysis (HID)
- Performs primary analysis:
  - For sequencing applications: Basecalling
  - For fragment analysis and HID applications: Sizing

## Dashboard

You can access the **Dashboard** from any screen by clicking the **Dashboard** tab.

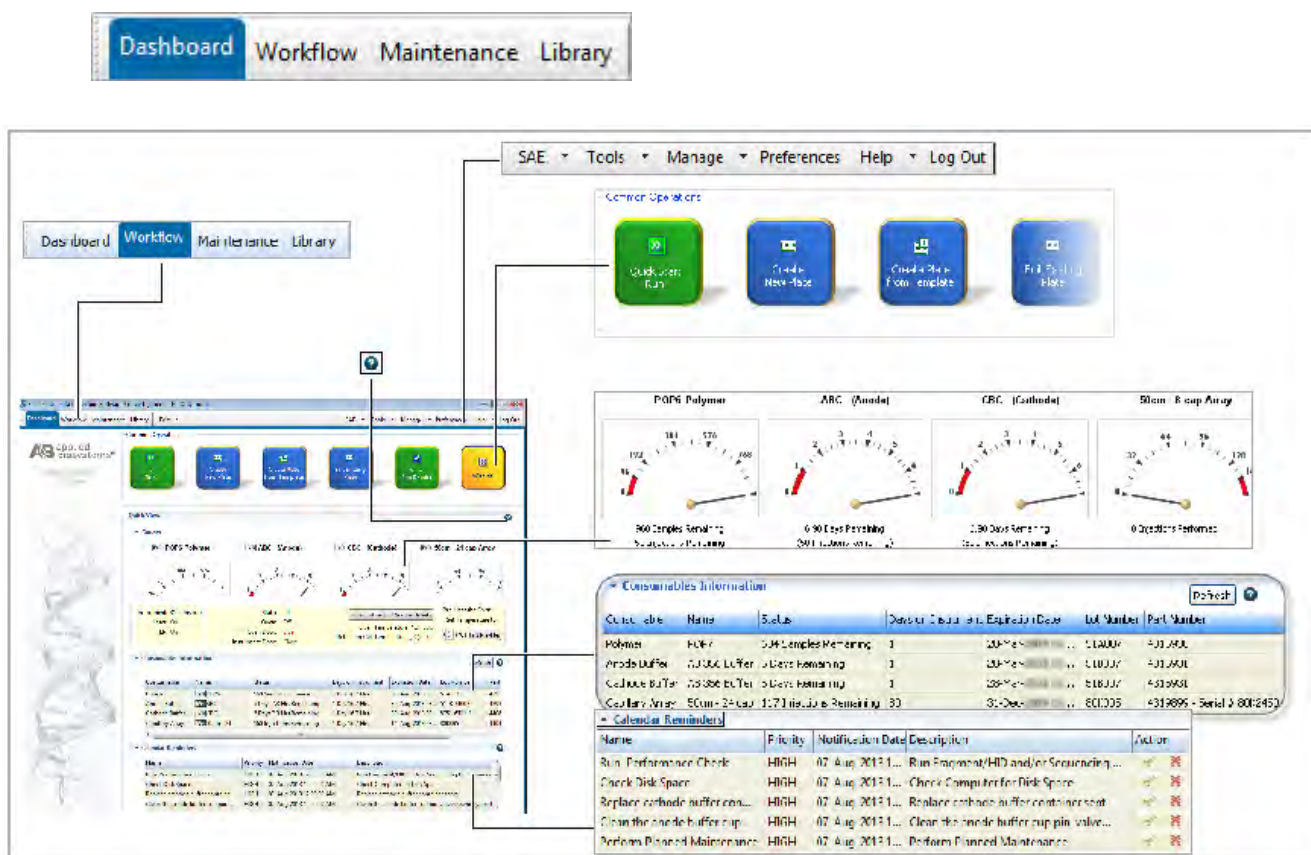




Figure 2 Dashboard overview

The Dashboard gives you quick access to the information and tasks you need to set up and run:

- **Workflow, Maintenance, and Library** tabs—Advances to the screens to set up, load, run, and review plates, maintenance wizards, and library items.
- Menu bar—Accesses administrative and tools functions.
- **Common operations**—Allows you to quick-start (load a plate that is set up), create or edit plates, view results, and access the Maintenance workflow.
- **Quick view**—Displays gauges that show the remaining usage of consumables and gives the status of instrument conditions. Consumable usage is automatically tracked by the instrument by RFID tags.
- **Consumables information**—Gives details for the installed consumables and indicates if any consumable is about to expire based on RFID tags.
- **Calendar reminders**—Displays the tasks listed in the schedule.
- Help icon —Displays a help topic specific to a screen or an area of the screen. All screens include  icons.

## Workflow

Click the **Workflow** tab at the top left of the screen to access the **Workflow** screen.



The **Workflow** tab contains the screens where you set up, load, and run plates, and view results.



Select a task in the navigation pane to access each screen.

The **Workflow** navigation pane is designed as a task workflow. Each screen contains a button that you can click to advance to the next screen in the workflow.

You can click **Dashboard** or any other tab item at any time to advance from the **Workflow**.

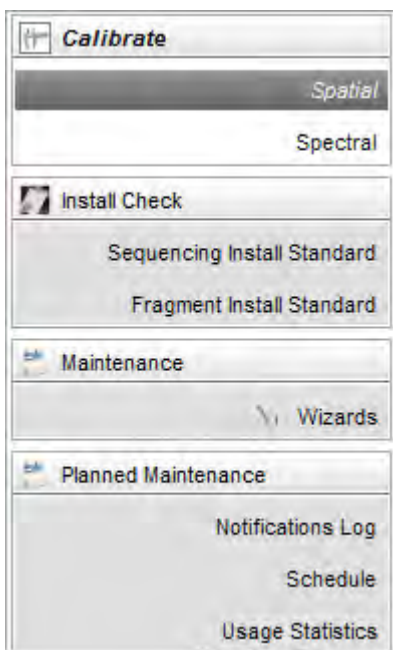
## Maintenance workflow

Select **Maintenance** in the menu bar to access the **Maintenance** workflow.



The **Maintenance** workflow contains the screens where you calibrate, run install checks, run maintenance procedures, and access records about instrument maintenance and service.

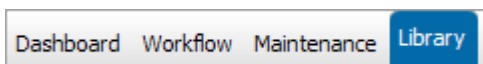
You can click **Main Workflow** or **Dashboard** or select any other menu item at any time to advance from the **Maintenance** workflow.



The **Maintenance** workflow is described in Chapter 10, “Maintain the instrument”.

## Library workflow

Click the **Library** tab at the top left of the screen to access the **Library**.



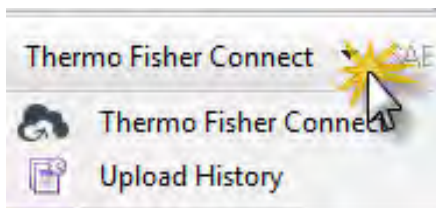
The Library contains items that you manage plates, assays, file name conventions, and results groups that you use to acquire and process data.

You can click **Workflow** or select **Dashboard** or any other menu item at any time to advance from the Library workflow.

## Thermo Fisher Connect menu

This option is *not* available if your system includes a license for the **Security, Audit, and E-signature** modules.

Select **Thermo Fisher Connect** in the menu bar to access:

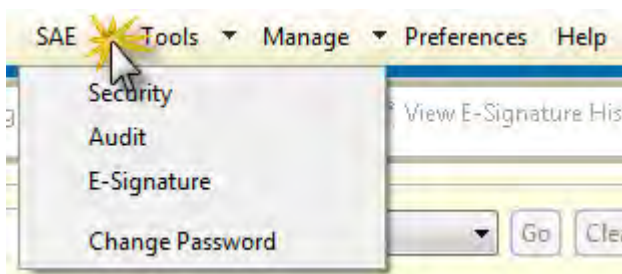


- The screen that allows you to link the instrument to your Thermo Fisher™ Connect Platform account
- An upload log for a list of all sample files uploaded to your Thermo Fisher™ Connect Platform account

## SAE menu

This option is available if your system includes a license for the **Security, Audit, and E-Signature** module.

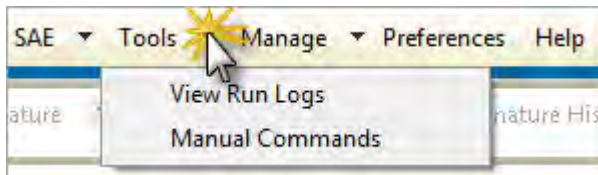
Select **SAE** in the menu bar to access:



- **Security, Audit, and E-signature** modules
- **Change Password** function

## Tools menu

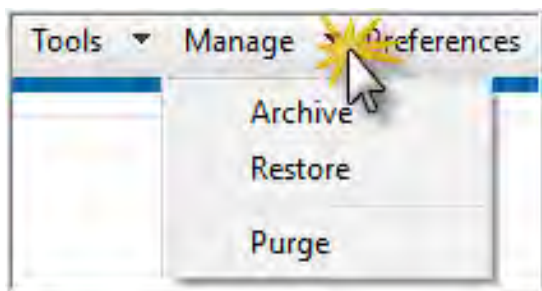
Select **Tools** in the menu bar to access:



- **View Run Logs** for reports of instrument runs
- **Manual Commands** to troubleshoot instrument performance

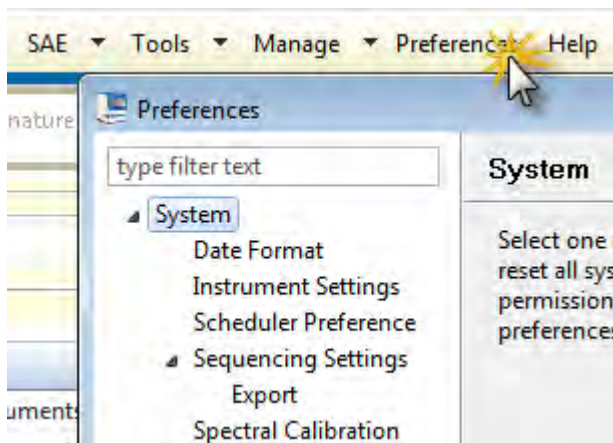
## Manage menu

Select **Manage** in the menu bar to access **Archive**, **Restore**, and **Purge** functions.



## Preferences menu

Select **Preferences** in the menu bar to set default parameters.



Preferences allow you to set system and user defaults for settings such as the date format, sample data file storage location, export file formats for sequencing data, and a variety of sequencing-specific settings.

## Help menu

Select **Help** in the menu bar to access software help.

The **Help** menu provides quick access to brief information about how to perform tasks on a screen. For details about tasks and other information, refer to the chapters in this user guide.

## Use the software without an instrument

You can install the software on a computer that is not connected to an instrument. You can use this stand-alone version of the software to:

- Create plates, protocols, and other library items, then import them into a version of the software that is installed on an instrument computer
- Review completed results

Do not select instrument-related functions in the stand-alone version of the software.

---

**IMPORTANT!** Do not rename the computer after the software is installed. The instrument computer has been assigned a unique name. Changing the name may cause the software to malfunction.

---

# 2

## Start the system

- Workflow ..... 32
- Start the computer and instrument ..... 33
- Start the software ..... 34
- Check system status in the Dashboard ..... 36
- Set preferences (optional) ..... 41

### Workflow

**Start the system**

---

**Power on the computer (do not log in), then power on the instrument (page 33)**

---

**When the green front panel indicator stops blinking, log in to Windows™ operating system, then start the software (page 34)**

---

**Check calendar reminders (page 36)**

---

**Check consumables status (page 37)**

---

**Replenish consumables (page 39)**

---



## Start the computer and instrument

---

**IMPORTANT!** The order in which you turn on the computer and instrument is critical for proper communication between the instrument and the computer. Follow the sequence of steps given in this section (power on computer but do not log in, power on instrument, log in to Windows™ operating system).

---

1. Power on the computer and monitor, but do not log in to the Windows™ operating system.
2. Verify that the instrument is connected to the appropriate power supply.



**CAUTION!** Do not unpack or plug in any components until a service representative has configured the system for the proper operating voltage.

---

**IMPORTANT!** Do not rename the computer after the software is installed. The instrument computer has been assigned a unique name. Changing the name may cause the software to malfunction.

---

3. Inspect the instrument interior. Ensure that:
  - a. The oven door is closed.
  - b. No objects are left inside the instrument.

---

**IMPORTANT!** Misplaced objects left inside the instrument can cause damage.

---

4. Close the instrument door.
5. Power on the instrument:



Power button

Tray button

Light button

- a. Press the power on/off button on the front of the instrument and wait for the green status light to turn on.

---

**Note:** If the door is open during power on, the yellow light will continue to flash until you close the door. See indicator descriptions in “Instrument front panel indicators” on page 19.

---

- b. If desired, press the Light button to turn on the interior light.
- c. Check the instrument status. Ensure the green status light is on and not flashing before proceeding. See indicator descriptions in “Instrument front panel indicators” on page 19.

6. Log on to the Windows™ operating system.

---

**IMPORTANT!** Use the same administrator Windows™ user account to log in to the instrument computer. Use of a non-administrator Windows™ user account, or use of different administrator Windows™ user accounts can interfere with software operation.

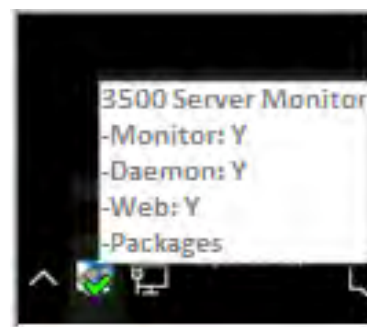
---

## Start the software


### Step one: Start the Server Monitor




1. After you log on to the Windows™ operating system, wait ~1 to 2 minutes.

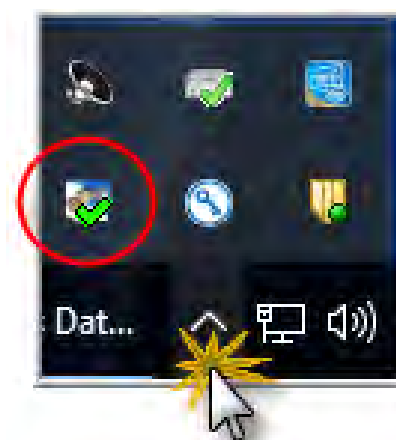
As the server monitor starts, the list of services is displayed at the bottom of the desktop.




2. Check the status of the server monitor (a background application that the software requires). In the Windows™ taskbar at the bottom right of the desktop, click the arrow to display the running tasks.

If the  Server Monitor icon is displayed, go to “Step two: Start the 3500 Series Data Collection Software v3.3” on page 34.

3. Select  **Applied Biosystems** **Server Monitor**. The  Server Monitor icon is displayed in the taskbar, then a status bubble is displayed. It takes ~1 minute for the Server Monitor to start up. When the  Server Monitor icon is displayed, go to “Step two: Start the 3500 Series Data Collection Software v3.3” on page 34 below.




---

**IMPORTANT!** If the Server Monitor icon does not change to , you cannot start the software. See “Step one: Start the Server Monitor” on page 34 for more information.

---

### Step two: Start the 3500 Series Data Collection Software v3.3

Select **Start** **Applied Biosystems** **3500**.

The 3500 Series Data Collection Software v3.3 splash screen is displayed for a few seconds, then the 3500 Series Data Collection Software v3.3 **Login** dialog box opens.



### Step three: Log in

The Login dialog box is displayed if your system includes a license for the Security, Audit, and E-signature module.

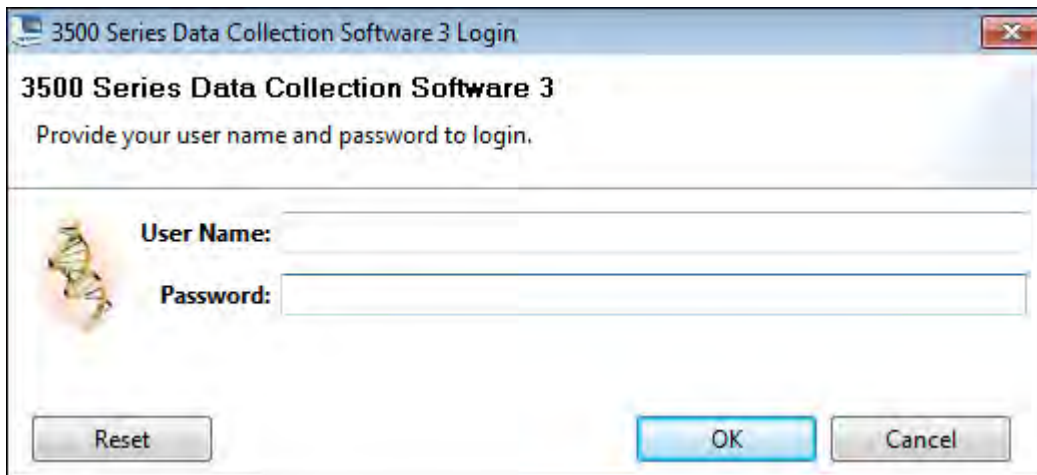
In the **Login** dialog box:

Enter your **User Name** and **Password**, then click **OK**. See your 3500 system administrator for login information.

---

**Note:** For information on creating user accounts, see Chapter 9, “Use Security, Audit, and E-Sig functions (SAE Module)”.

---



## Check system status in the Dashboard

Check calendar reminders and consumables status in the **Dashboard**.

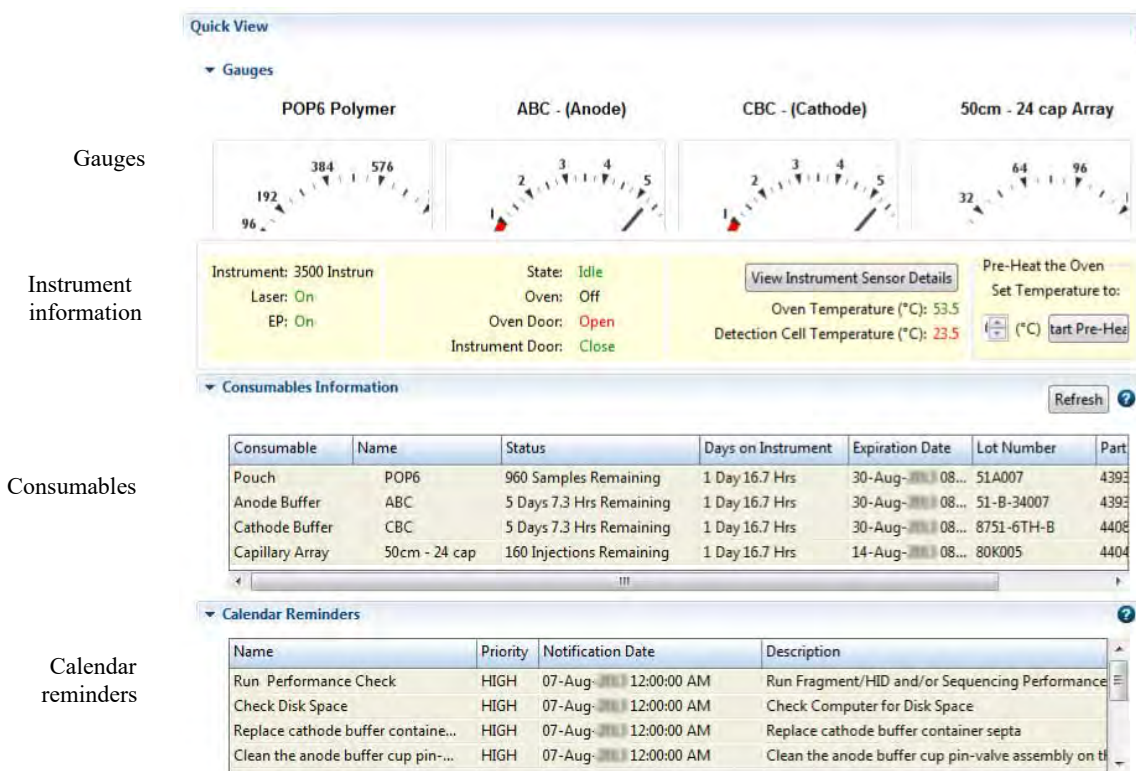


Figure 3 Dashboard

## Check calendar reminders

The **Calendar Reminders** section displays reminders for the tasks listed in the schedule (see “As-Needed instrument maintenance tasks” on page 254). You can set the time to trigger calendar reminders in **Preferences**.

1. Review the **Calendar Reminders** pane.

Name	Priority	Notification Date	Description	Action
Run Install Check	HIGH	13-Sep-2013 12:00:00 AM	Run Install Check	✓ ✗
Perform Planned Maintenance	HIGH	13-Sep-2013 12:00:00 AM	Perform Planned Maintenance	✓ ✗
Clean the anode buffer cup pin-...	HIGH	03-Oct-2013 12:00:00 AM	Clean the anode buffer cup pin-valve assembly on the polymer del...	✓ ✗
Replace cathode buffer containe...	HIGH	13-Sep-2013 12:00:00 AM	Replace cathode buffer container septa	✓ ✗
Restart computer, Instrument	MEDI...	03-Oct-2013 12:00:00 AM	Restart computer, Instrument	✓ ✗

2. Perform any scheduled tasks, then click to mark it as complete, (or click to mark it as dismissed if you do not perform the task). Actions are recorded in the **Notifications Log** (for more information, see “Review the Notifications Log” on page 256).
3. Perform any daily, monthly, or quarterly tasks that are not listed in the Calendar Reminders pane (see “Maintenance schedule” on page 251).

## Check consumables status

1. Click **Refresh** to update consumable status.

The **Consumables** pane displays expiration dates and lot numbers (determined from the RFID tags on the consumable containers).

Consumables Information <span style="float: right;">Refresh ?</span>						
Consumable	Name	Status	Days on Instrument	Expiration Date	Lot Number	Part Number
Pouch	POP6	960 Samples Remaining	1 Day 19.6 Hrs	23-Aug-2013 08...	51A007	4393716
Anode Buffer	ABC	5 Days 4.4 Hrs Remai...	1 Day 19.6 Hrs	30-Aug-2013 08...	51-B-34007	4393925
Cathode Buffer	CBC	5 Days 4.4 Hrs Remai...	1 Day 19.6 Hrs	30-Aug-2013 08...	8751-6TH-B	4408258
Capillary Array	50cm - 24...	160 Injections Remai...	2 Days 14.6 Hrs	15-Aug-2013 08...	80K005	4404688 - Serial # 8902020

**Note:** The **Expiration Date** for consumables is displayed in red if the consumable is within the following days of expiration: Pouch 7 days, Buffers 7 days, Capillary array 1 day.

Consumables Information						
Consumable	Name	Status	Days on Instrument	Expiration Date	Lot Number	Part Number
Pouch	POP6	960 Samples Remaining	1 Day 19.1 Hrs	12-Aug-2013 08...	51A007	4393716
Anode Buffer	ABC	5 Days 4.9 Hrs Remai...	1 Day 19.1 Hrs	14-Aug-2013 08...	51-B-34007	4393925
Cathode Buffer	CBC	5 Days 4.9 Hrs Remai...	1 Day 19.1 Hrs	14-Aug-2013 08...	8751-6TH-B	4408258
Capillary Array	50cm - 24...	160 Injections Remai...	2 Days 0.0 Hrs	07-Aug-2013 08...	80K005	4404688 - Serial

2. Check the consumables gauges for the number of injections, samples, or days remaining for a consumable. See “Instrument consumables handling, usage limits, and expiration” on page 22 for information.

When <10% of the allowed use of the consumable remains, the gauge moves into the red warning range. The consumable also displays in red in the Consumables pane.



**IMPORTANT!** We recommend that you add a calendar reminder to the schedule for polymer and buffer replacement. Set the notification to display 2 days before the polymer should be replaced.

## How the polymer sample and injection counters calculate usage

The polymer sample counter decrements only for wells that contain sample, but the polymer injection counter decrements for each injection, regardless of whether all wells contain sample. The sample limit and the corresponding injection limit may not coincide. The first limit that is reached depends on whether you perform partial or full injections.

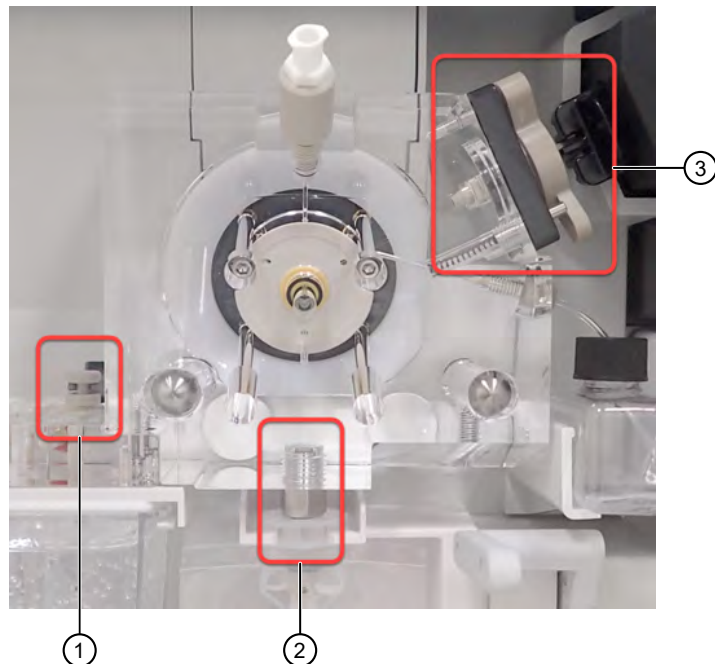
Example: Instrument configuration: 24-capillary, 960 sample polymer pouch		
Partial injection example (not all wells contain sample)	1 injection with 24 samples + 49 injections with 1 sample = 73 samples, 50 injections	The 50 injection count limit is reached before the 960 sample count limit.
Full injection example (all wells contain sample)	40 injections with 24 samples = 960 samples, 40 injections	The 960 sample count limit is reached before the 50 injection count limit.

## Check for leaks and spills

1. Open the front doors.
2. Inspect the instrument interior.
3. Wipe any spills.



4. Check for leaks around the buffer-pin valve, check valve, and array port lock.



- ① Buffer-pin valve
- ② CV (check valve) fitting
- ③ Array port lock

5. Remove dried residue and ensure that the array port lock is securely tightened.

## Check buffer fill levels

Check the fill levels on buffers. Verify that the buffer level is at the top of the fill line and check that the seal is intact. The meniscus must line up at or above the fill line. Ensure that the septa on the CBC are properly seated.

---

**IMPORTANT!** Replace the buffer if the buffer level is too low.

---

## Replenish consumables

If any consumables are expired or if buffer fill level is too low, replenish the consumables as described in:

- “Replenish polymer or change polymer type” on page 263

---

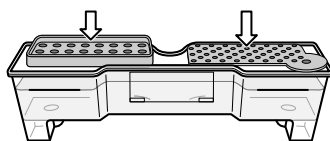
**IMPORTANT!** Wear gloves while handling polymer, the capillary array, septa, ABC, or CBC.

---

- “Prepare the Anode Buffer Container (ABC)” on page 258
- “Prepare the Cathode Buffer Container (CBC)” on page 259
- “Fill capillary array with fresh polymer” on page 265
- “Install or change the capillary array” on page 266

## Ensure proper installation of CBC septa

When you install the CBC buffer septa, press firmly to seat the septa.



---

**IMPORTANT!** Look at the CBC from the side and ensure that there is no gap between the container and the lip of the septum.

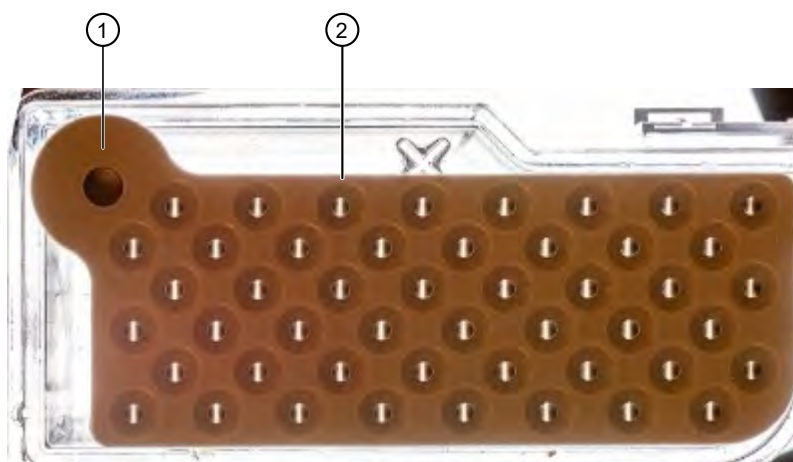
---

**IMPORTANT!** Ensure the septa are securely seated to prevent displacement of the septa during operation. Inspect the underside of the CBC lid to ensure that all capillary washing septum blades are fully engaged and unobstructed.

---

**IMPORTANT!** A correctly inserted capillary washing septum shows a clear, linear slit in all wells. To easily view the slits, illuminate the CBC from the bottom, such as with an LED screen, and observe the CBC from above. If any holes do not show a clear, linear slit, firmly press down on those specific holes to ensure that the septum blades are visually engaged and the slit of light is unobstructed.

---



**Figure 4** Illuminated CBC with the capillary washing septum correctly in place

- ① Starter tab positioned in alignment hole
- ② Linear slit visible

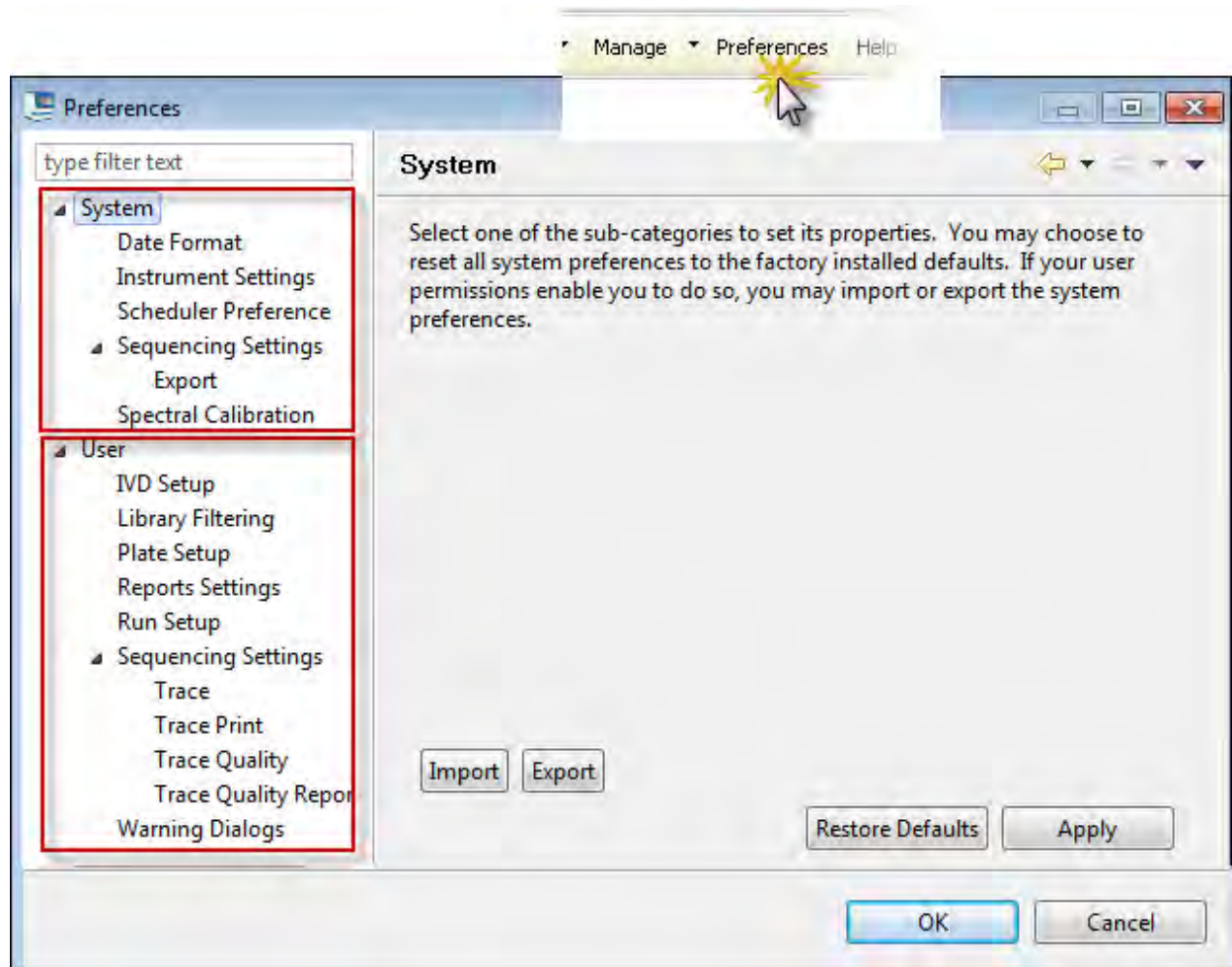
For more information about installing the septa, see “Prepare the Cathode Buffer Container (CBC)” on page 259.



## Set preferences (optional)

### Overview

To access the **Preferences** dialog box, select **Preferences** in the toolbar. You have the option to set any or all preferences.



**Note:** The **type filter text** field at the top of the dialog box is not used.

These system settings apply to all users:

- Date Format
- Instrument Settings (instrument name, reagent use, message boxes, and run logs)
- Scheduler Preference (trigger time for calendar reminders)
- Sequencing Export Settings
- Spectral Calibration (number of allowed borrowing events)

These user preferences are saved individually for each user.

- Library filtering
- Plate Setup
- Reports Settings
- Run Setup
- Sequencing Settings (review and report settings)
- Warning dialogs

---

**Note:** Users can also save user preferences while viewing tables. See “Customize a table” on page 94.

---

## System preferences

In the **Preferences** dialog box, click a system preference, select a setting, then click **Apply** to save the preference.

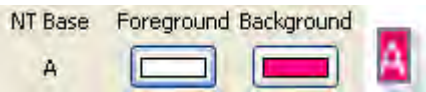

System preference	Sets
Date Format	Date and time format for the software.
Instrument Settings	<ul style="list-style-type: none"> <li>• Instrument name (appears in the <b>Dashboard</b>, reports, file name conventions, instrument sensor details, view sequencing results.)</li> </ul> <p><b>Note:</b> If you have multiple instruments, you can assign each instrument a unique instrument name.</p> <ul style="list-style-type: none"> <li>• Suppress the messages that are displayed when at the start of a run that indicate the number of days left before a consumable expires or should be replaced.</li> <li>• Number of runs to preserve in the <b>Run Log</b> (accessed by selecting <b>Tools ▶ View Run Logs</b>).</li> </ul>

(continued)

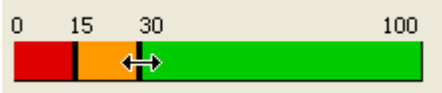
System preference	Sets
<b>Instrument Settings for reagent use</b>	<ul style="list-style-type: none"> <li>• Allow runs with reagents that exceed limits.               <ul style="list-style-type: none"> <li>– By default, the software allows use of reagents that are expired or exceed on-instrument limits. This setting allows a user to dismiss expiration or limit warnings, then continue the run.</li> </ul> <p>An Administrator can prevent the use of reagents that are expired or exceed on-instrument limits by deselecting reagents in the <b>Instrument Settings</b> screen.</p> <p>By default, all reagents are selected, which means that a user can dismiss a reagent usage limits and/or expiration warning and continue to run.</p> <p>Deselect the reagents that will not allow runs unless they are within on-instrument limits (to set a "hard stop").</p> <p>If you do not have Administrator role, these options are not active.</p> </li> <li>• Enable warning messages.               <ul style="list-style-type: none"> <li>– You can control the display and timing of warnings that are related to reagent usage limits and expiration.</li> <li>– Expiration warnings are displayed when a reagent is expired or exceeds on-instrument limits.</li> <li>– Pre-expiration warnings are displayed the following number of days before a reagent is expired:                   <ul style="list-style-type: none"> <li>– ABC and CBC: 7 days</li> <li>– Array and polymer: 14 days</li> </ul> </li> </ul> </li> </ul>
<b>Scheduler Preference</b>	Time for calendar reminders to be displayed in the <b>Dashboard</b> (see “Check calendar reminders” on page 36).
<b>Spectral Calibration</b>	Number of allowed borrowing events for spectral calibration (see “What you see during a spectral calibration” on page 138).
<b>Sequencing Settings Export</b>	<p>Default file types for files exported during a sequencing run. Exported files are stored in the same directory as the .ab1 files:</p> <ul style="list-style-type: none"> <li>• *.annotation.txt — Information from the <b>Annotation</b> tab in the sequencing trace view such as data collection time, run time start finish</li> <li>• *.phd.1, *.scf — Sequencing files</li> <li>• *.fsta, *.qual, *.seq — Reference files - specify Entire Sequence or Post-trim Sequence Only</li> </ul>

## User preferences

In the **Preferences** dialog box, click a user preference, select a setting, then click **Apply** to save the preference.

User preference	Sets
IVD Setup Workflow	Not supported.
Library Filtering	<p>Default filter for items displayed in the <b>Open Plate from Library</b> dialog box, the <b>Plates</b> library, and the <b>Assays</b> library. You can set the filter to include only one application type, 8- and/or 24-capillary-specific items, or items that contain in their names the text you specify. Use an asterisk (*) wildcard character to indicate that text may precede or follow the text you specify. Excluded text is not case-sensitive.</p> <p>Example: To exclude only items named "ABC", enter ABC . To exclude items named "ABCDE", enter ABC* . To exclude items named "123ABC", enter *ABC .</p> <p>You can disable filters in each location to display all items.</p>
Plate setup	Default settings for plate name.
Reports Settings	<p>Default font and text size and custom logo in reports.</p> <p><b>Note:</b> You can override this setting in each report view.</p>
Run Setup	<ul style="list-style-type: none"> <li>Default storage location for data files in file name conventions and results groups.</li> </ul> <p><b>Note:</b> You can override this setting in file name conventions and results groups.</p> <ul style="list-style-type: none"> <li><b>Pause After Last Injection</b>—When enabled, allows reinjection of the last injection by pausing after the last injection is complete (before completing the run).</li> </ul>
Sequencing Settings Trace	<p>Default settings for color representation of nucleotide and quality value bars in the <b>Trace View</b> in <b>View Sequencing Results</b>:</p> <ul style="list-style-type: none"> <li><b>NT (nucleotide) Base Color</b>—Click an NT or mixed base Foreground or Background color block, then select a color for the letter annotation or the highlight color for the letter annotation.</li> </ul>  <ul style="list-style-type: none"> <li><b>Pure Base and Mixed Base QV Colors</b>—Sets the colors and ranges for pure and mixed base QVs (quality values) displayed in the <b>Trace View</b>:</li> </ul>  <ol style="list-style-type: none"> <li>Click a pure base or mixed base color bar to select a new color.</li> <li>Place the mouse pointer over a slider, then drag to set a new range.</li> </ol> <p>We recommend that you set the following ranges for QVs:</p> <ul style="list-style-type: none"> <li>Pure bases: Low QV &lt; 15, Medium QV = 15 to 19, High QV = 20+ (default).</li> <li>Mixed bases: Low QV &lt; 5, Medium QV = 5 to 10, High QV &gt; 10 (investigate to determine the best range for your application).</li> </ul>

(continued)

User preference	Sets
<b>Sequencing Settings Trace Print</b>	Settings for sequencing trace reports: Type of trace data, specific print settings, and Y-Scale.
<b>Sequencing Settings Trace Quality</b>	<p>Quality ranges for:</p> <ul style="list-style-type: none"> <li>• <b>QC report</b>—Trace Score and CRL</li> <li>• <b>Plate report</b>—Trace Score</li> </ul> <p>Set colors and ranges:</p> <ol style="list-style-type: none"> <li>a. Click a color bar to select a new color.</li> <li>b. Place the mouse pointer over a slider, then drag to set a new range.</li> </ol> 
<b>Sequencing Settings Trace Quality Report</b>	<p>Content and formatting used in QC, Plate, Trace Score, CRL, QV20+, and Signal Strength reports:</p> <ul style="list-style-type: none"> <li>• <b>Sort data</b>—Sort data in <b>Trace Score</b>, <b>CRL</b>, <b>QV20+</b>, and <b>Signal Strength Reports</b> based on Run Name or Capillary Number.</li> <li>• <b>Signal based on</b>—Base signal in QC and <b>Signal Strength Reports</b> based on Average Raw Signal Intensity or Average Raw Signal to Noise Ratio.</li> <li>• <b>Display well image by</b>—Specify the thumbnail option for Plate Reports: Wider thumbnail without file name or Smaller thumbnail without file name.</li> </ul>
<b>Warning Dialogs</b>	Suppress warning messages for deleting an injection or exporting a library item.

# 3




## Use the instrument with the Thermo Fisher™ Connect Platform

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■ Register and obtain a Thermo Fisher™ Connect Platform account .....	47
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■ Set up the data storage location and email notifications .....	48
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### Thermo Fisher™ Connect Platform features

This option is *not* available if your system includes a license for the **Security, Audit, and E-signature** module.

If the instrument is connected to a network, you can use the Thermo Fisher™ Connect Platform feature. The Thermo Fisher™ Connect Platform provides the following functions:

-  Automatically transfer data files from the instrument to your Thermo Fisher™ Connect Platform account.
-  Receive instrument status email notifications.
-  View instrument status on InstrumentConnect or a mobile device.

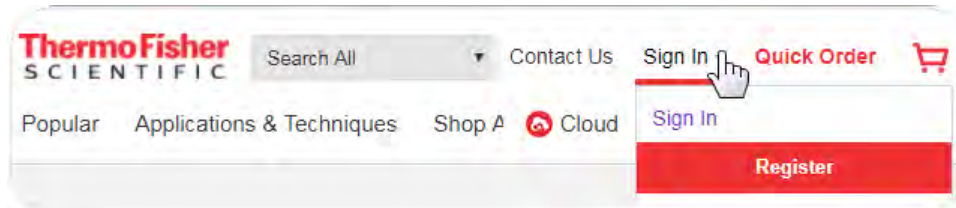
---

**IMPORTANT!** The instrument communicates with the computer by Ethernet connection. Do not make any changes to the computer ethernet/internet connections during a run or during calibration.

---

## Register and obtain a Thermo Fisher™ Connect Platform account

1. Go to [www.thermofisher.com](http://www.thermofisher.com).
2. On the home page, select **Sign In** ▶ **Register**.

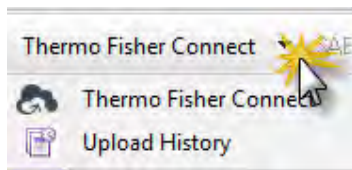


3. Fill in all information, then click **Create account**.

## Connect the instrument to your Thermo Fisher™ Connect Platform account

This option is not available if your system includes a license for the Security, Audit, and E-Signature module. The **Thermo Fisher Connect** menu is not active.

1. In any screen, select **Thermo Fisher Connect** ▶ **Thermo Fisher Connect**.



**Manage Thermo Fisher Connect Profile**

Link to Thermo Fisher Connect by entering your username and password. Using cloud profile allows for run files, instrument status, error conditions and notification to become available via Thermo Fisher web and mobile applications.

User ID:

Password:

User ID	Last Used	Active Profile	Unlink Account
yoke.lim@lifetech.com	2018-09-20 01:18:41	<input checked="" type="radio"/>	<input type="button" value="Unlink Account"/>

**Manage Thermo Fisher Connect Storage Location**

Select a folder to export your run files in Thermo Fisher Connect

Enable Destination

Status: **Not Connected**

**Manage Thermo Fisher Connect Notification**

**Receive Notifications**

Notifications related to run instrument, run status and error conditions will be sent to Thermo Fisher web and mobile applications.

2. Enter the **User ID** and **Password** for your Thermo Fisher™ Connect Platform account, then click **Link Account**.

**Manage Thermo Fisher Connect Profile**

Link to Thermo Fisher Connect by entering your username and password. Using cloud profile allows for run files, instrument status, error conditions and notification to become available via Thermo Fisher web and mobile applications.

User ID:

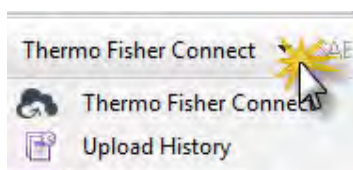
Password:

An email is sent to the email address associated with your account, and the instrument is listed in the screen on the Thermo Fisher™ Connect Platform (see “Monitor a run from InstrumentConnect” on page 51).

## Set up the data storage location and email notifications

When an instrument is linked to your Thermo Fisher™ Connect Platform account, you can store run data in your Thermo Fisher™ Connect Platform account. You can also have email notifications sent to your Thermo Fisher™ Connect Platform account email address.

1. In any screen, select **Thermo Fisher Connect** ▶ **Thermo Fisher Connect**.





2. In the middle of the screen, click your **User ID** to connect the instrument to your Thermo Fisher™ Connect Platform account.

The screenshot shows two main sections of the software interface. The top section, titled "Manage Thermo Fisher Connect Profile", includes a text box for "User ID" and a "Password" field, with "Cancel" and "Link Account" buttons. Below this is a table with the following data:

User ID	Last Used	Active Profile	Unlink Account
yoka.lm@fietech.com	2018-09-20 01:18:41	<input checked="" type="radio"/>	Unlink Account

The bottom section, titled "Manage Thermo Fisher Connect Storage Location", features a red circular icon with a white cloud, a text box for "Select a folder to export your run files in Thermo Fisher Connect", and an "Enable Destination" checkbox. The status is "Not Connected" and the current path is "/ROOT/Personal Files/3500/hid". A "Browse Cloud Destination" button is also present.

3. Select the **Enable Destination** checkbox, then select the storage location in your Thermo Fisher™ Connect Platform account.

When a run is complete, the data is stored in the results group folder that is specified in the plate record.

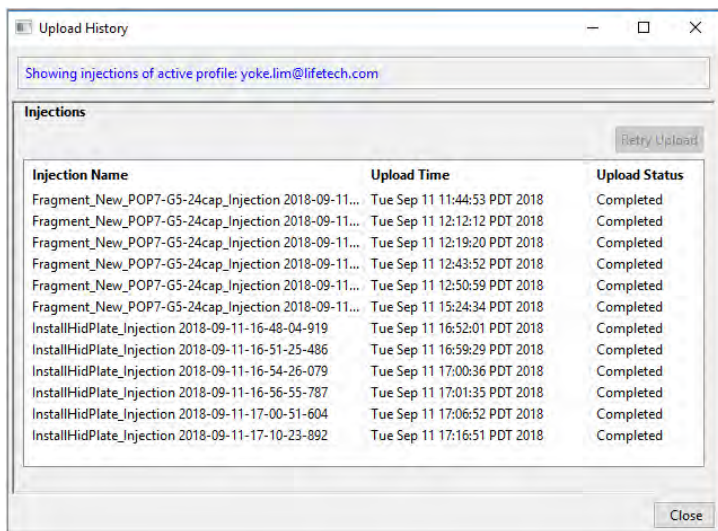
The data will be automatically uploaded to your account whenever your **User ID** is the active ID. Results are saved in your account folders named by plate and injection, not in results group folders.

4. Select the **Receive Notifications** checkbox.

Run status emails will be sent to the email address associated with your Thermo Fisher™ Connect Platform account.

## View your upload history

To view a list of injections (which includes a set of sample files) that have been uploaded to your Thermo Fisher™ Connect Platform account, select **Thermo Fisher Connect** ▶ **Upload History**.



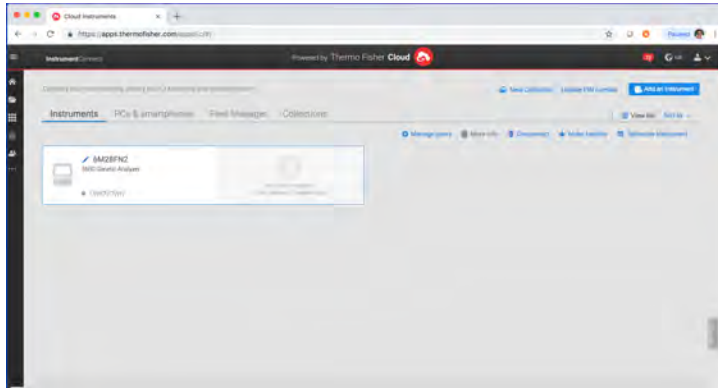
Sample file names are retained in the list for 30 days.

Possible upload status conditions are listed below.

Upload Status	Description
Pending	Files are waiting to be uploaded.
Processing	Upload is in process.
Completed	Upload is complete.
Failed	Files were not uploaded. Click <b>Retry Upload</b> .

## Monitor a run from InstrumentConnect

1. Sign in to [thermofisher.com/connect](https://app.thermofisher.com/connect).
2. In the left panel, then click  to access InstrumentConnect.



---


**Note:** The **Add an Instrument** function is not supported for the instrument. See “Connect the instrument to your Thermo Fisher™ Connect Platform account” on page 47.

---

3. Click the instrument to display instrument status.

## Monitor a run from a mobile device

The instrument must be connected to your Thermo Fisher™ Connect Platform account before you can monitor it. See the “Connect the instrument to your Thermo Fisher™ Connect Platform account” on page 47.

1. On your mobile device, download the InstrumentConnect app from the Apple Store or from Google™ Play.
2. On your mobile device, launch  InstrumentConnect.
3. Touch the instrument to monitor.



## View notifications from the instrument on your Thermo Fisher™ Connect Platform account

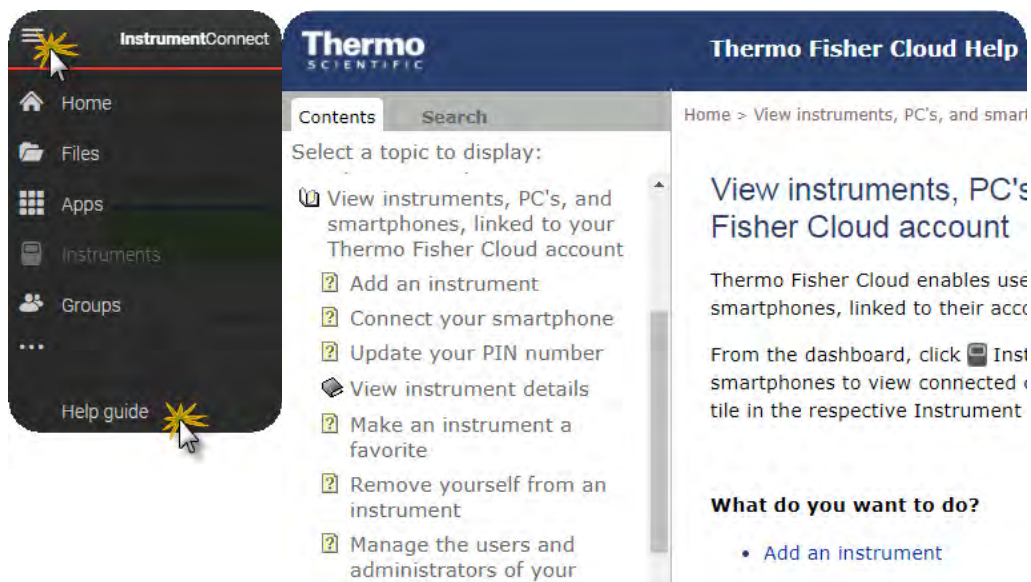
1. In any screen in the Thermo Fisher™ Connect Platform, click .



2. Click a notification, then click **Dismiss** or **Dismiss all** to dismiss the notification.

## For more information on using InstrumentConnect

In the top left of any screen in InstrumentConnect, click ☰, then select **Help guide**.



## Thermo Fisher™ Connect Platform administrators for an instrument

### First user who links is assigned administrator role

The first user who links the instrument to their Thermo Fisher™ Connect Platform account is assigned administrator role for the instrument.

Additional instrument administrators can be assigned, and user roles can be changed after linking.

### Instrument administrator functions


An administrator can perform the following tasks from InstrumentConnect.

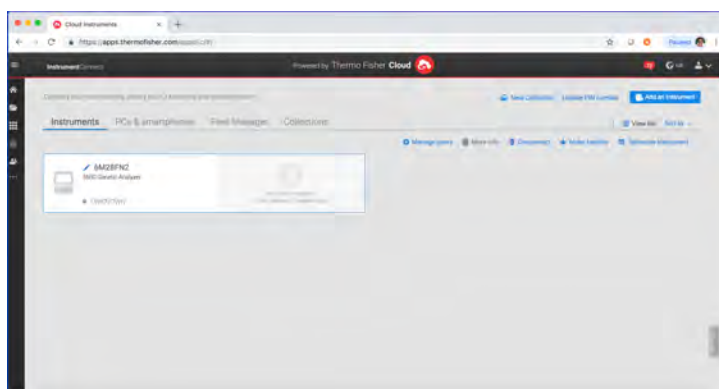
- Access the **Manage users** function to see a list of all accounts that are linked to the instrument.
- Assign administrator role to one or more users.
- Remove an account from an instrument.
- Disconnect the instrument from InstrumentConnect.
- Change the instrument name.

## Manage the users and administrators of your instrument


Any user with administrator role can manage users for an instrument or disconnect an instrument from InstrumentConnect.


If an administrator...	The software...
Assigns Administrator role to a user	Allows the user to perform all administrator functions (see “Instrument administrator functions” on page 53).
Removes a user	Unlinks the instrument from their Thermo Fisher™ Connect Platform account.
Disconnects the instrument	<ul style="list-style-type: none"> <li>• Unlinks the instrument from all Thermo Fisher™ Connect Platform accounts.</li> <li>• Removes the instrument from InstrumentConnect.</li> </ul>

1. Sign in to [thermofisher.com/connect](https://thermofisher.com/connect).
2. In the left panel, click  to access InstrumentConnect.
3. Select the instrument.



**Note:** The **Manage users** and other administrator functions are not enabled until you select an instrument.

4. To assign the Administrator role to a user or to remove a user, click  **Manage users**, then perform the following tasks as needed.

To...	Do this...
Assign the Administrator role to an additional user	Select the <b>Admin</b> checkbox, then click <b>Close</b> .
Remove a user	Click  , then click <b>Confirm</b> .

## Unlink individual users from an instrument

You cannot unlink individual users from an instrument in InstrumentConnect. To unlink a user in the data collection software, select **Thermo Fisher Connect** ▶ **Thermo Fisher Connect**, select the **User ID**, then click **Unlink Account**.

You can disconnect the instrument from InstrumentConnect. However, doing so unlinks *all* accounts and removes the instrument, and all user data for that instrument, from InstrumentConnect.

You can *remove* a user from the instrument. However, doing so deletes the user data from the instrument.

For more information, see “Manage the users and administrators of your instrument” on page 54.

# 4

## Set up and run

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## Setup workflow

### Workflow

#### Prepare and check the instrument, sample plates, and dashboard system

1. “Prepare the instrument” on page 57
2. “Prepare sample plates” on page 69 and “Load the plate in the instrument” on page 72
3. “Check system status in the Dashboard” on page 36

#### Plate Settings

Select a workflow for plate settings:

- **Create and assign new plate settings.**
  - a. “Create or import a plate” on page 58
  - b. “Assign plate contents” on page 61
  - c. “Print the plate layout” on page 66
  - d. “Link the plate” on page 72
- **Start a run with preprepared plate settings.**

“Quick Start a run” on page 73

#### Set up and run

1. “Load plates for run and create the injection list” on page 74
2. “Review, modify, or export the injection list in Preview Run” on page 78
3. “Start the run from Preview Run” on page 79
4. “Check sequence or sample quality and re-inject samples” on page 83

## Prepare the instrument

1. In the **Dashboard**, check consumables status (see “Check consumables status” on page 37).  
Ensure that:
  - Consumables are not expired
  - Adequate injections remain for consumables
2. Ensure that buffer levels are at the fill lines (see “Check buffer fill levels” on page 39).

3. Set the oven temperature, then click **Start Pre-heat**.

Pre-heat the oven and detection cell while you prepare for a run (detection cell temperature is set by the software). Pre-heating helps mitigate subtle first-run migration rate effects. The pre-heat function automatically turns off after 2 hours.

We recommend that you pre-heat the oven for at least 30 minutes before you start a run if the instrument is cold.

Temperatures are displayed in red as they warm to the set-points. When temperatures are at the set-point they are displayed in green. Temperatures may fluctuate slightly when they reach the set-point as they stabilize.

4. Check the pump assembly for bubbles and run the **Remove Bubble wizard** if needed (see “Remove bubbles from the polymer pump” on page 268).

## Create or import a plate

---







**Note:** If you are running a stand-alone version of the software (a version that is not installed on the instrument computer), you can create plates, then export them for use on the instrument computer.

---

### About plate templates

The software includes plate templates that you can use as a starting point to create a plate. Plate template names reflect the run module associated with the plate. The run module contains data collection settings.

Example sequencing plate templates are shown below.

  Seq_Std_BDTv3.1_xL-POP7	Sequencing	For the analysis of the Sequencing Install Standard (BigDye Terminator v3.1...
  Std_Seq_xL-POP6	Sequencing	For read lengths of 600 bp or greater and a run time of 2 hours - 24 capill...
  Std_Seq_xL-POP7	Sequencing	For read lengths of 850 bp or greater and a run time of 2 hours - 24 capill...

For a list of the run time and size range collected for each run module, see Appendix B, “Run modules and dye sets”.

You can also create your own templates. In addition to defining plate parameters, a plate template can also contain a list of the appropriate assays for an application. For more information, see “Create a plate template” on page 97.

## Create a plate from a template

The software includes factory-provided plate templates that you can use as a starting point to create a plate (you can also create your own plate templates). In addition to pre-defined plate parameters, a plate template can also contain a list of the appropriate assays, file name conventions, and results groups for an application.

1. In the **Dashboard**, click **Create Plate From Template** to display the **Open Plate Template from Library** dialog box.



2. In the **Define Plate Properties** screen, enter the plate name and select the number of wells on the plate.
  - Find templates by selecting an attribute, entering the text to search for, then clicking **Go**. (Click **Clear** to clear the field and enter different search criteria).
  - Select a template, then click **Open**.

A screenshot of the "Define Plate Properties" dialog box. The title bar contains "New Plate", "Open Plate", "Save Plate", and "Close Plate" buttons. The main area is titled "Plate Details" and contains several fields: "\* Name:" with a text input field containing "Enter plate name"; "\* Number of Wells:" with three radio buttons for "96", "96-Fast", and "384", where "96" is selected; "\* Plate Type:" with a dropdown menu showing "Sequencing"; "\* Capillary Length:" with a dropdown menu and the unit "cm"; and "\* Polymer:" with a dropdown menu.

---

**IMPORTANT!** Enter only alpha-numeric characters in the software. Special characters may not be correctly displayed in some software screens, may cause problems with plate, file, folder, user account, and/or library item names, and may interfere with starting a run and/or importing and exporting library items.

---

**IMPORTANT!** If you copy/paste sample or plate information into the Assign Plate Contents screen or into a plate import file, copy from a plain text editor such as Notepad. Do not copy from a word processing program such as Microsoft™ Word™, which may include invisible, non-ASCII characters. Non-ASCII characters in plate or sample information may cause a run to stop or may prevent a run from starting.

---

- **96**—Select if you are using a 96-well standard reaction plate or 8-strip standard tubes with a retainer.
  - **96-Fast**—Select if you are using a 96-well Fast reaction plate or 8-strip fast tubes with a retainer.
  - **384**—Select if you are using a 384-well reaction plate (24-capillary instruments only).
3. (Optional) Enter **Owner**, **Barcode**, and **Description** for the plate. For more information on these parameters, see “Plates library” on page 166.
  4. (Optional) In the bottom section of the screen, specify auto-analysis settings for the plate. Refer to the instructions provided with the secondary analysis software.
  5. Click **Save**.
  6. Click **Assign Plate Contents**, then go to “Assign plate contents” on page 61.

## Import a plate

1. Do either of the following:
  - Create a plate on another computer where the software is installed, then export (see “Import and export a plate” on page 97).
  - Create a plate import file (see “Create a plate import file” on page 96).


---

**IMPORTANT!** If you copy/paste sample or plate information into the Assign Plate Contents screen or into a plate import file, copy from a plain text editor such as Notepad. Do not copy from a word processing program such as Microsoft™ Word™, which may include invisible, non-ASCII characters. Non-ASCII characters in plate or sample information may cause a run to stop or may prevent a run from starting.

---

2. Access the **Assign Plate Contents** screen: Click the **Workflow** tab in the **Dashboard**, then select **Assign Plate Contents** in the navigation pane.



3. Click  **Import**, then select the plate import file.
4. Click **Assign Plate Contents**.

## Assign plate contents

You assign the following information to the wells in a plate before you can run the plate:

- **Sample names and sample types** (required)—Identifies the well positions of each sample for data collection and processing.
- **Assay** (required)—Specifies the parameters that control data collection and primary analysis (basecalling or sizing). All named wells on a plate must have an assigned assay. For more information on assays, see “Assays library” on page 169.
- **Filename convention** (*optional*)—Specifies file naming. For more information, see “File name convention overview” on page 173.
- **Results group** (*optional*)—Specifies sample data file storage. For more information on assays, see “Results Group overview” on page 178.

## Access the Assign Plate Contents screen

1. Access the **Assign Plate Contents** screen from:



- The **Define Plate Properties** screen by clicking **Assign Plate Contents** (described above).
  - The navigation pane by selecting **Assign Plate Contents**.
  - The **Dashboard** by clicking the **Workflow** tab, then selecting **Assign Plate Contents** in the navigation pane.
2. Click **Show In Wells** to specify the attributes to display in wells.  
Figure 5 shows the Plate View of the Assign Plate Contents screen.

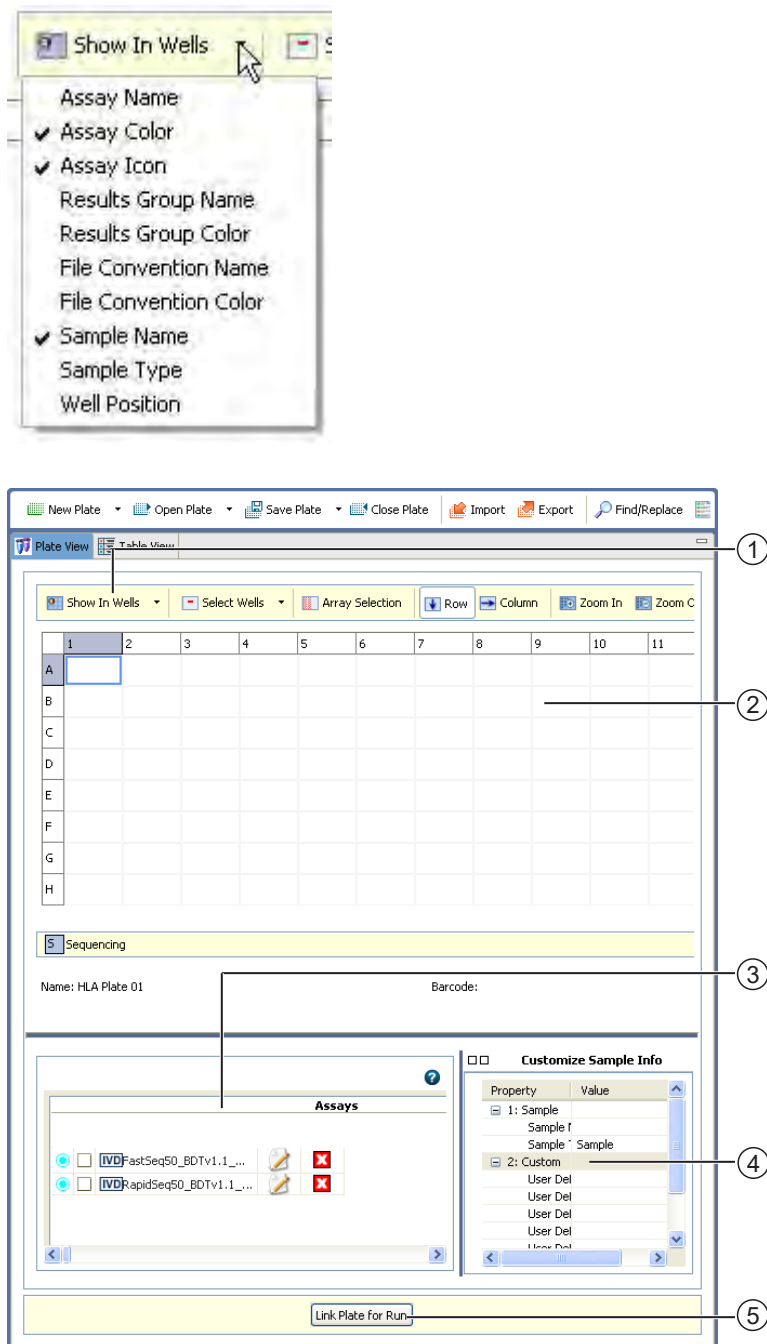


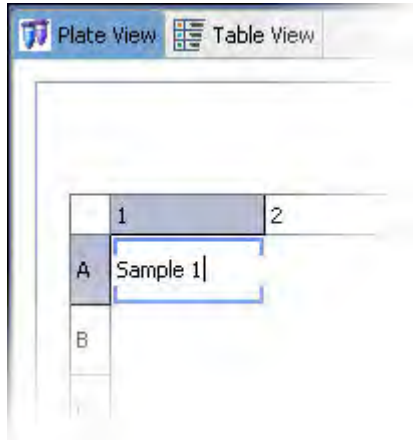
Figure 5 Assign plate Contents

- ① Show well attributes
- ② Name samples
- ③ Assign assays, file name conventions, and results groups
- ④ Assign sample types and user-defined fields
- ⑤ Link plate for run

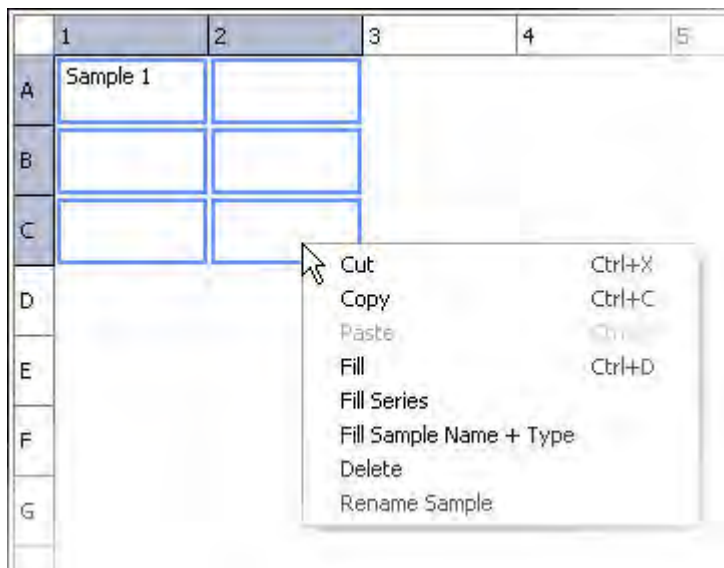
## Name samples and assign sample types in the plate view

**Note:** For other ways to name samples, see “Name samples in the plate view” on page 91 and “Use the table view” on page 93.

1. Click a well, type a sample name directly into the well, then press **Enter**.



2. Click-drag to select multiple wells.
3. Right-click and select **Fill** or **Fill Series** to populate the selected fields.



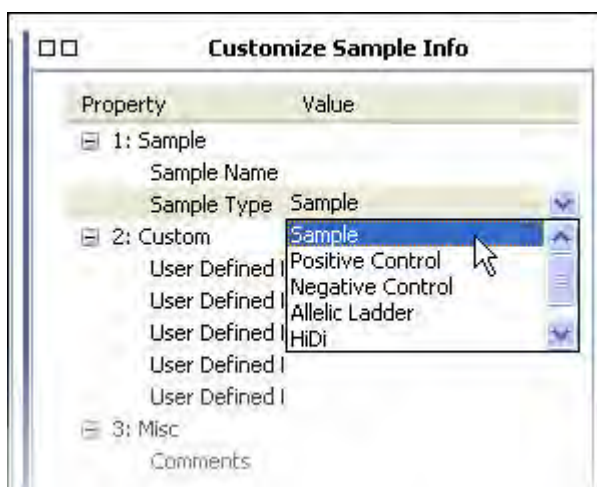
**Note:** To use Fill Series, type a number as the last character of the named well. The number will increment for each well in the series.

**Note:** You can copy and paste sample names instead of using fill commands.

- At the bottom-right of the **Assign Plate Contents** screen, expand the **Customize Sample Info** pane.



- In the Plate View, click-drag to select the wells of interest.
- Specify the **Sample Type** for the selected wells, then press **Enter**.



- (Optional) Specify **User Defined Fields** and **Comments**. User Defined Fields contain additional attributes you can assign to a plate and are displayed only in Table View.

---

**IMPORTANT!** Enter only alpha-numeric characters in the software. Special characters may not be correctly displayed in some software screens, may cause problems with plate, file, folder, user account, and/or library item names, and may interfere with starting a run and/or importing and exporting library items.

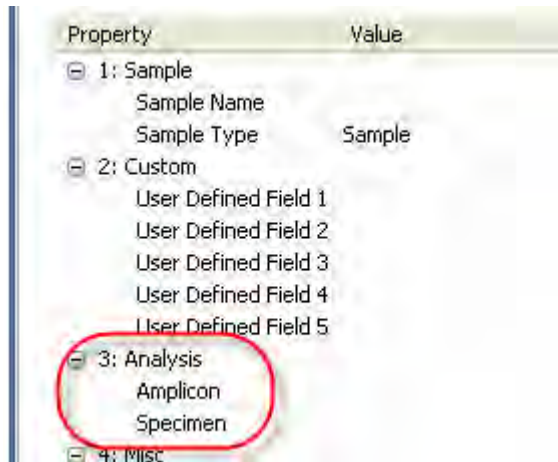
---

**IMPORTANT!** If you copy/paste sample or plate information into the Assign Plate Contents screen or into a plate import file, copy from a plain text editor such as Notepad. Do not copy from a word processing program such as Microsoft™ Word™, which may include invisible, non-ASCII characters. Non-ASCII characters in plate or sample information may cause a run to stop or may prevent a run from starting.

---



- For sequencing assays, specify **Amplicon** and **Specimen**.

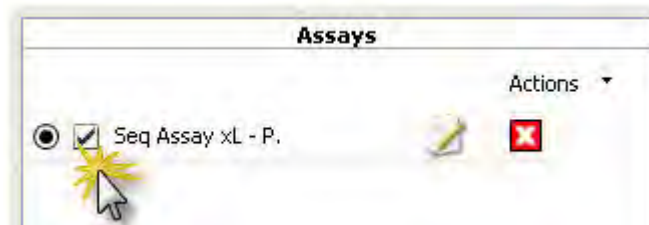


- Repeat steps step 6 through step 8 to assign the Sample Type for all named wells.
- Go to “Assign assay, file name convention, and results group in the plate view” on page 65.

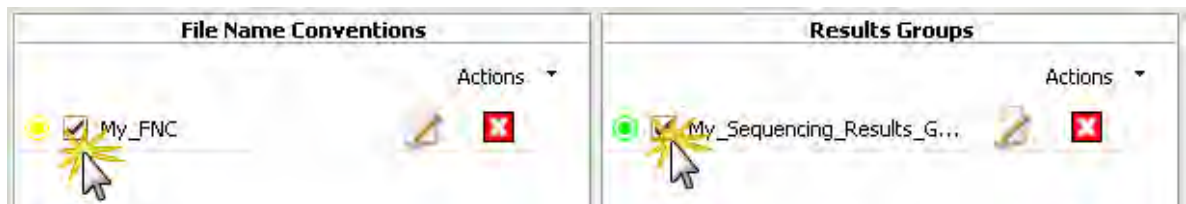
## Assign assay, file name convention, and results group in the plate view

**Note:** If a file name convention or results group you created is not listed for the plate, go to “Add assays, file name conventions, and results groups to a plate” on page 95.

- Select the wells for which to specify an assay.
- Select the checkbox next to the assay name to assign the assay to the selected wells.



- Repeat for file name conventions and results group.



- Select **Save Plate**.
- Go to “Print the plate layout” on page 66.

## How file location in file name conventions and results groups work

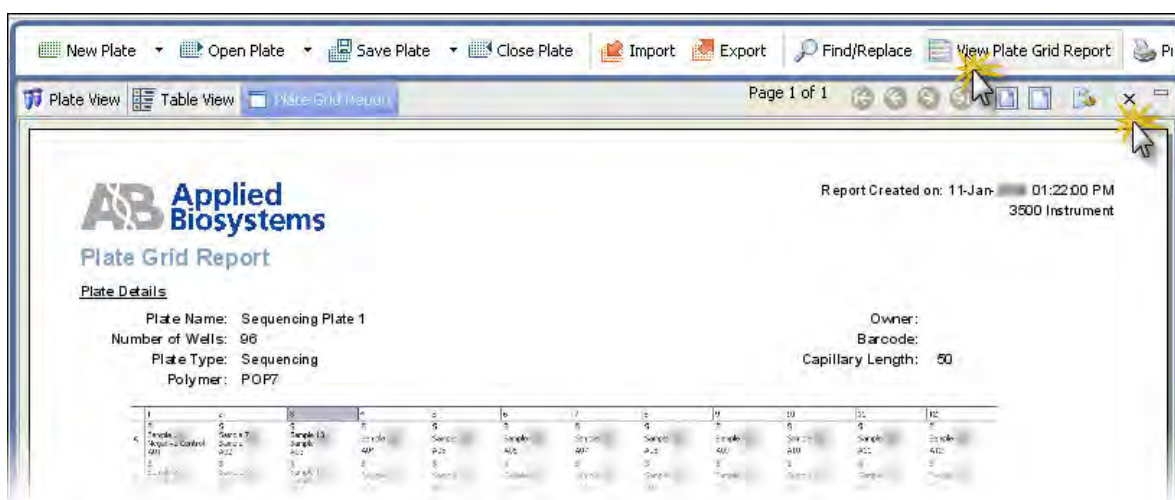
If you do not specify a file name convention, data files are named in this format: <sample name>\_<well>.

If you do not specify a results group, files are stored in the location specified in the file name convention or in **Preferences** > **User** > **Run** (see “User preferences” on page 44).

If you specify both a file name convention and a results group, files are stored in the location specified in the results group.

## Print the plate layout

1. In the **Assign Plates for Run** screen, click **View Plate Grid Report**.



2. Select **Print Preview** or **Print** as needed.
3. To save the report electronically (PDF), print the report and select a PDF printer.
4. Close the report.
5. Go to “Prepare and assemble sample plates” on page 67.

# Prepare and assemble sample plates

**IMPORTANT!** Do not use warped or damaged plates.

## Capillary-to-plate mapping

The capillary-to-plate mapping for the default injection order is shown below. The numbers in the wells represent capillary numbers. If you change the injection order in the injection list, injection order in the injection list differs from the following examples.

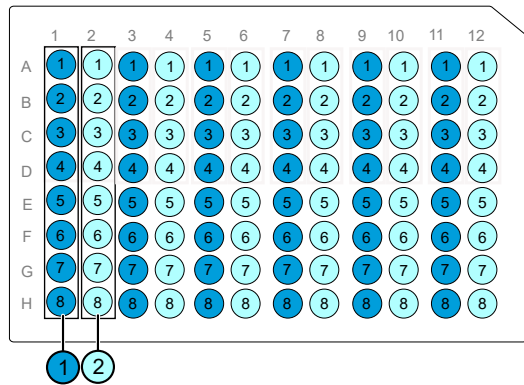


Figure 6 3500 96-well plate capillary-to-plate mapping (8 capillary)

- Injection 1 (wells A1–H1)
  - Injection 2 (wells A2–H2)
- This pattern repeats for a total of 8 injections

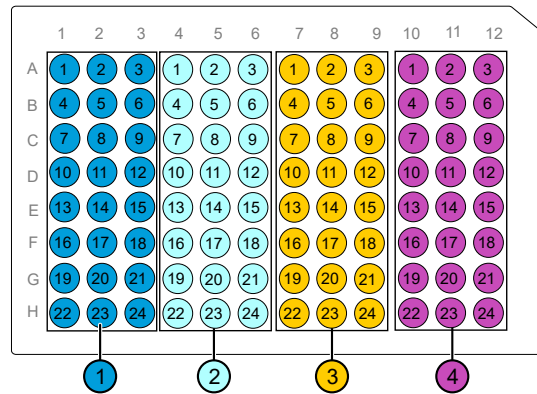


Figure 7 3500xL 96-well plate capillary-to-plate mapping (24 capillary)

- Injection 1 (wells A1–H3)
- Injection 2 (wells A4–H6)
- Injection 3 (wells A7–H9)
- Injection 4 (wells A10–H12)

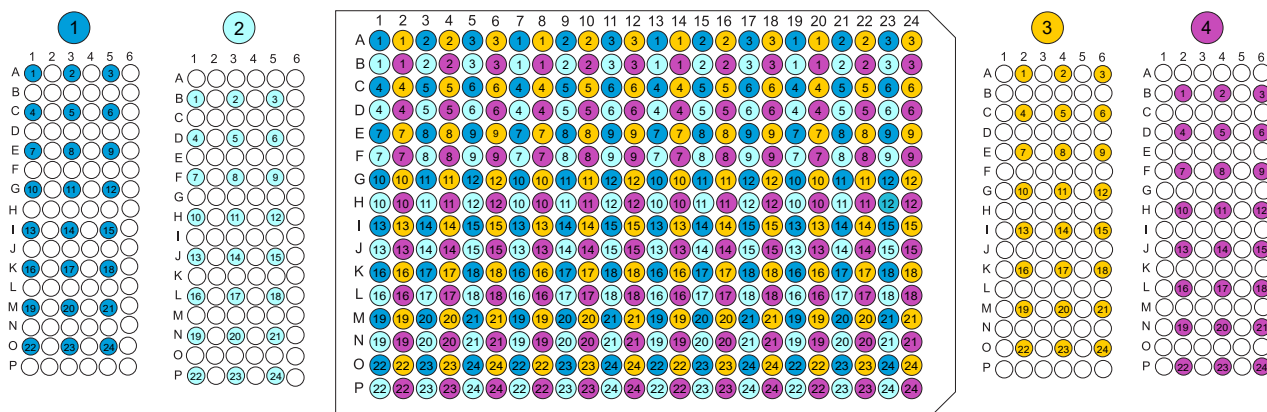


Figure 8 3500xL 384-well plate capillary-to-plate mapping (24 capillary only)

- Injection 1 (wells A1, A3, A5; wells C1, C3, C5; wells E1, E3, E5; wells G1, G3, G5; wells I1, I3, I5; wells K1, K3, K5; wells M1, M3, M5; wells O1, O3, O5)
- Injection 2 (wells B1, B3, B5; wells D1, D3, D5; wells F1, F3, F5; wells H1, H3, H5; wells J1, J3, J5; wells L1, L3, L5; wells N1, N3, N5; wells P1, P3, P5)
- Injection 3 (wells A2, A4, A6; wells C2, C4, C6; wells E2, E4, E6; wells G2, G4, G6; wells I2, I4, I6; wells K2, K4, K6; wells M2, M4, M6; wells O2, O4, O6)
- Injection 4 (wells B2, B4, B6; wells D2, D4, D6; wells F2, F4, F6; wells H2, H4, H6; wells J2, J4, J6; wells L2, L4, L6; wells N2, N4, N6; wells P2, P4, P6)

This pattern repeats for a total of 16 injections

## Allelic ladder run requirements

We recommend that you inject one allelic ladder for each set of 24 samples in HID runs:

- **8-capillary instruments**—One allelic ladder per 3 injections
- **24-capillary instruments**—One allelic ladder per 1 injection

Allelic ladders that are injected under the same conditions are recommended to accurately genotype samples in the secondary analysis software (GeneMapper™ *ID-X* Software v1.3 or later).

---

**IMPORTANT!** Variation in laboratory temperature can cause changes in fragment migration speed that can, in turn, cause sizing variation. We recommend the frequency of allelic ladder injections described above to account for normal variation in fragment migration speed. However, during internal HID validation studies, verify the required allelic ladder injection frequency to ensure accurate genotyping of all samples in your laboratory environment.

---

## Results group for one allelic ladder per run folder

For a 24-capillary instrument, create a results group that specifies an injection folder, then select this results group for all injections on the plate.

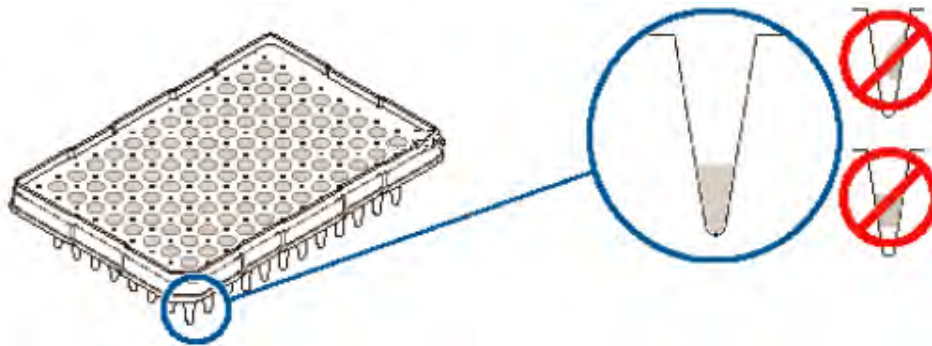
For an 8-capillary instrument, create one results group for each set of three injections on the plate (each results group specifies a results group name folder). For more information, see “Results Group example 2: store re-injections in separate folders” on page 185.

## Prepare sample plates

1. Pipet samples into the plate according to the plate layout (see “Print the plate layout” on page 66).
2. Briefly centrifuge the plate.
3. Verify that each sample is positioned correctly in the bottom of its well.

---

**IMPORTANT!** If the contents of any well contain bubbles or are not located at the bottom of the well, briefly centrifuge the plate, remove the plate from the centrifuge, and verify that each sample is positioned correctly in the bottom of its well.



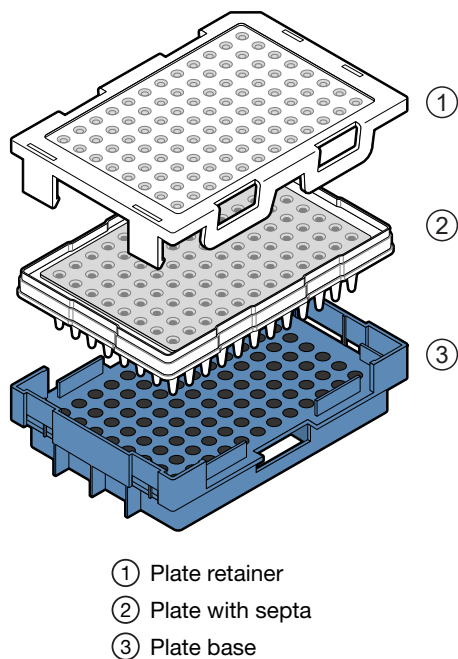
4. Store the plate on ice and protected from light until you prepare the plate assembly and load the plate in the instrument.

## Prepare the plate assembly

Prepare the plate assembly on a clean, level surface. Wear gloves when handling septa. Do not heat plates that are sealed with septa.

### 96-well plate assembly

**IMPORTANT!** Use the correct plate base for the plate in use. Using the wrong plate base may affect performance. See Appendix D, “Catalog numbers” for plate assembly specifications and catalog numbers.



1. Align the holes in the septa with the wells of the plate, then press down firmly on the septa until the septa lies flat on the plate.
2. Place the plate into the plate base.
3. Snap the plate retainer (cover) onto the plate, septa, and plate base.
4. Verify that the holes of the plate retainer and the septa are aligned. If holes are not aligned, take it apart, then re-assemble.

**IMPORTANT!** The array tips will be damaged if the plate retainer and septa holes do not align correctly.

5. If the contents of any well contain bubbles or are not located at the bottom of the well, briefly centrifuge the plate, remove the plate from the centrifuge, and verify that each sample is positioned correctly in the bottom of its well.

## 8-strip tube standard or fast assembly

**IMPORTANT!** Use the correct plate base for 8-tube standard or fast strips. Using the wrong plate base may affect performance. See Appendix D, “Catalog numbers” for plate assembly specifications and catalog numbers.

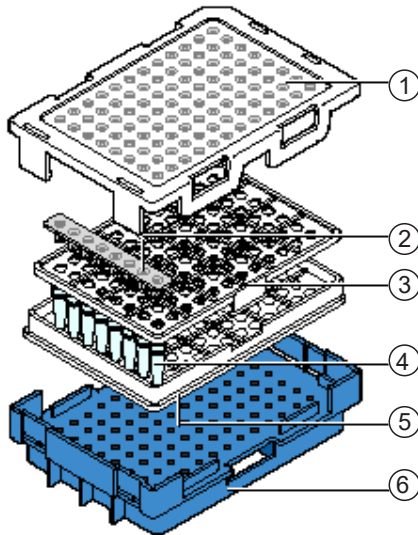


Figure 9 8-strip standard tube assembly

- ① Plate retainer
- ② Septa
- ③ Retainer
- ④ 8-strip tubes
- ⑤ 96-well tray
- ⑥ Plate base

1. Place the tubes in the 96-well tray.

**IMPORTANT!** The array tips will be damaged if the plate retainer and septa strip holes do not align correctly.

2. (8-strip standard tube only) Place the retainer on the tubes.
3. Align the holes in the septa strip with the retainer (8-strip standard tube) or the tubes (8-strip fast tube), then firmly press down.
4. Place the tray-tube-retainer assembly into the plate base.
5. Snap the plate retainer (cover) onto the plate, septa, and plate base.

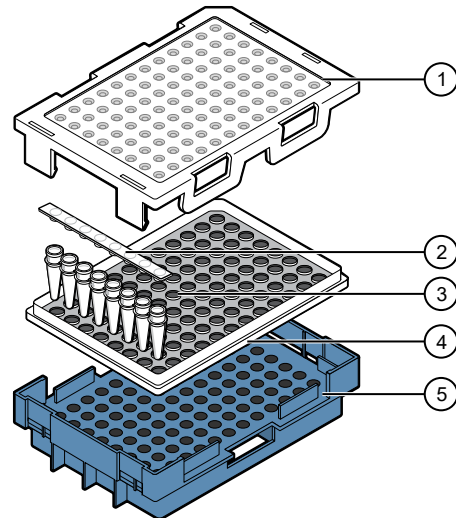


Figure 10 8-strip fast tube assembly

- ① Plate retainer
- ② Septa
- ③ 8-strip tubes
- ④ 96-well tray
- ⑤ Plate base



6. Verify that the holes of the plate retainer and the septa strip are aligned. If holes are not aligned, re-assemble and then assemble the plate assembly.
7. If the reagents of any well contain bubbles or are not located at the bottom of the well, briefly centrifuge the plate, remove the plate from the centrifuge, and verify that each sample is positioned correctly in the bottom of its well.

### 384-well plate assembly

---

**IMPORTANT!** Use the correct plate base for 384-well plates. Using the wrong plate base may affect performance. See Appendix D, “Catalog numbers” for plate assembly specifications and catalog numbers.

---

1. Place the sample plate into the plate base.
2. Place the septum on the plate and press down to seat.
3. If the reagents of any well contain bubbles or are not located at the bottom of the well, briefly centrifuge the plate, remove the plate from the centrifuge, and verify that each sample is positioned correctly in the bottom of its well.

### Load the plate in the instrument

1. Click the Tray button on the front panel to move the autosampler to the front position, then open the instrument door.
2. Place the plate in the autosampler with the labels facing you (or the instrument door) and the notched corner of the plate in the notched corner of the autosampler.
3. Close the instrument door to initialize the instrument.

### Link the plate

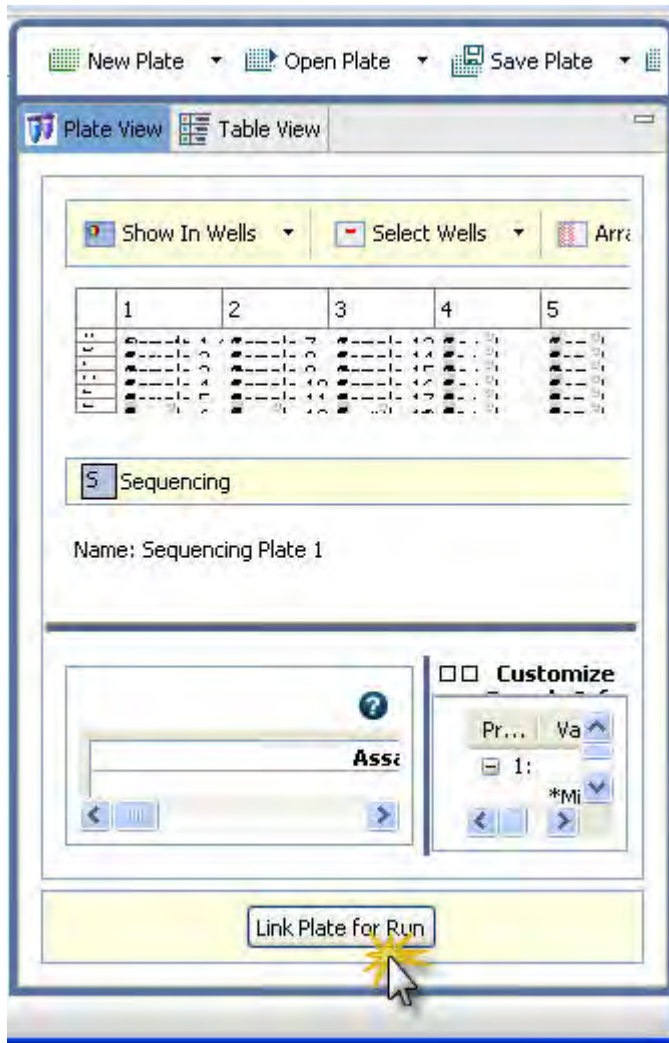
1. In the **Assign Plates for Run** screen, click **Link Plate for Run**.

---

**Note:** By default, plate A position is selected.

---





2. Go to “Load plates for run and create the injection list” on page 74.

## Quick Start a run

Load the plate in the instrument before proceeding (see “Load the plate in the instrument” on page 72).

You can start a run in the **Dashboard** by selecting a plate with plate contents already assigned.

1. In the Dashboard, click **Quick Start Run** to display the **Select Plate from Library** dialog box.



2. Select a plate, then click **Load Plate**.
3. Click **Start Run** from the **Load Plates for Run** screen.

---

**Note:** If an install check for the run application type (Sequencing or Fragment) has not been performed, a message is displayed and the run does not start.

---

## Load plates for run and create the injection list

Load the plate in the instrument (see “Load the plate in the instrument” on page 72) and link the plate (“Link the plate” on page 72) before proceeding.

1. Access the **Load Plates for Run** screen (Figure 11) from:
  - The **Assign Plate Contents** screen by clicking **Link Plate for Run**.
  - The navigation pane by selecting **Load Plates for Run** in the navigation pane.



- The **Dashboard** by clicking the **Workflow** tab, then selecting **Load Plates for Run** in the navigation pane.
2. Review the consumables information and the calibration information and ensure the status is acceptable for a run.
  3. Enter a **Run Name** or use the default run name: <Start Instrument Run Date/Time Stamp> YYYY-MM-DD-hh-mm-ss-SSS (milliseconds), for example, “Run 2014-06-10-17-33-46-522” where the run start date is February 5 2009 and the run start time is 15:03:42:096.

---

**Note:** An instrument run begins when you click **Start Run** (on the **Load Plates for Run** screen) and ends when the last injection on the last plate has completed. For example, if you link two plates, then start the run, both plates and any duplicate injections or re-injections are part of the same instrument run. An injection is an instance of 8 or 24 samples (depending on instrument configuration) processed simultaneously under the same conditions.

When you access the **Load Plates for Run** screen by clicking **Load Plates for Run** on the **Assign Plate Contents** screen, the plate is automatically linked (indicated by the active **Unlink** button).

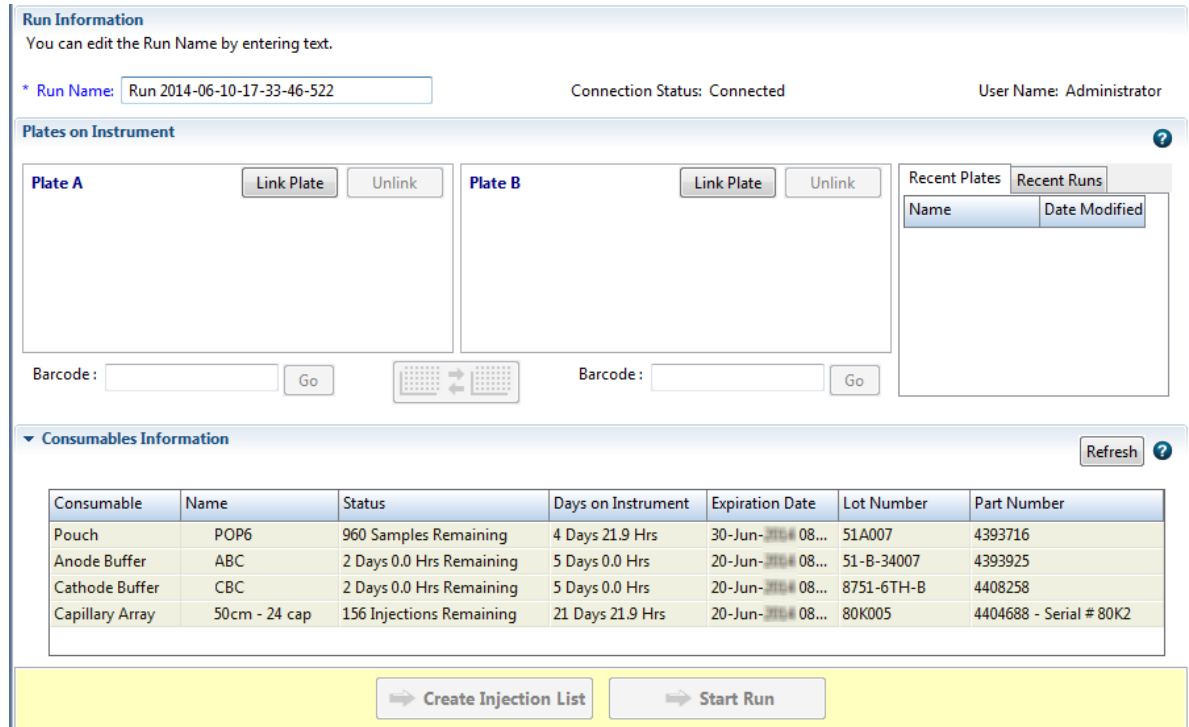



Figure 11 Load Plates for Run

4. If needed, click **Unlink**, then follow the steps in “Link a plate (if a plate is not linked)” on page 76.



5. As needed, click **Switch Plates** (  ) to assign the plate to the other position in the autosampler.

6. Click either of the following:

- **Create Injection List**—Displays the Preview Run screen where you can modify the injection list before starting the run. Go to “Review, modify, or export the injection list in Preview Run” on page 78.
- **Start Run**—Displays the Monitor Run screen. Go to “Monitor the run” on page 80.

---

**Note:** If an install check for the run application type (Sequencing or Fragment) has not been performed, a message is displayed and the run does not start.

---

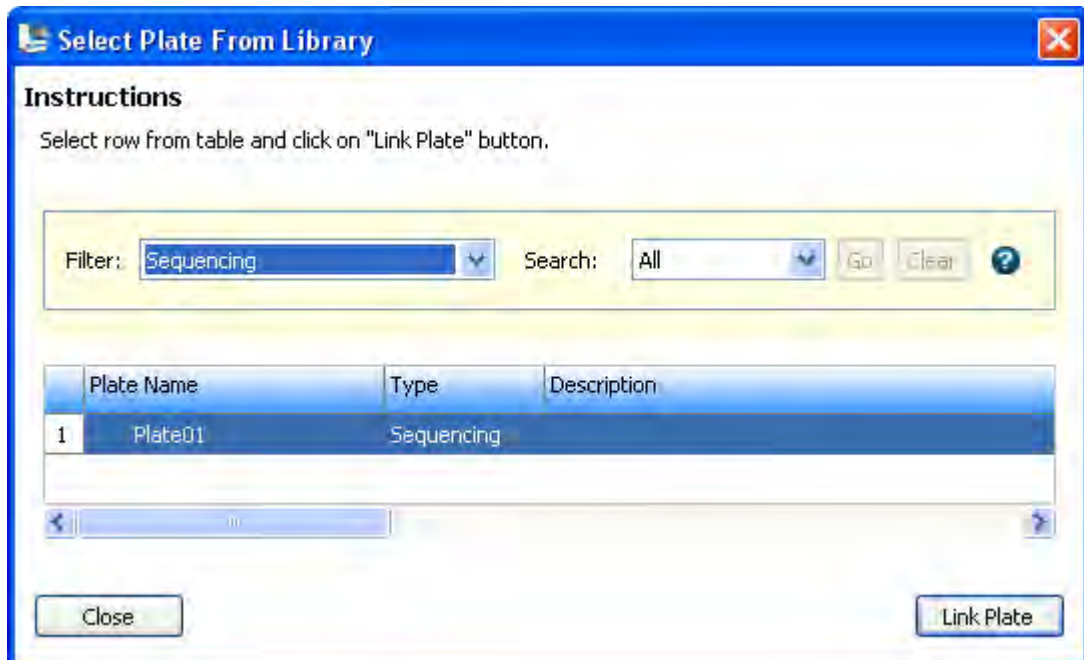
## Link a plate (if a plate is not linked)

If you access the **Load Plates for Run** screen from the navigation pane, a plate may not be linked (indicated by the active Link Plate button).



To link a plate:

1. Click **Link Plate** to display the **Select Plate from Library** dialog box.



2. Select a plate, then click **Link Plate**.
3. Do either of the following:
  - Click **Create Injection List**, then go to “Review, modify, or export the injection list in Preview Run” on page 78
  - Click **Start Run**, then go to “Monitor the run” on page 80

---

**Note:** If an install check for the run application type (Sequencing or Fragment) has not been performed, a message is displayed and the run does not start.

---

## Link a plate from the Recent Plates or Recent Runs tab

Instead of clicking **Link Plate** to select a plate, you can click-drag a plate from the **Recent Plates** tab (pending plates) or the **Recent Runs** tab (processed plates).



## Review, modify, or export the injection list in Preview Run

The **Preview Run** screen allows you to modify the injection list before you start the run.

1. Access the Preview Run screen (Figure 12) from:
  - The **Load Plates for Run** screen by clicking **Create Injection List**.
  - The navigation pane by selecting **Preview Run**.
  - The **Dashboard** by clicking the **Workflow** tab, then selecting **Preview Run** in the navigation pane.

The screenshot displays the 'Preview Run' interface. At the top, there are navigation icons: 'Move Up in List', 'Move Down in List', 'Delete', and 'Duplicate'. Below this is the 'Injection List' section, which shows 12 injections created across Plate A and Plate B. The list includes columns for Type, Assay, Instrument Protocol, and Plate. To the right of the list is a grid representing the plate layout, with rows labeled A through H and columns 1 through 12. Each cell in the grid contains 'Samp'. Below the grid, there are fields for 'Name: Plate01' and 'Barcode: IVD'. At the bottom of the Injection List section, there is a 'Legend' with 'Duplicate Injection' and 'Re-Injection' options. Below the Injection List is the 'Consumables Information' section, which includes a 'Refresh' button and a table with columns for Consumable, Name, Status, Days on Instrument, Expiration Date, Lot Number, and Part Number. The table lists four consumables: Pouch, Anode Buffer, Cathode Buffer, and Capillary Array.

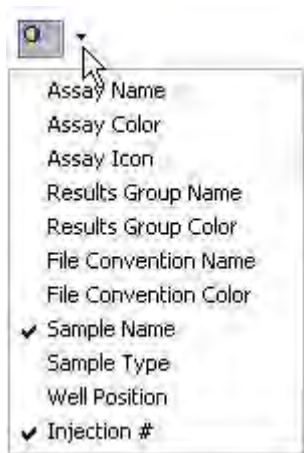
Type	Assay	Instrument Protocol	Plate
1	FastSeq50_BDTv1.1...	FastSeq50_POP6_E	Plate01[]
2	FastSeq50_BDTv1.1...	FastSeq50_POP6_E	Plate01[]
3	FastSeq50_BDTv1.1...	FastSeq50_POP6_E	Plate01[]
4	FastSeq50_BDTv1.1...	FastSeq50_POP6_E	Plate01[]
5	FastSeq50_BDTv1.1...	FastSeq50_POP6_E	Plate01[]
6	FastSeq50_BDTv1.1...	FastSeq50_POP6_E	Plate01[]
7	FastSeq50_BDTv1.1...	FastSeq50_POP6_E	Plate01[]
8	FastSeq50_BDTv1.1...	FastSeq50_POP6_E	Plate01[]
9	FastSeq50_BDTv1.1...	FastSeq50_POP6_E	Plate01[]
10	FastSeq50_BDTv1.1...	FastSeq50_POP6_E	Plate01[]
11	FastSeq50_BDTv1.1...	FastSeq50_POP6_E	Plate01[]
12	FastSeq50_BDTv1.1...	FastSeq50_POP6_E	Plate01[]

Consumable	Name	Status	Days on Instrument	Expiration Date	Lot Number	Part Number
Pouch	POP6	952 Samples Remaining	0.8		51A007	
Anode Buffer	ABC	6.22 Days Remaining	0.8		51-B-04007	
Cathode Buffer	CBC	6.22 Days Remaining	0.8		6751-6TH-B	
Capillary Array	50cm - 8 cap	159 Injections Remaining	0.8		80K005	

Figure 12 Preview Run screen



2. Click the icon above the plate to specify the attributes to display in the plate view.








3. Click the **Plate** tabs to display **Plate A** or **Plate B**.

The **Preview Run** screen contains an injection list and a plate view. The injection list is linked to the plate view. Click an injection to select the associated wells in the plate view.

---

**IMPORTANT!** If the injection list is blank, make sure that you clicked **Create Injection List** on the **Load Plates for Run** screen.

---

4. To modify the injection list at any time before a run or during a run, select an injection, then click  **Move Up**,  **Move Down**, and  **Delete** as needed.
5. To specify a duplicate injection (a replicate injection that uses the same instrument protocol as the original injection), select an injection, then click .  
Sample data files for each duplicate injection can be saved in a separate folder in the results group folder if specified in the results group.
6. To export the injection list, click  **Export**.

## Start the run from Preview Run

When the injection list is configured, click **Start Run**. The **Monitor Run** screen is automatically displayed.

---

**IMPORTANT!** You must re-inject samples before the run completes unless the Pause after last injection preference is set.

---

**Note:** If an install check for the run application type (Sequencing or Fragment) has not been performed, a message is displayed and the run does not start.

---

## Export the injection list from Preview Run

The injection list can be exported in a CSV, XLS, or TXT export file. The export file lists samples in the order in which they are displayed on the screen.

1. Select **Preview Run** in the left pane.
2. Click **Export**.

## Monitor the run

The **Monitor Run** screen (Figure 13) is automatically displayed when you click **Start Run** in the **Load Plates for Run** screen or the **Preview Run** screen. The current injection is highlighted in green in the plate view. The injection list is linked to the plate view. Click an injection to select the associated wells in the plate view. A selected injection is highlighted in green in the plate view.

The screenshot shows the Monitor Run interface. At the top, there are control buttons: Move Up in List, Move Down in List, Delete, Duplicate, Re-Inject, Pause Run, Resume Run, Abort Injection, and Terminate Injection. Below this is a status bar with the following information:

- Connection Status: Connected
- User Name: Administrator
- Last Login Time: 10-Sep-2010 06:48:17 AM
- Run Name: Run 09-10-06-55-28-906
- Run Status: Running
- Estimated Time Remaining: 17:29:45

The main section is titled "Injection List Details" and shows "12 injections created - 12 in Plate A - 0 in Plate B". It contains a table with the following columns: Injection, Type, Assay, and Instrument Protocol.

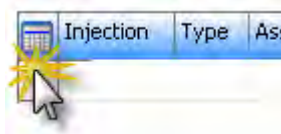
Injection	Type	Assay	Instrument Protocol
1	Active	FastSeq50_BDTv1.1_...	FastSeq50_POP6_E
2	Not Started	FastSeq50_BDTv1.1_...	FastSeq50_POP6_E
3	Not Started	FastSeq50_BDTv1.1_...	FastSeq50_POP6_E
4	Not Started	FastSeq50_BDTv1.1_...	FastSeq50_POP6_E
5	Not Started	FastSeq50_BDTv1.1_...	FastSeq50_POP6_E
6	Not Started	FastSeq50_BDTv1.1_...	FastSeq50_POP6_E
7	Not Started	FastSeq50_BDTv1.1_...	FastSeq50_POP6_E
8	Not Started	FastSeq50_BDTv1.1_...	FastSeq50_POP6_E
9	Not Started	FastSeq50_BDTv1.1_...	FastSeq50_POP6_E
10	Not Started	FastSeq50_BDTv1.1_...	FastSeq50_POP6_E
11	Not Started	FastSeq50_BDTv1.1_...	FastSeq50_POP6_E
12	Not Started	FastSeq50_BDTv1.1_...	FastSeq50_POP6_E

Below the table is a legend with icons for Not Started, Active, Aborted, Completed, Re-Injection, Duplicate, and Flags. To the right of the injection list is a plate view grid for Plate A and Plate B. The grid shows 12 columns (1-12) and 8 rows (A-H). The first column of each row is highlighted in green, indicating the active injection. The grid cells contain "Samp" followed by the column number.

At the bottom of the plate view, there are fields for "Name: Plate01" and "Barcode:".

Figure 13 Monitor Run screen

1. Click the Table Settings button, then specify the columns to show or hide in the injection list.



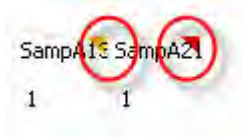


2. (Optional) Specify the attributes and/or display sample details:

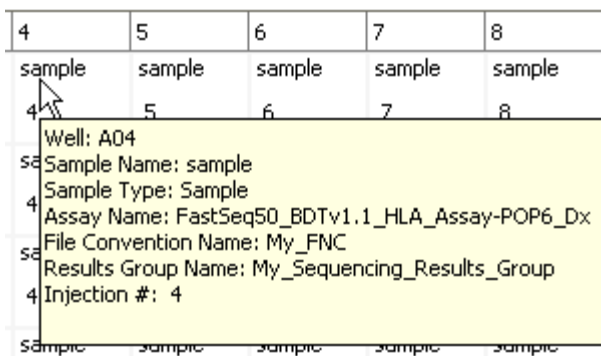
- Click the icon above the plate to specify the attributes to display in the plate view. In addition to the attributes available in **Preview Run**, a **Flag** attribute is available.



If you select the **Flag** attribute, green marks are displayed for wells with Average QV values that are within range, yellow marks are displayed for wells with Average QV values that are in the suspect range, and red marks are displayed for wells with Average QV values that are out of range.



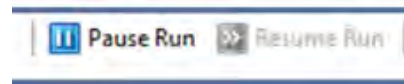
- Place the mouse pointer over a well to display sample details.



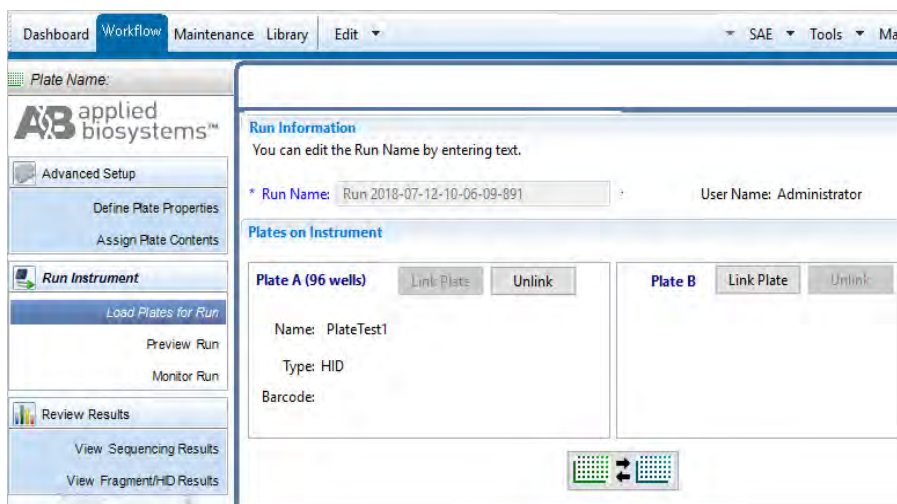
## Pause a run and load a new plate (flexible plate loading)

The software allows you to load an additional plate in the instrument at any time during a run, and move injections from the new plate to the top of the injection list.

1. In the **Workflow** tab, click **Monitor Run** in the left pane.
2. In the **Monitor Run** screen, click **Pause Run**.





3. Click **OK** to accept the message that indicates that the instrument will pause after completing the current injection.
4. When the run pauses, click **Load Plate for Run** in the left pane.
5. If both plate positions are filled in the **Load Plate for Run** screen, click **Unlink** for one of the positions, then remove the plate.



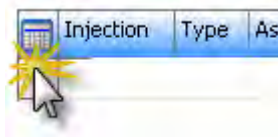
6. Install the new plate, click **Link Plate**, then select the plate you want to load.
7. At the bottom of the **Load Plate for Run** screen, click **Create Injection List**.
8. Click **Monitor Run** in the left pane.
9. As needed, change the injection order in the **Monitor Run** screen.  
 You can move injections from the newly loaded plate up in the injection list to inject from the newly loaded plate before the first plate has finished running.
10. Click **Resume Run**.

## Check sequence or sample quality and re-inject samples

When an injection is complete, it is flagged with  in the **Injection** and **Analysis** columns. If the software detects a problem with offscale data or low quality samples, the injection is also flagged with .

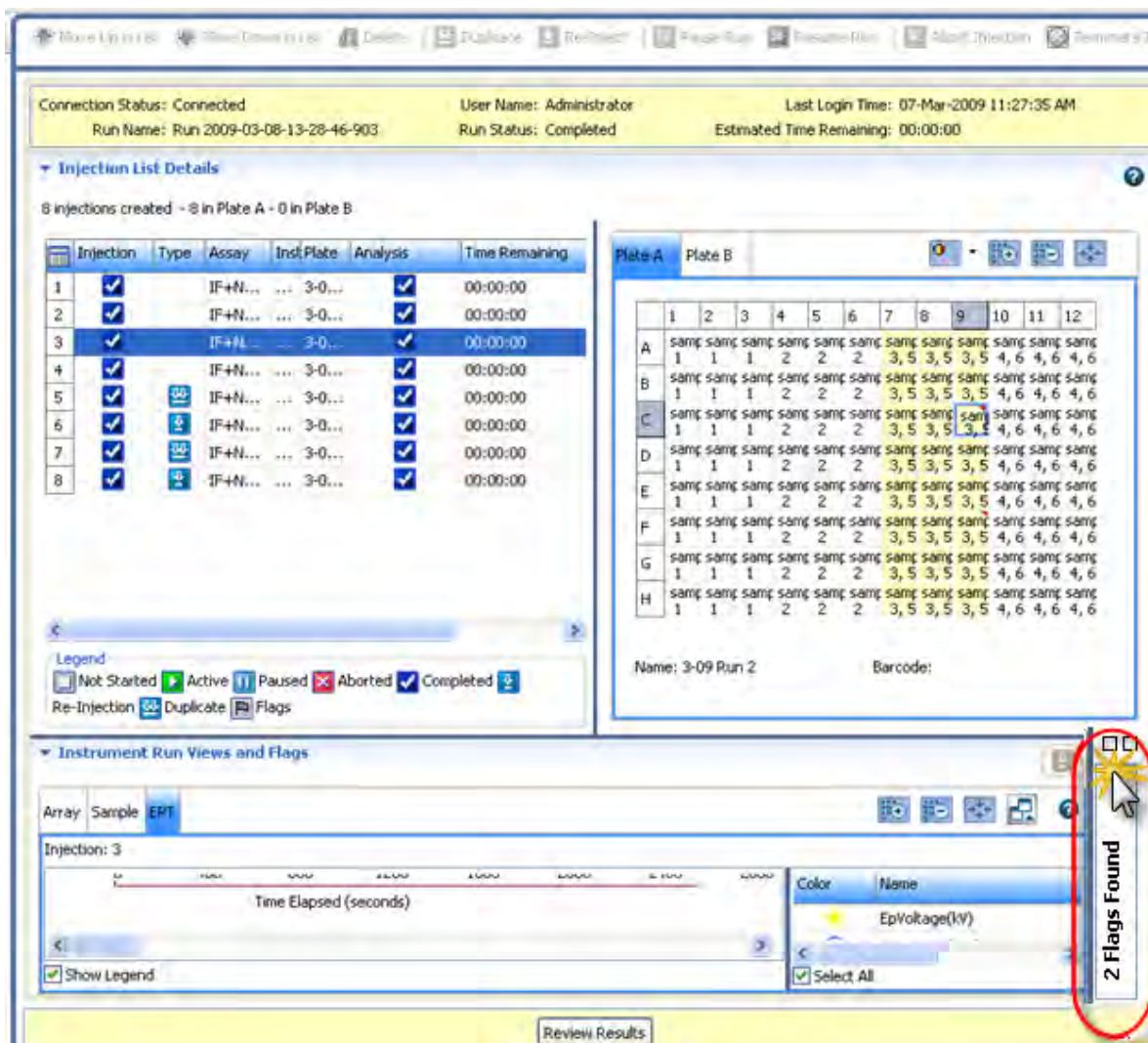
	Injection	Type	Assay	Inst	Plate	Analysis	Time Remaining	Flags
1	<input checked="" type="checkbox"/>		IF+N...	...	3-0...	<input checked="" type="checkbox"/>	00:00:00	

**Note:** If the **Injection**, **Analysis**, or **Flag** columns are not displayed, you can click the Table Settings button, then show them in the injection list.

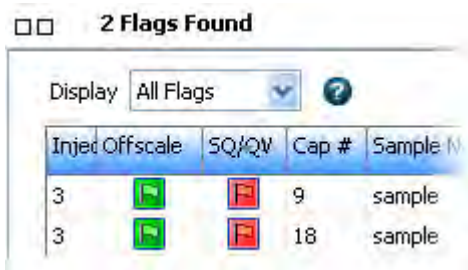


## Check sequence or sample quality

1. Expand the **Flag** pane at the bottom right of the screen.






The flag table displays a quick preview of sample quality and identifies samples that may need investigation. The flag table is linked to the plate view.













2. Click a flag to select the associated well in the plate view:

**Note:** If no samples are listed in this pane, no flags were found and the samples have passed quality checks.

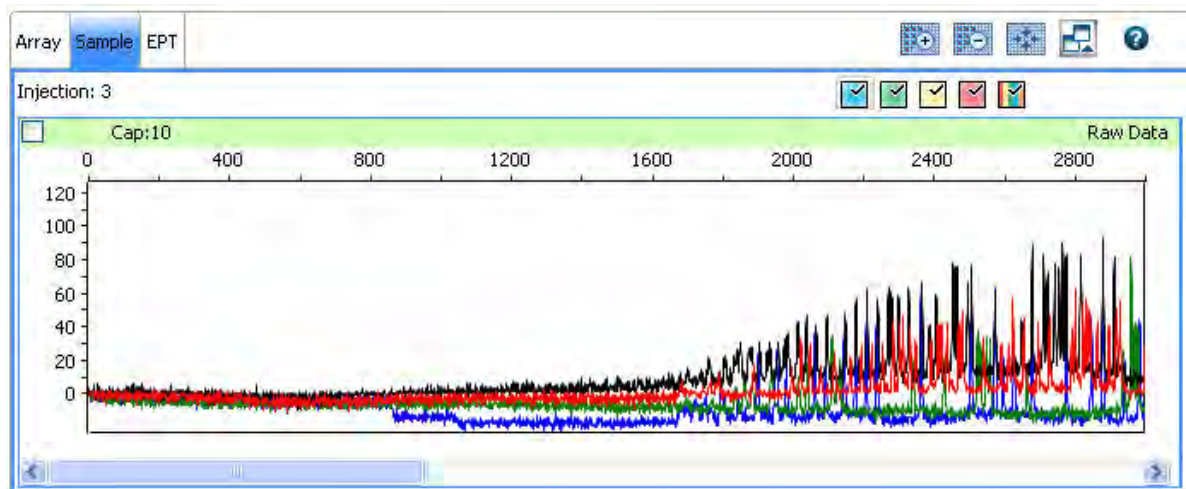
-  All samples passed
-  At least one sample is in the suspect range and requires review
-  At least one sample is offscale or is in the fail range

3. To filter the flag table, select a flag type. To sort the table, double-click column headers.

The flags you may see in the flag table are:

Flag/Symbols	Description
Offscale  (green or red)	 (red) At least one data point in the analysis range has saturated the CCD camera.  <b>Note:</b> In the <b>View Results</b> screen, an offscale sample is flagged with  .
QV: Average Quality Value (sequencing)  (green, yellow, red)	 (yellow) or  (red) The Average Quality Value (based on CRL, Trace Score, and QV20+ results) is in the Suspect or Fail range. For information, see “Basecalling protocol—QV settings” on page 205.
SQ: Sizing Quality (fragment)  (green, yellow, red)	 (yellow) or  (red) The Sizing Quality is in the Suspect or Fail range. For information, see “Sizecalling protocol—QC settings” on page 211.  <b>IMPORTANT!</b> Normalization is not applied to samples with  (red) Sizing Quality.

4. Click a row in the flag table, then click the Sample tab in **Instrument Run Views** to display the associated data in the Sample view.








## Re-inject samples from the Monitor Run screen

A re-injection physically re-injects all samples in the capillary array. You can specify whether to collect data for all or only selected samples in the array.

By default, you can specify a re-injection before the run completes. To allow re-injections after a run is complete, set the **Pause After Last Injection** preference (see “User preferences” on page 44).

1. Select the injections or wells to re-inject:

**Note:**  Re-inject is dimmed if you select an injection that contains more than one results group, or if you select flags in the flags table that correspond to samples with different results groups. To enable  Re-inject, select samples that specify the same results group.

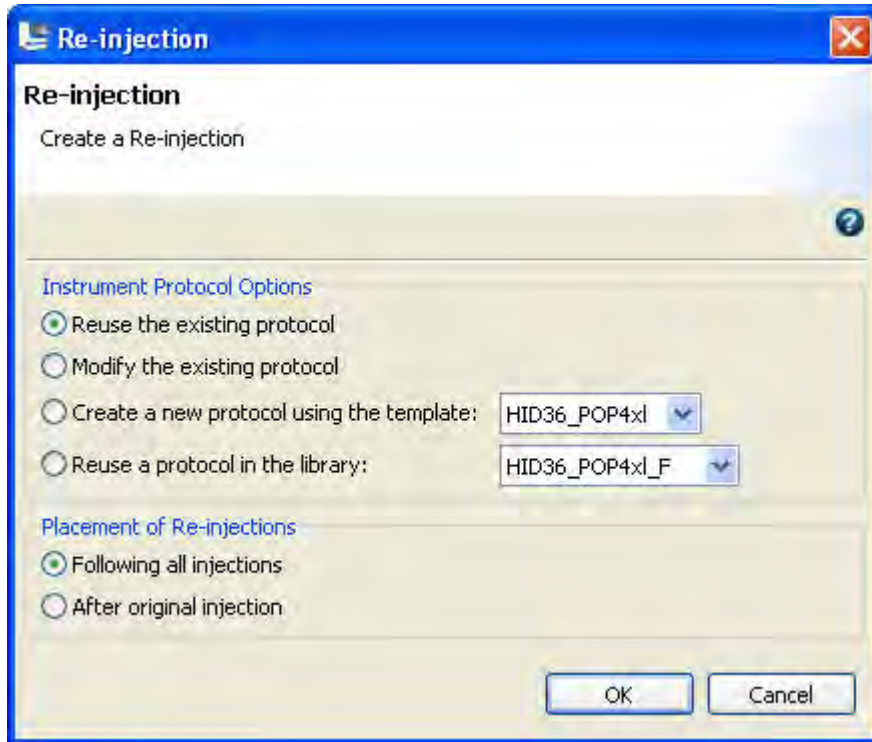
To collect data for all wells in an injection	<ol style="list-style-type: none"> <li>1. Select the injection in the injection list.</li> <li>2. Click  <b>Re-inject</b>.</li> </ol>
To collect data for only specific wells <b>Note:</b> You can also re-inject specific samples in <b>Review Results</b> .	<ol style="list-style-type: none"> <li>1. Select the injection.</li> <li>2. Select in the array view the capillary that corresponds to the well or sample of interest (see “Array view” on page 99).</li> <li>3. Click  <b>Re-inject</b>.</li> </ol>
To collect data for only samples that contain flags	<ol style="list-style-type: none"> <li>1. Select the samples in the flag table (see “Check sequence or sample quality” on page 84).</li> <li>2. Click  <b>Re-inject</b>.</li> </ol>

**Note:** If you are running an HID plate, see “Re-inject HID allelic ladder samples” on page 88.

2. In the **Re-injection** dialog box, select options, then click **OK**.

**Note:** Sample data files for each re-injection can be saved in a separate folder in the results group folder if specified in the results group.





## If you select a protocol other than the original

If you select a protocol other than the original, the software:

- Creates a copy of the assay specified for the re-injected well (Original\_Assay-1).
- Adds the new or modified instrument protocol to Original\_Assay-1.
- Assigns Original\_Assay-1 to the re-injected well only.
- Saves the plate (the software does not save the copy of the assay to the library).

## How re-injections are displayed in the plate view

If the Injection Number attribute is selected for display in the plate view, the number of the original injection and the re-injection are shown.

	1	2
A	sample 1	1, 2
B	sample 2	1, 2
C	sample 3	

- ① Sample 1 selected for re-injection
- ② Re-injection number listed for all samples in the re-injection

---

**Note:** If you select only specific wells for the re-injection (which physically re-injects all samples for the capillary array but collects data only for the selected wells), the re-injection number is displayed for all samples in the re-injection, not just the samples selected for data collection.

---

## Re-inject HID allelic ladder samples

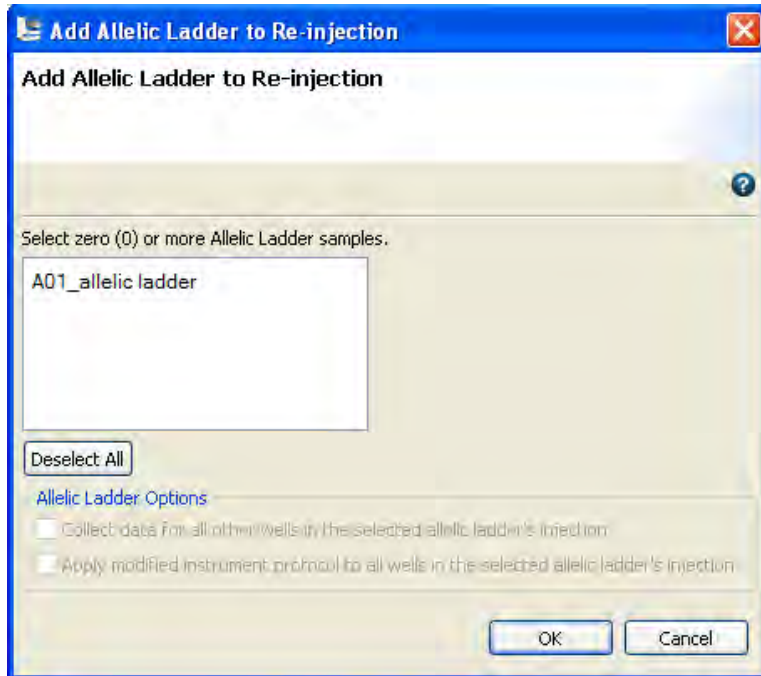
If you select to re-inject a sample that includes an allelic ladder in its results group, but the allelic ladder is not part of the injection, the software prompts you to select one or more allelic ladder samples to re-inject.

For example:

- You are running an 8-capillary instrument, and you have specified one results group for each set of three injections (for more information, see “Results Group example 3: store one allelic ladder per run folder (8-capillary instruments)” on page 188)
- The allelic ladder sample is in Injection 1.
- You select for re-injection a sample that is in injection 2.



- The software prompts you to select one or more allelic ladder samples to re-inject. The allelic ladders available to select are from the same plate and within the same results group as the original injection. If the results group does not contain an allelic ladder sample, the software does not prompt you to select one for re-injection.



Complete the following actions in the **Add Allelic Ladder to Re-injection** dialog box:

1. Select one or more allelic ladder samples.

---

**IMPORTANT!** The software does not display the well location of allelic ladder samples in this dialog box. To identify allelic ladder samples for re-injection, include the well position in the allelic ladder sample name when you assign plate contents.

---

2. Select whether to collect data for the remaining samples in the allelic ladder re-injection.
3. Select whether to apply a modified instrument protocol to the allelic ladder re-injections, or whether to use the original instrument protocol for the allelic ladder re-injection(s). You will select the modified protocol in the next screen.

---

**IMPORTANT!** Allelic ladders that are injected under the same conditions are recommended to accurately genotype samples in the secondary analysis software (GeneMapper™ ID-X Software v1.3 or later).

---

4. Click **OK**.
5. Specify the remaining re-injection settings as described in “Re-inject samples from the Monitor Run screen” on page 86.




## Review completed injections in Review Results

You can review results for any completed injections. Select the injection, then click **Review Results**. The samples for the injection are loaded in the Samples Table in Review Results. For more information, see Chapter 5, “Review sequencing results”.

## Pause, resume, or stop a run


### Pause and resume

As needed, click:


-  **Pause**—Pauses the run after the current injection completes (the  symbol is not displayed in the injection list because the injection continues to completion).
-  **Resume**—Resumes the run.

### Abort or terminate




As needed, click:

-  **Abort**—Immediately aborts the current injection and pauses the instrument run. You can resume the run or terminate the injection list. Do not click Delete to stop an injection.

---

**IMPORTANT!** You can stop the current injection only when the front panel indicator is blinking green. If you click  **Abort** when the front panel indicator is solid green, the physical injection is already completed (although the software is still processing the information) and a message is displayed indicating that there is no injection in process.



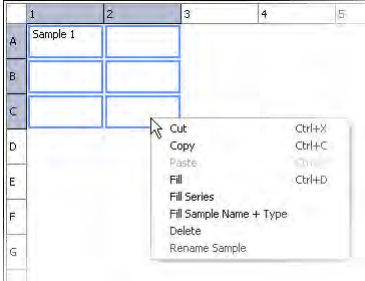
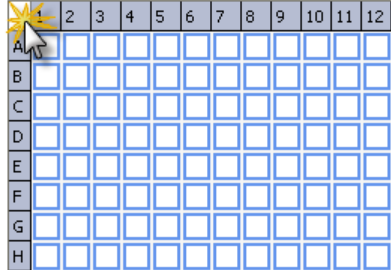
---

-  **Terminate injection list**—Stops the instrument run. Terminate is active only after you click  Pause or  Abort.

## More features in Assign Plate Contents

### Name samples in the plate view

To name samples in the **Plate View**:

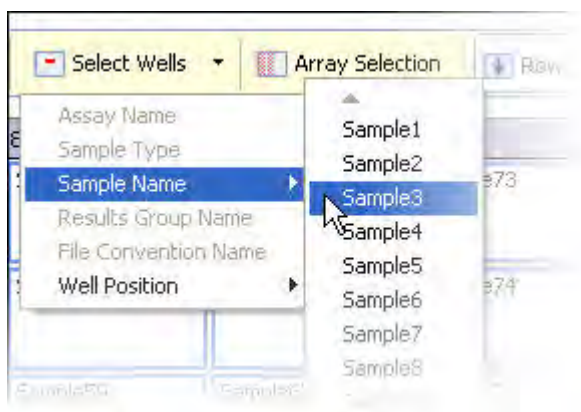
<p>To name one sample</p>	<ul style="list-style-type: none"> <li>Click a well, then type a sample name directly into the field, then press <b>Enter</b>. <i>or</i></li> <li>Copy and paste a name from another well.</li> </ul> <p>To set the direction for the cursor when you press <b>Enter</b>:</p> <p>Click  <b>Row</b> to set the Enter key to move the cursor vertically to the next row.</p> <p>Click  <b>Column</b> to set the Enter key to move the cursor horizontally to the next column.</p>
<p>To name multiple samples</p>	<ul style="list-style-type: none"> <li>Click a named well.</li> <li>Click-drag multiple wells.</li> <li>Right-click and select <b>Fill</b> or <b>Fill Series</b> to populate the selected fields.</li> </ul> <p><b>Note:</b> To use <b>Fill Series</b>, type a number as the last character of the named well). You can also copy and paste sample names.</p> 
<p>To name all wells at one time</p>	<ul style="list-style-type: none"> <li>Select all wells.</li> <li>Select assays, file name conventions, and results group for the plate.</li> <li>Enter name and select sample type (in the <b>Customize Sample Info</b> pane) for the whole plate.</li> </ul> 

## Customize the plate view

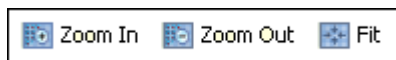
1. Click **Show In Wells** to specify the attributes to display in wells.



2. Click **Select Wells** to select wells with a specific attribute.



3. Click **Zoom In**, **Zoom Out**, and **Fit** as needed.



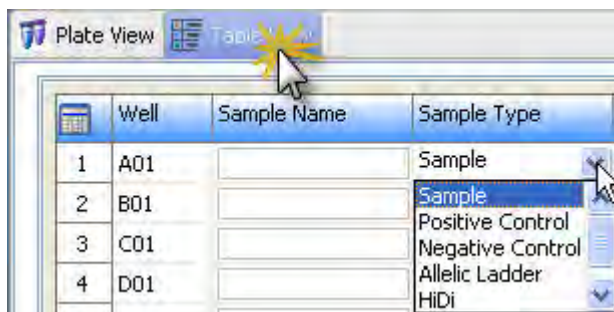
## View the capillary-to-plate map


Click **Array Selection** to select wells by injection. Click again to turn off array selection.



## Use the table view

1. Click **Table View**.

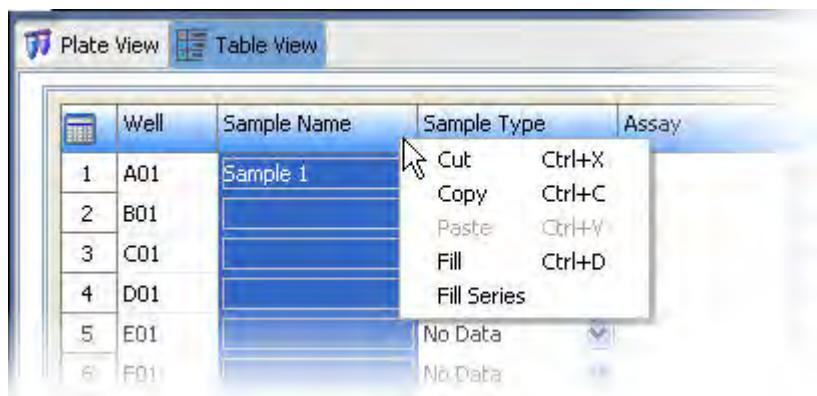


2. Click the **Sample Name** field, then type a name.
3. Click  next to each field, then select a setting.
4. Right-click a column header, then select **Fill** or **Fill Series** to populate the selected fields (to use Fill Series, type a number as the last character of the named well).

---

**Note:** You can double-click column headers to sort columns. Multi-column sorting is supported (see “Sort by one or multiple columns” on page 94 below).

---



## Sort by one or multiple columns

Double-click column headers to sort. To sort by multiple columns:

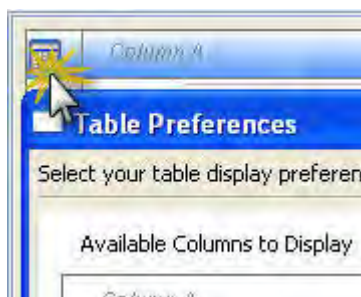
- Double-click a column header to sort the column.
- Alt+Shift-click another column header to sort another column.
- Alt+Shift-click a third column header to sort a third column.

Numbers in the column headers reflect sort order.



## Customize a table

Click the **Table Settings** button, then specify the columns to show or hide.

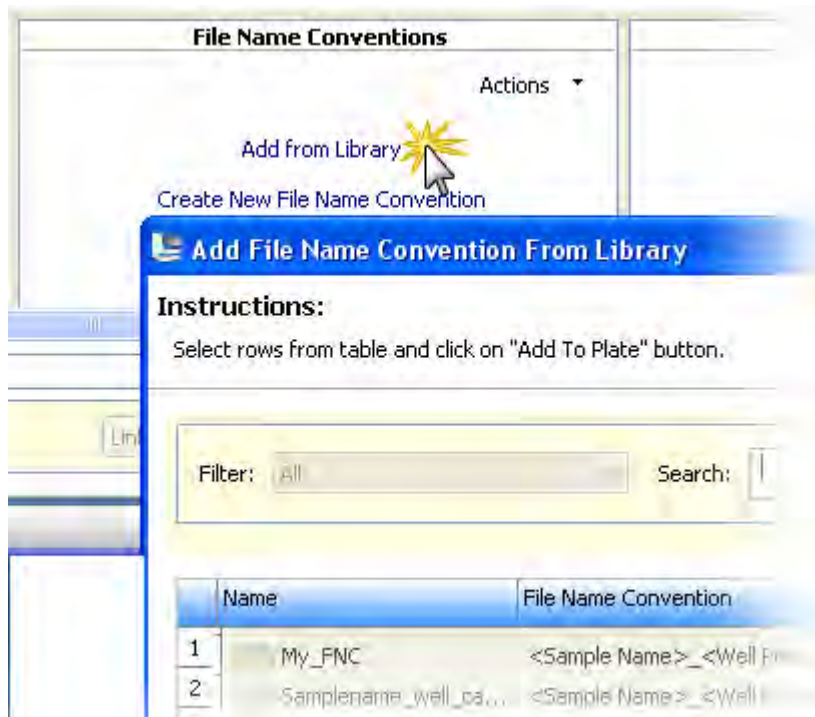


Click:

- **Apply**—To use the settings for this session only.
- **Save to Preferences**—To save for future use by all users. Preferences are saved for the logged-in user.
- **Restore Defaults**—To restore factory-default settings.

## Add assays, file name conventions, and results groups to a plate

To add an assay, file name convention, or results group from the library, click **Add from Library** at the bottom of the **Assign Plate Contents** screen.



## Create a plate import template

The software allows you to import plate information from files that you create in another application. To create a template for importing plate information, set up a plate in the software and then export it to create a file that contains the correct header and column information for importing:

1. In the **Dashboard**, click **Create Plate from Template**.



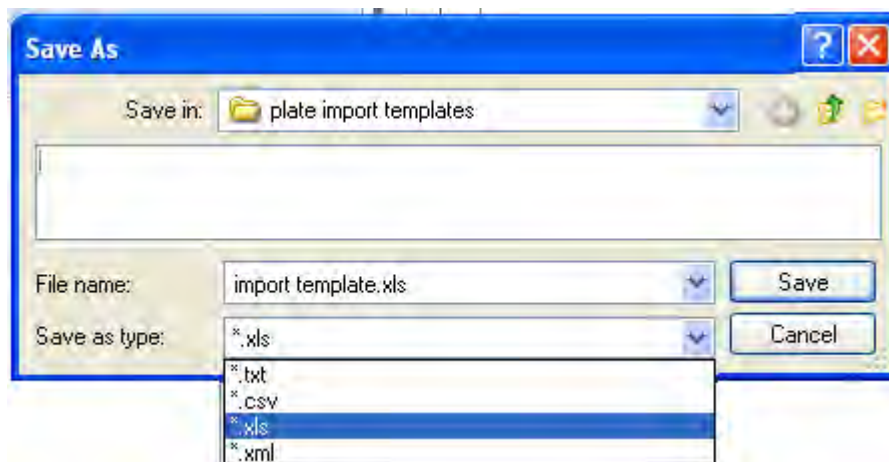
2. In the **Open Plate Template from Library** dialog box:
  - a. Select a filter to display the plate template type of interest.
  - b. Select a plate template, then click **Open**.
3. Enter a name for the plate, then specify the capillary length and polymer type for the plate.
4. Click **Assign Plate Contents**.



- In the **Assign Plate Contents** screen, click  **Export**.

**Note:** Before you click Export, you can assign other plate elements to the plate import template as described in “Assign plate contents” on page 61.

- Select a file type for the plate import template.



- Enter a name and location for the plate record template.

- Click **Save**.

The figure below shows the format of the exported plate.

	A	B	C	D	E	F	G	H
1	3500 Plate Layout File Version 1.0							
2								
3	Plate Name	Application Type	Capillary Length (cm)	Polymer	Number of Wells	Owner Name	Barcode Number	Comments
4		Sequencing	50	POP6	96			
5								
6	Well	Sample Name	Assay	File Name	Results Group	Sample Type	User Defined Field 1	User Defir L
7	A01							

## Create a plate import file

- Open a plate import template (see “Create a plate import template” on page 95).
- Save the plate import template under a new name.
- Enter sample names (required).



4. (Optional) Enter information for the remaining columns. Note: If you specify assay, results group, or file name convention names, the names you enter must exactly match the names of existing items in the library.

---

**IMPORTANT!** If you copy/paste sample or plate information into the Assign Plate Contents screen or into a plate import file, copy from a plain text editor such as Notepad. Do not copy from a word processing program such as Microsoft™ Word™, which may include invisible, non-ASCII characters. Non-ASCII characters in plate or sample information may cause a run to stop or may prevent a run from starting.

---

5. Save the plate import file.

## Edit a plate

You can edit a plate from:

- **Library**—Select a plate, then click **Edit**.
- **Dashboard**—Click **Edit Existing Plate**.
- **Define Plate Properties** screen—Select **Open Plate** ▶ **Edit Existing Plate**.
- **Assign Plate Contents** screen—Select **Open Plate** ▶ **Edit Existing Plate**.

## Import and export a plate

You can import and export plates from:


- **Plates library**—Plates in .xml format for use on another 3500 instrument. See “Import and export a library entry” on page 165.
- **Define plate properties**—Plates in TXT, CSV, and XLS format—Files you create that contain plate information in a specific format.
- **Assign Plate Contents**—Plates in TXT, CSV, and XLS format—Files you create that contain plate information in a specific format.

## Create a plate template

A plate template contains default settings that you can edit when you create a plate from the template.

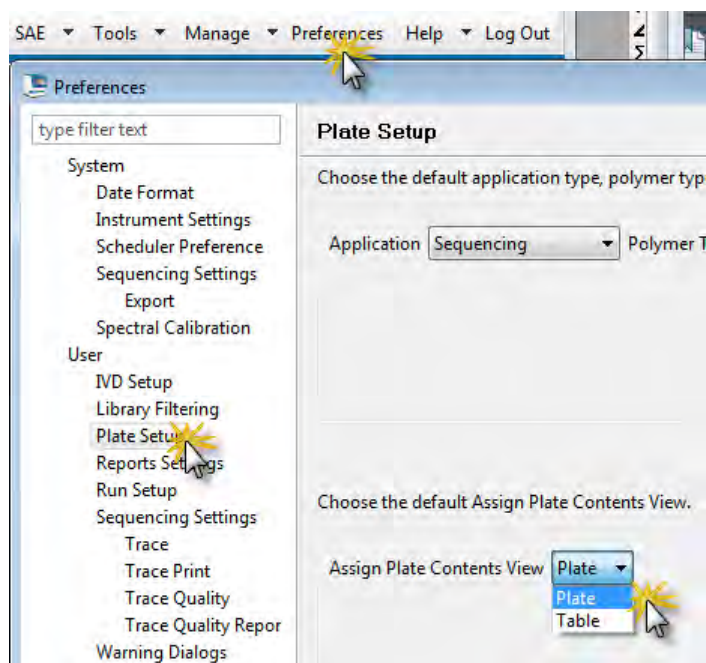
1. Create a plate (see “Create a new plate” on page 167).
2. (Optional) Add sample names and sample types (see “Name samples and assign sample types in the plate view” on page 63).
3. (Optional) Add the assays, file name conventions, and results groups appropriate for this plate template’s application (see “Add assays, file name conventions, and results groups to a plate” on page 95).

Adding assays, file name conventions, and results groups to the plate template automatically displays these items in the **Assign Plate Contents** screen when you open the plate template. You do not have to add these items from the library for each plate you create.

4. (Optional) Click **Show In Wells** to specify the attributes to display in wells in the template.
5. Select **Save Plate ▶ Save As Template**. The software displays the template icon  below the plate layout.

## Specify the default plate type for the Open Plate dialog box

Specify the default plate type for the **Open Plate** dialog box in **Preferences**.







## Save electronic version of reports

When you print any report, you can select a PDF printer to save the report to PDF.

## More features in Monitor Run

### Review the Instrument Run views

Select an injection, then click an instrument run view tab. As needed:

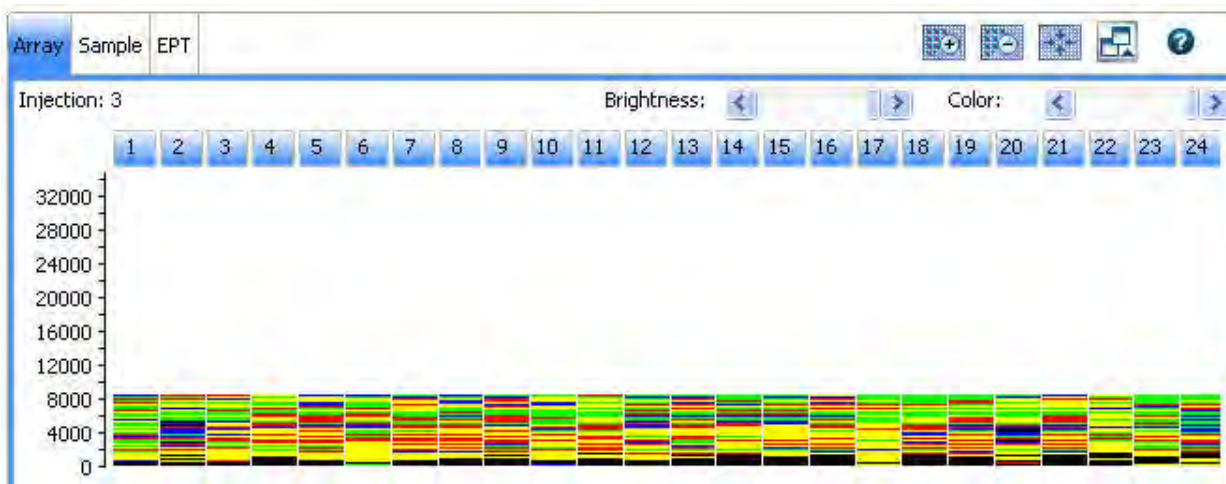
- Click    to zoom in and out.
- Click  to detach a view and display it in a separate window that you can move around on the screen.

To locate a detached view, click the 3500 task bar icon.



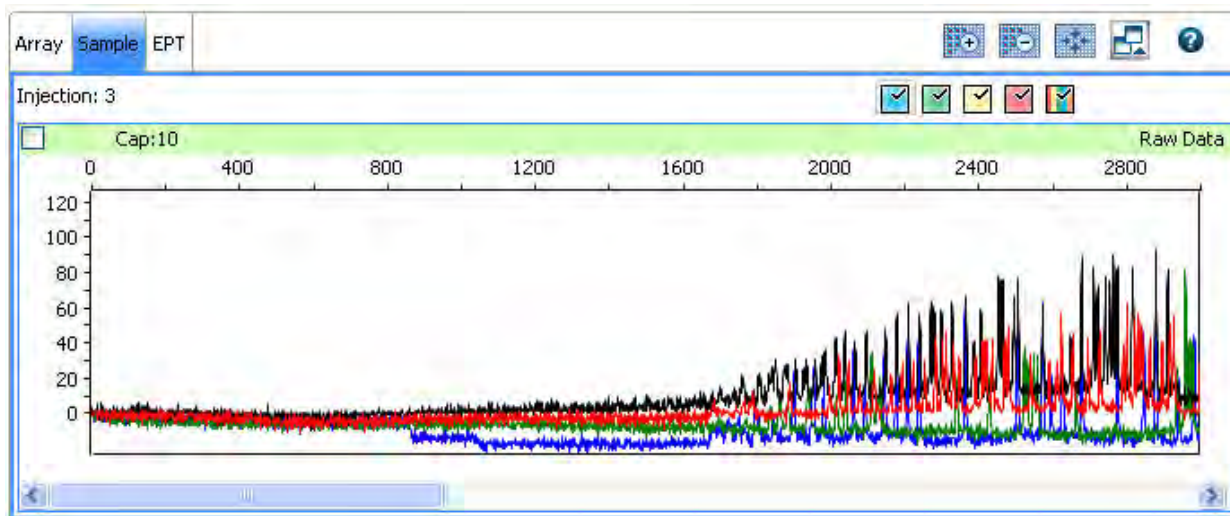
## Array view

The **Array** view shows the color data (based on the dominant fluorescence color) for each capillary as a function of instrument scan number (time). Adjust the brightness and color by using the slider bars above the view.



## Sample view

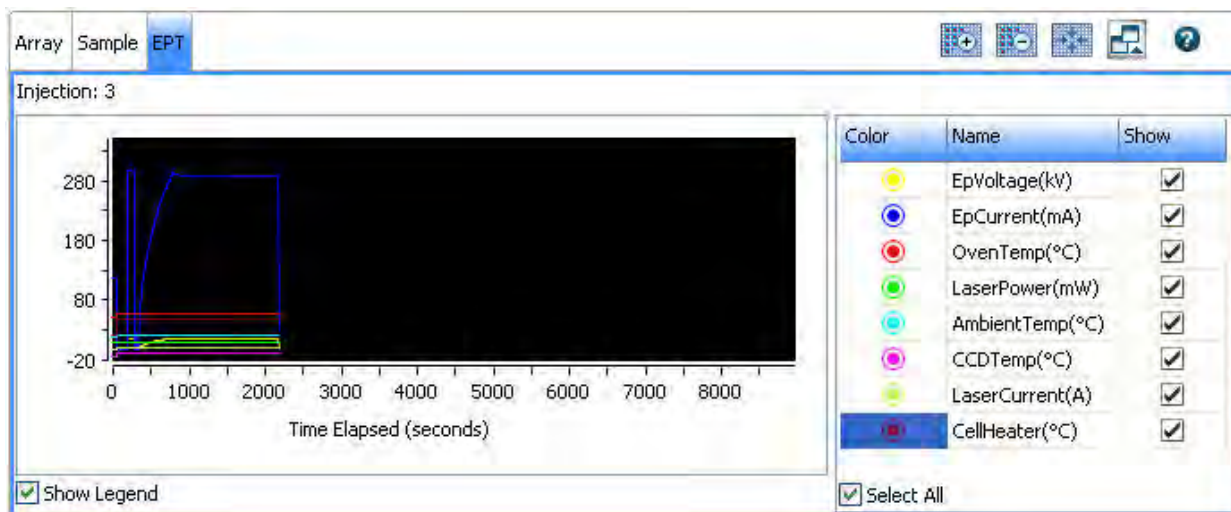
The **Sample** view shows the relative dye concentrations as a function of instrument scan number (time) for the selected capillary. You can select and deselect the dye colors to display.



## EPT view

The **EPT** view (ElectroPhoresis Telemetry) shows instrument data conditions (laser power, temperatures, electrophoresis voltage) as a function of time. In the legend to the right of the **EPT** view, you can select and deselect the traces to display in the view.

You can view the EPT plot for completed or terminated runs.





# Review sequencing results

- Workflow ..... 101
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## Workflow



## Access the View Sequencing Results screen


Access the View Sequencing Results screen from:

- The Monitor Run screen by clicking **Review Results**.
- The navigation pane by selecting **View Sequencing Results**.
- The Dashboard by clicking **View Run Results**.



## Review results for the currently running sequencing plate

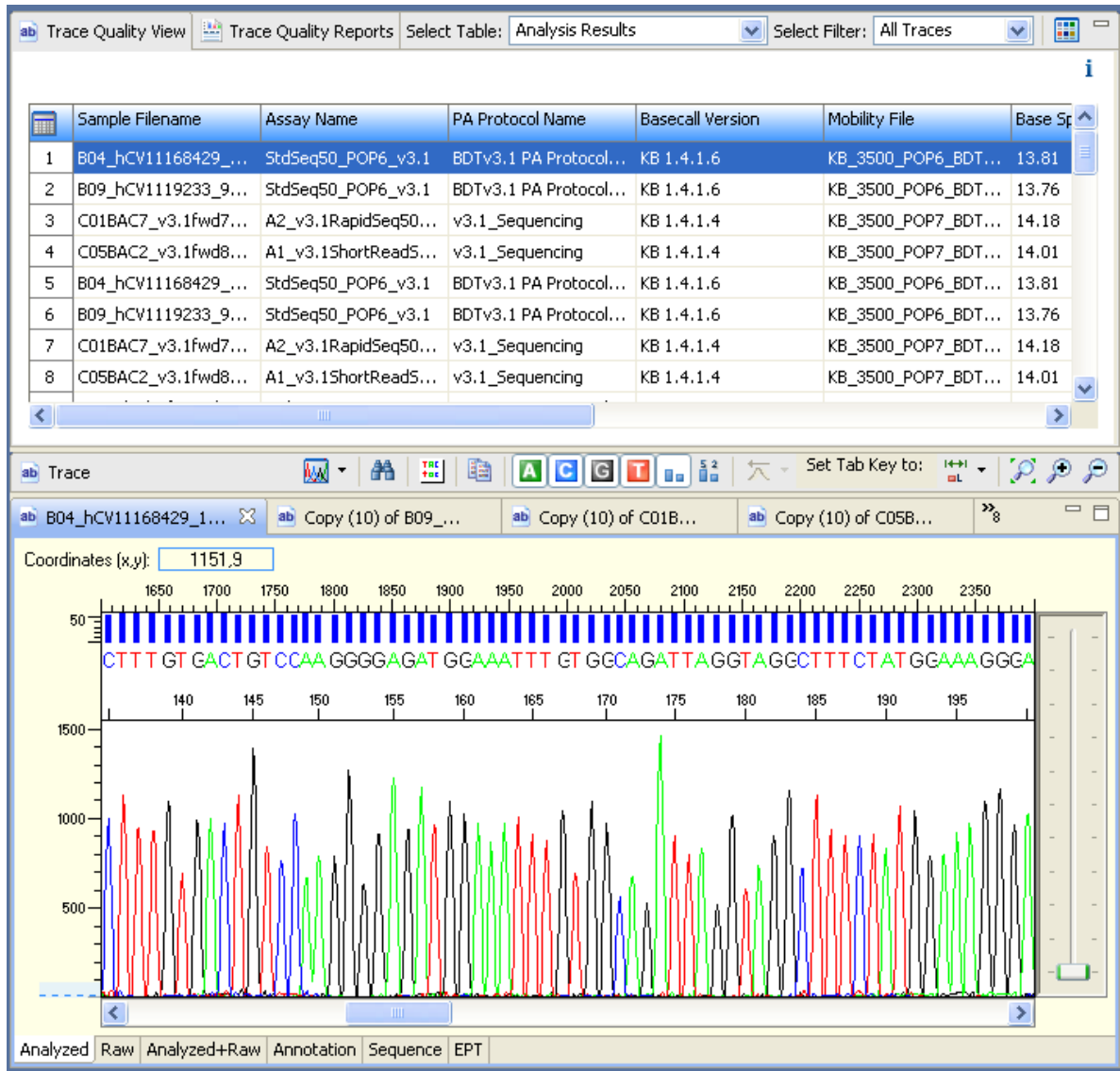
To view results for completed injections in the current run while a run is in progress:

1. Navigate to **View Sequencing Results** ▶ **Trace Quality View**.
2. Select one or more samples, then click  **Open Trace** to display the data in the Trace pane.

---


**Note:** The basecaller version listed in the basecalling protocol is limited to a 3-digit number. The version listed in sequencing results is a 4-digit number. The fourth digit is an internal number used by the software.

---



## Review previously run sequencing samples

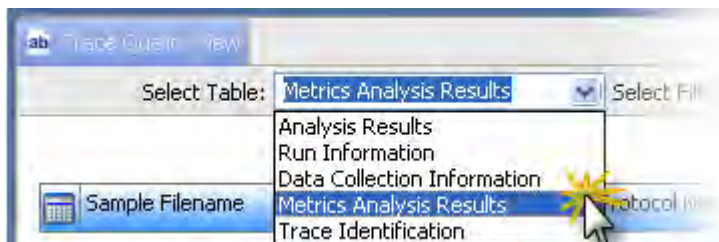
If you access the View Sequencing Results screen when no run is in progress and no plate is linked, no samples are listed. (If the plate from the most recent run is linked, the results from that plate are displayed.)

To view results for samples other than those from the most recent run, click  **Import**, then select the samples to review.

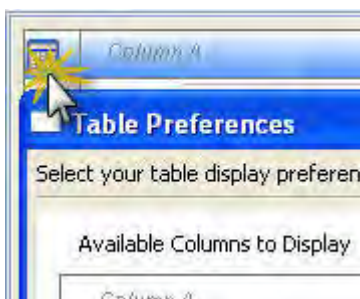


## Review sequence quality

1. Display **Metric Analysis** results to review sample basecalling and trimming results.



2. Click the **Table Settings** button, then specify the columns to show or hide.



3. Double-click column headers to sort columns. Multi-column sorting is supported (see “Sort by one or multiple columns” on page 94).

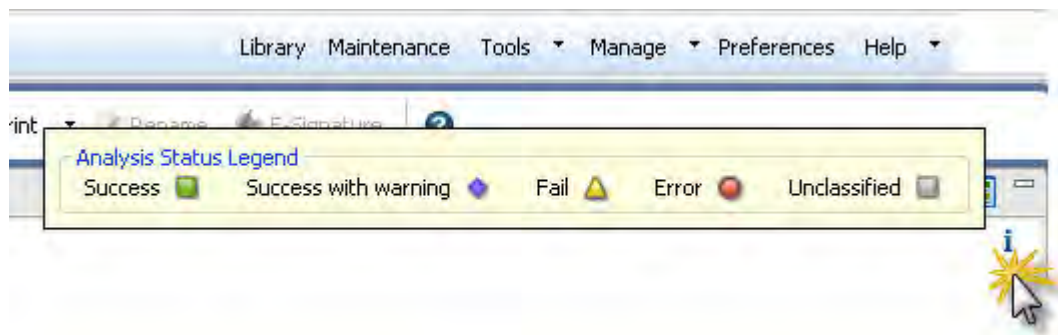


4. Review the results:






Result	Description
Trace Score	The average basecall Quality Value (QV) of basecalls in the clear range sequence of a trace. The <i>clear range</i> is the region of the sequence that remains after excluding the low-quality or error-prone sequence at the 5' and 3' ends. The clear range is calculated by the KB Basecaller using QVs.
CRL	The longest uninterrupted segment of basecalls with an average Quality Value (QV) $\geq 20$ . In addition to evaluating the QV of a basecall, the software considers the QV of adjacent basecalls within a 21-bp moving window to determine a contiguous read length based on quality values: the software starts from the 5' end and calculates the average QV across a moving window size of 21, sliding 1 bp at a time, to the 3' end. The resulting longest contiguous segment is determined as the CRL.
QV20+	The total number of bases in the entire trace with Quality Value $\geq 20$ .
Trace Score Quality CRL Quality QV20 Quality	Pass/fail/check determined by the settings in the <b>Basecalling protocol QV Settings</b> tab.
PUP Score	A measure of noise or pull-up that is determined by taking the mean of the ratios of signal strength calculated for each basecalled peak: primary peak/secondary peak under the primary peak. A higher value indicates less baseline or secondary noise. A lower value indicates an elevated baseline or secondary noise. Example 1: Main called base signal strength is 1,000 RFU and the largest secondary peak beneath it is 10 RFU; PUP=100 Example 2: Main called base signal strength is 1,000 RFU and the largest secondary peak beneath it is 100 RFU; PUP=10

5. Review warnings:

- a. Scroll to the right of the **Metric Analysis** table to display the Warning column.
- b. Display the **Analysis Status** legend.




## c. Review warnings:

Result	Description
 <b>Success</b>	Basecalling and trimming successful.
 <b>Success with warning</b>	Basecalling successful, trimming not successful. Warning messages are listed in the <b>Warning/Error Message</b> column (default position is the last column in the table).
 <b>Fail</b>	Basecalling and trimming failed, no results generated.
 <b>Error</b>	Basecalling and trimming failed due to internal software error, no results generated.
 <b>Unclassified</b>	No analysis performed.

6. (Optional) Click **Minimize** and **Restore** to collapse and expand the samples table.

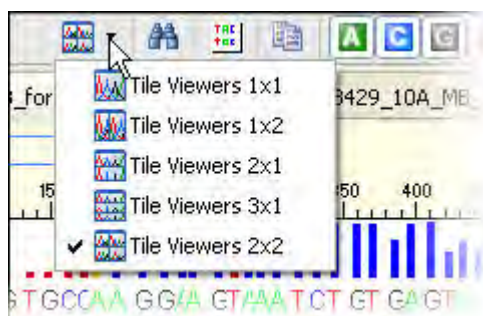
## Review traces

1. Select the samples of interest in the samples table, then click  **Open Trace**.
2. Select items from the trace toolbar to manipulate the trace as needed. Place the mouse pointer over a button for the description of the button.



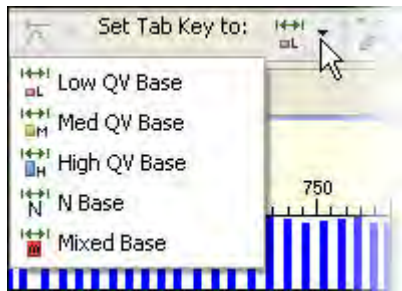
3. (Optional) Modify trace display:

- Use the **Tile Viewer** options to display up to four traces at a time.

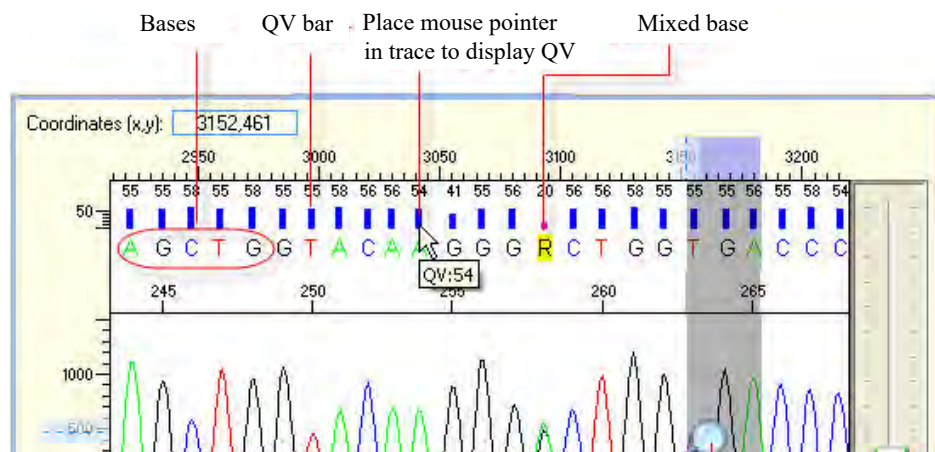


- Set trace colors in **Preferences** (see “Overview” on page 41).

4. Set the category of base for the **Tab** key.



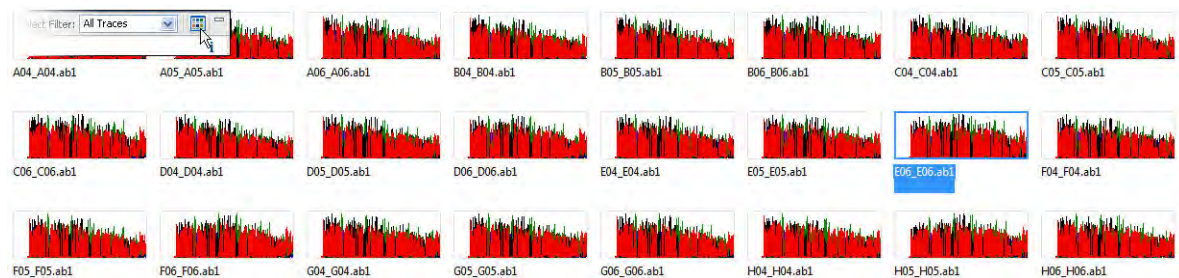
5. Review traces: press **Tab** to review bases from left to right in a trace. Press **Shift+Tab** to move right to left.



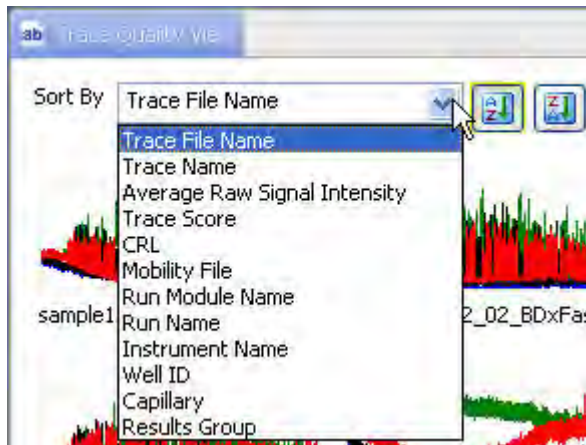
6. Click the tabs at the bottom of the trace pane for different views of the data.

## Display thumbnails

1. Click the **View Thumbnails** button to display results as thumbnails.



- Sort as needed.



- To compare signal across all samples on a plate, select **Uniform Y Scaling**.
- Click the **View Tables** button to close the thumbnail pane.

## Understand Quality Values (QVs)

### Quality value ranges

We recommend the following ranges for QVs (set in Preferences, see “Overview” on page 41):

- Pure bases: Low QV < 15, Medium QV = 15 to 19, High QV = 20+ (default).
- Mixed bases: Low QV < 5, Medium QV = 5 to 10, High QV > 10 (investigate to determine the best range for your application).

### Pure base versus mixed base QVs


Pure bases and mixed bases have the same probability of error for the associated basecall ( $10^{-q/10}$ ). Note the following:

- High-quality pure bases typically have QVs of 20 or higher.
- The distribution of quality values for mixed bases differs dramatically from that of pure bases.
- Mixed bases have a maximum QV of 20.
- Review all mixed base calls.

## Quality values (QV) and probability of error (Pe)

QV	Pe	QV	Pe
1	79.0%	30	0.10%
5	32.0%	35	0.032%
10	10.0%	40	0.010%
15	3.2%	45	0.0032%
20	1.0%	50	0.0010%
25	0.32%	60	0.00010%


## Re-inject samples from Review sequencing results

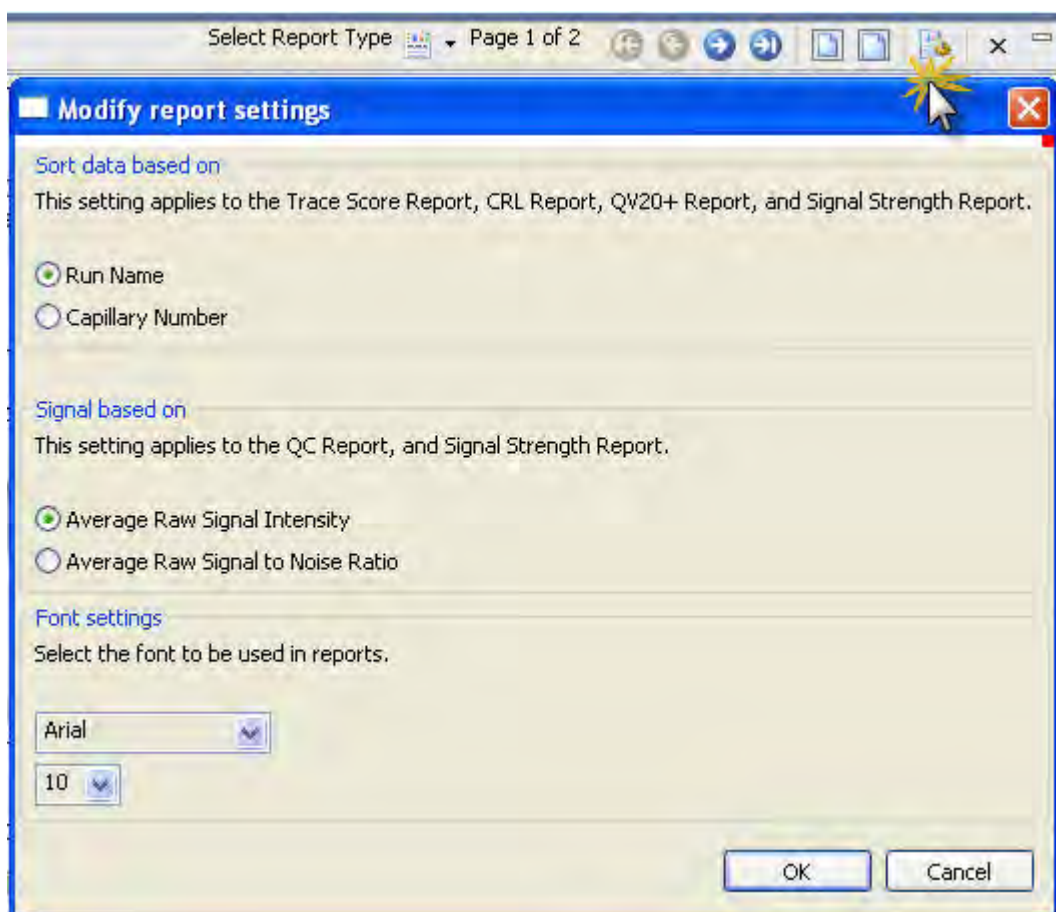
Before the run completes, select a sample with suspect or failing flags, then click  **Re-inject**. For information on making a re-injection before a run completes, see “Re-inject samples from the Monitor Run screen” on page 86.


## View, print, and save (PDF) trace quality reports

### View Trace Reports

**Note:** You can set defaults for the reports in **Preferences** (see “Set preferences (optional)” on page 41).

1. Click  **View Trace Reports**, then select a report type to view and print.
2. (Optional) Modify report settings. You can specify additional report settings in Preferences (see “Set preferences (optional)” on page 41).



3. Double-click different elements in the QC report to open the Trace view and display the associated sample.
4. To print the report, click  **Print**, then preview or print.
5. To save the report electronically (PDF), print the report and select a PDF printer.

## Report options

- **QC**—One-page bar chart that shows trace score statistics and results for each selected sample.
- **Plate**—One-page per plate for all selected samples that shows the well-location thumbnail raw data traces with color-coded headers that reflect Trace Score quality.
- **Trace Score, CRL, and QV20+**—One-page bar chart that shows trace score, CRL, or QV20+ statistics and results for each selected sample.
- **CRL Distribution**—One-page bar chart that shows CRL statistics and CRL results distribution for all selected samples.
- **Signal Strength**—One-page graph that shows the average sequencing dye signal strength for all selected samples.

## Export sequencing results

1. Filter the table of interest.
2. Select an export option: Results, Reports, or Traces.
3. Select the export options and the location for the export file, then click **OK**.  
The file(s) are exported to the specified location with the following naming conventions:
  - **Results**—`export_ReportName.txt`
  - **Reports**—`ReportName.*` (\* is the format you selected: .txt, .xls, .pdf, or .html)
  - **Traces**—`FileName.*` (\* is the format you selected: .annotation.txt, .phd.1, .scf, .fsta, .qual, or .seq)

## Modify sequence data

To edit, modify, or further analyze sequence data, import the sample data files into a secondary analysis software application such as SeqScape™ Software 3 (or later), MicroSEQ™ ID Analysis Software v3.0 (or later), Variant Reporter™ Software 2 (or later), and Sequence Analysis (SeqA) Software 6 (or later).





# Review fragment/HID analysis results

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## Workflow





## Access the View Fragment/HID Results screen

Access the View Fragment Results screen from:

- The Monitor Run screen by clicking **Review Results**.
- The navigation pane by clicking **View Fragment Results**.
- The Dashboard by clicking **View Run Results**.



## Export the injection list from Samples view

The injection list can be exported in a CSV, XLS, or TXT export file. The export file lists samples in the order in which they are displayed on the screen.

1. Select **View Fragment/HID results** in the left pane.
2. Create a table setting that includes **Injection Start Date** column.
3. Sort the table by sample file name, then by **Injection Start Date** column (which also includes the time of the injection).
4. Click **Export**.

## Review results for the currently running fragment/HID analysis plate

If you access the View Fragment Results screen while an instrument run is in progress, the samples table lists results for completed injections in the current run.

Select one or more samples in the samples table to display their data in the plot view and sizing table view.

The screenshot displays the 'View Fragment Results' software interface, which is divided into three main sections: a 'Samples View' table at the top, a 'Plot View' in the middle, and a 'Sizing Table View' at the bottom.

**Samples View:** This section contains a table with columns for Sample Name, Sample Type, Size Standard, Assay Name, Offscale, and Sizing Quality. Three samples are listed, all with 'Sample' as the type, 'GS600LIZ' as the size standard, and 'TM13\_G5' as the assay name. All 'Offscale' and 'Sizing Quality' indicators are green, signifying successful analysis.


**Plot View:** This section displays four chromatograms for different sample files: 1ng-6-B03.fsa, 1ng-7-C01.fsa, 1ng-8-C02.fsa, and 1ng-9-C03.fsa. Each plot shows 'Analyzed Data' with a y-axis ranging from 0 to 3000 and an x-axis from 80 to 400. The chromatograms show multiple peaks of varying heights and colors (blue, green, red, yellow).

**Sizing Table View:** This section provides a detailed table of peak data. It includes columns for Dye Color, Dye/Sample Peak, Sample File Name, Size, Height, and Area in Point. The table lists 11 peaks from the analyzed data.

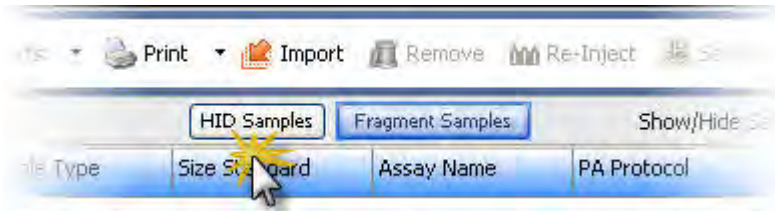
	Dye Color	Dye/Sample Peak	Sample File Name	Size	Height	Area in Point
49	Blue	B, 52	1ng-7-C01.fsa	327.21	1246	7962
50	Blue	B, 55	1ng-9-C03.fsa	327.18	1369	8360
51	Blue	B, 55	1ng-6-B03.fsa	327.16	1218	7966
52	Yellow	Y, 68	1ng-8-C02.fsa	325.75	59	424
53	Green	G, 57	1ng-6-B03.fsa	325.5	1190	8002
54	Green	G, 57	1ng-8-C02.fsa	325.49	1230	8275
55	Green	G, 57	1ng-7-C01.fsa	325.45	1224	8036
56	Green	G, 60	1ng-9-C03.fsa	325.42	1250	8009
57	Red	R, 66	1ng-6-B03.fsa	325.37	51	225
58	Blue	B, 54	1ng-6-B03.fsa	323.2	1339	8754
59	Blue	B, 54	1ng-8-C02.fsa	323.2	1434	8402

## Review previously run fragment analysis/HID samples

If you access the **Results** screen when no run is in progress and no plate is linked, no samples are listed. (If the plate from the most recent run is linked, the results from that plate are displayed.)

To view results for samples other than those from the most recent run, click , then select the samples to review.

By default, the Fragment Samples view is selected. If you are importing HID files, click **HID Samples**.




















## Review sample quality

1. In the samples view, click the **Table Settings** button, then specify the columns to show or hide.



2. Double-click **Offscale**, **Pull-Up (fragment)**, **Broad Peak (HID)**, and **SQ columns** to sort suspect and failing flags to the top of the table. Multi-column sorting is supported (see “Sort by one or multiple columns” on page 94).

Offscale	Spectral PullUp	Sizing Quality 1
		

Flag/ Symbols	Description
<b>Normalization Limit</b> 	<ul style="list-style-type: none"> <li>—Sample was collected with a normalization size standard, <b>SS Norm Factor</b> is within range.</li> <li>—Sample was collected with a normalization size standard, sample <b>SS Norm Factor</b> is not within range.</li> <li><b>No Data</b>—Normalization is enabled, but <b>Sizing Quality</b> is .</li> <li><b>NO</b>—Sample was not collected with a normalization size standard.</li> <li><b>N/A</b>—Sample was not collected on a 3500 instrument.</li> </ul> <p>For more information, see “Review normalized data” on page 117.</p> <p><b>Note:</b> If the <b>Sizing Quality</b> is , normalization is not applied, even if the <b>SS Norm Factor</b> is within the normalization range.</p>
<b>SS Norm Factor</b>	The size standard normalization factor that is applied to all peaks. See “Size standard normalization feature” on page 331. This factor is saved in the data file and applied during GeneMapper™ <i>ID-X</i> Software analysis if normalization is enabled in the GeneMapper™ <i>ID-X</i> Software Analysis Method ► Peak Detector tab.
<b>Avg Normalization PH</b>	The averaged peak height of the size standard peaks that were used to calculate the size standard normalization factor.
<b>Offscale</b> 	 At least one data point in the analysis range has saturated the CCD camera. <b>Note:</b> In the <b>Monitor Run</b> screen, an offscale sample is flagged with  .
<b>Spectral Pull-Up</b> (fragment analysis only) 	 At least one peak contains a pull-up peak. A <i>pull-up peak</i> is identified when the peak height of the minor peak is $\leq X\%$ of and within $\pm Y$ data point of the major peak, where X and Y are values you specify.
<b>Broad Peak</b> (HID analysis only) 	 At least one peak exceeds the Broad Peak threshold. Broad peaks affect Sizing Quality. See Chapter 8, “Manage library resources”. <b>Note:</b> The value displayed when you place the mouse pointer over a Broad Peak flag is an internal value and does not reflect the peak width.
<b>SQ: Sizing Quality</b> 	 The <b>Sizing Quality</b> is in the <b>Fail</b> or <b>Suspect</b> range. Place the mouse pointer over a flag to display the Sizing Quality value for the sample.


- Click a flag in the samples table, or select samples in the samples table to display the associated data in the plot view and sizing table view.
- (Optional) Modify the sample view:
  - Right-click the **Size Standard** field to view the size standard for a sample.
  - Click **Minimize** and **Restore** to collapse and expand the samples table.

## Review normalized data

Normalization corrects for instrument, capillary, and injection variability. When specified in the primary analysis protocol, the software calculates a size standard normalization factor for each sample. The size standard normalization factor is used as a multiplier to adjust the peak height of the sample peaks relative to the size standard peaks.

A sample is normalized if it is collected with a normalization size standard (specified in the primary analysis protocol [sizecalling or QC] in the assay).

---

**Note:** If the **Sizing Quality** is , normalization is not applied, even if the size standard normalization factor is within the normalization limits set in the instrument protocol. Ensure that you use the normalization size standard appropriate for your application.


---

## How normalization is applied

To normalize, the software:

1. Determines if the data was collected on a 3500/3500xL Genetic Analyzer.
2. Determines if the sample was collected with a normalization size standard definition file (normalization is enabled).
3. If normalization is enabled, the software calculates a size standard normalization factor for the sample using multiple size standard fragments. The size standard normalization factor is calculated by dividing the **Normalization Target** from the instrument protocol by the observed average peak height of the size standard fragments in the samples.
4. Compares the size standard normalization factor to the thresholds (set in the instrument protocol).
5. If the calculated size standard normalization factor is within the normalization factor range, multiplies the peak heights of the sample by the calculated size standard normalization factor.
6. If the calculated size standard normalization factor is outside the normalization factor range, multiplies the peak heights of the sample by the maximum or minimum normalization factor threshold setting. For example, if the normalization factor range is 0.3 to 3.0 and the calculated size standard normalization factor is 5, the software applies a size standard normalization factor of 3.0.
7. Displays normalization information in the Samples view.

## Normalization factor in secondary analysis

If normalization is applied in the 3500 Series Data Collection Software v3.3, the calculated size standard normalization factor is stored with the raw data and is applied to the raw data in the GeneMapper™ Software 5 and the GeneMapper™ ID-X Software v1.2 or later secondary analysis software. You can turn normalization off and on in the analysis method used in the GeneMapper™ Software 5 and GeneMapper™ ID-X Software v1.2 or later secondary analysis software. If normalization is not applied in the 3500 Series Data Collection Software v3.3 (either a normalization size standard was not used, or sizing failed , normalization cannot be applied in the secondary analysis software.

## Review plots

1. Select the samples of interest in the samples table.
2. Select items from the plot toolbar to manipulate the plot as needed. Place the mouse pointer over a button for the description of the button.




---

**IMPORTANT!** If you first view a 4-dye sample, then view a 5-dye sample, you must manually select the fifth dye. It is not automatically selected when you switch to a 5-dye sample.


---

3. Click  to apply scaling settings to plots: Enter the range for Y axis and X axis, then click the **Zoom** buttons.

---





**IMPORTANT!** You must open Plot Settings each time you access the View Results screen, then click **Zoom**. Scaling settings are not automatically applied when you access this screen, or when you click Apply.

---

To apply scaling settings to all samples in the samples table, select all of the samples in the samples table to display them in the plot view, specify the scaling settings, click **Zoom**, then click **Page Up** and **Page Down** in the plot view to move through the samples. If the  button is dimmed, the Plot Settings dialog is open. Click the **3500** task bar icon, then select **Plot Settings**.



4. Display multiple plots as needed: In the Plot Settings Display tab, select **Checkerboard**.
5. Click a peak to label it (to label all peaks, see “Label peaks” on page 119).


## Zoom on data

1. Place the pointer *above the top* of the plot or *to the left* of the plot at the start of the area you want to zoom, then click to turn the pointer to .
2. With the  still *above* the plot or *to the left* of the plot, click-drag to the end of the area you want to zoom. Do not drag the  inside the plot area. Doing so changes  back to a pointer and does not zoom as expected.




You can also click zoom and fit buttons to zoom   .

## Change plot settings


Click  (Plot Settings) in the plot view toolbar. For information on plot settings, click  in the plot settings tabs.

If the  button is dimmed, the **Plot Settings** dialog is open. Click the 3500 task bar icon, then select Plot Settings.

## Overlay samples

1. Select samples in the samples view to display the plots.
2. Click  **Overlay All**.  
When  **Combine Dyes** is selected, the plot view displays one plot with all samples and all dyes. When  **Separate Dyes** is selected, the plot view displays one plot per dye. Each dye plot contains all samples.

## Label peaks

1. Select samples in the samples view to display the plots.
2. Click  (Plot Settings) in the plot view toolbar, then select the **Labels** tab.

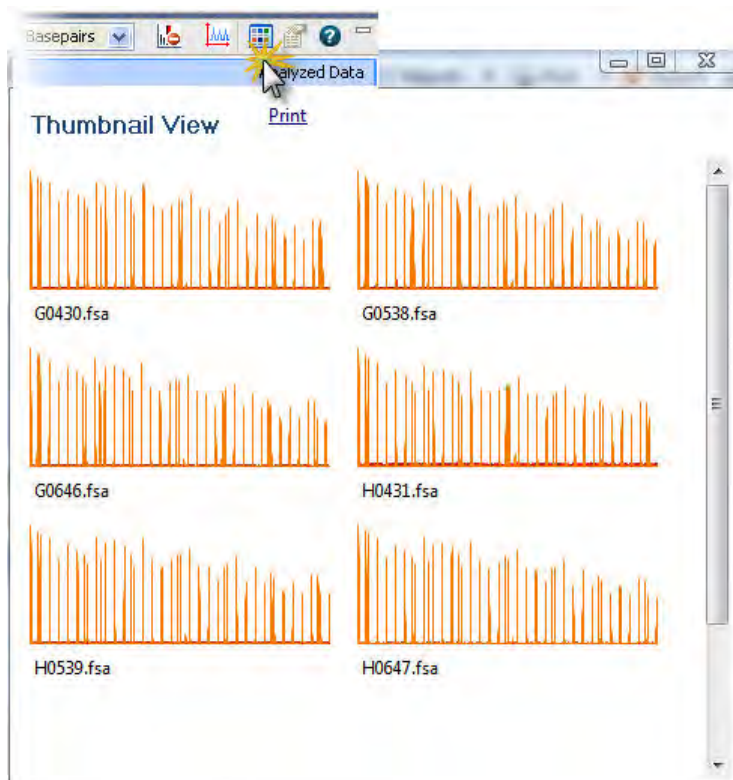


3. Label peaks:

If you have ...	Then ...
Already specified default labeling preferences	<ol style="list-style-type: none"> <li>1. Select <b>Show Peak Labels</b>.</li> <li>2. Click <b>Label Peaks</b>.</li> <li>3. Click <b>Apply</b>.</li> </ol> <p><b>IMPORTANT!</b> You must open <b>Plot Settings</b> each time you access the <b>View Results</b> screen, then click <b>Label Peaks</b>. Labeling settings are not automatically applied when you access <b>View Results</b>, or when you click <b>Apply</b>.</p>
Not specified default labeling preferences	<ol style="list-style-type: none"> <li>1. In <b>Labels to Show</b>, select the needed labels.</li> <li>2. In <b>Labeling Options</b>: <ul style="list-style-type: none"> <li>• Select <b>Show Peak Labels</b>.</li> <li>• To label all peaks with the selected labels, click <b>Label Peaks</b> (make sure <b>All</b> is selected).</li> <li>• To label selected peaks, select the category from the <b>Label Peaks</b> list (<b>Height, Area, Size</b>), specify the range to label for the selected category (for example, if you select <b>Height</b>, specify the height range of the peaks to label), then click <b>Label Peaks</b>.</li> <li>• Select <b>Retain Labels</b>.</li> </ul> </li> <li>3. Click <b>Save to Preferences</b> to save these settings for future use. You can change preferences at any time.</li> <li>4. Click <b>Apply</b>.</li> </ol>


## View thumbnails

Click the **View Thumbnails** button to display the traces for the samples selected in the samples view and the dyes selected in the plot view.



## Rename samples

To rename sample files:

1. In the **Sample Name** column, select the samples to rename, or click the Sample Name column header to select the entire column.
2. Click  **Rename**.
3. In the **Search** field, enter the sample name to change.
4. In the **Rename** field, enter the new name.
5. Click **Search**, then click **Rename**.



## Sort by one or multiple columns

Double-click column headers to sort. To sort by multiple columns:

- Double-click a column header to sort the column.
- Alt+Shift-click another column header to sort another column.
- Alt+Shift-click a third column header to sort a third column.

Numbers in the column headers reflect sort order.



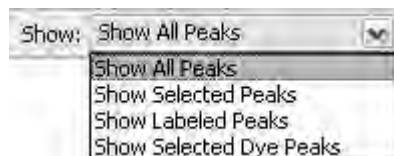
## Review sizing

The Sizing Table View displays:

- **For fragment samples**—All dyes
- **For HID samples**—Size standard dye only (orange or red)

## Set up the sizing table

1. Select samples in the samples table to display the plots.
2. In the sizing table, click the **Table Settings** button, then specify the columns to show or hide.
3. Filter the table as needed.



4. Double-click column headers to sort columns. Multicolumn sorting is supported (see “Sort by one or multiple columns” on page 94).
5. Selecting rows in the sizing table, then click **Label Selected Peaks**.

## Examine the size standard plot


1. In the plot view toolbar, deselect all dye colors except the size standard dye color (red or orange).
2. In the sizing table, select the size standard peaks of interest.

3. Click **Label Selected Peaks** to label the size standard peaks in the plot view.


**Note:** If labels are not displayed, click  (Plot Settings) in the plot view toolbar, then select **Show Labels** in the Labels tab. Click **Save to Preferences** to retain this setting.

4. Ensure that all size standard peaks are present and correctly labeled.


## Overlay the sizing curve

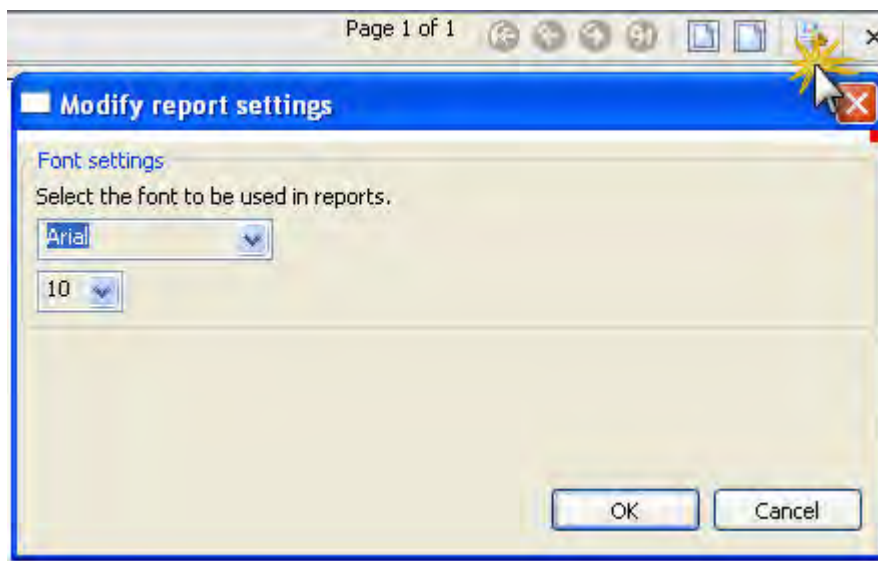
1. Click  (Plot Settings) in the plot view toolbar.
2. Select **Overlay Sizing Curve** in the Display tab.

## Re-inject samples from Review fragment results

Before the run completes, select a sample with suspect or failing flags, then click  **Re-inject**. For information on making a re-injection before a run completes, see “Re-inject samples from the Monitor Run screen” on page 86.

## View, print, and save (PDF) sample quality reports

1. Select the samples of interest in the samples table.
2. Click  **Reports**, then select a report type to view and print. Reports are displayed in the sizing table view at the bottom of the screen.  
Reports are displayed in the sizing table view at the bottom of the screen.
3. (Optional) Modify report settings.



4. To print the report, click  **Print**, then preview or print.

## Report options

- **Sizing**—One page per selected sample that shows the quality ranges set in the sizecalling or QC protocol, the quality values for the sample, and the electropherogram for the sample. Plot zooming is not retained in the report.
- **Overlay**—One page for all selected samples that shows the size standard dyes overlaid with the size standard curves.
- **Plate**—One page per plate for all selected samples that shows the well-location thumbnail traces with color-coded headers that reflect sizing quality. Plot zooming is not retained in the report.

## Export sizing results

1. Set up the sizing table (see “Set up the sizing table” on page 121). All rows and columns displayed in the sizing table are exported.
2. Click **Export Results**.

## Modify fragment analysis or HID data

To edit, modify, or further analyze fragment analysis or HID data, import the sample data files into a secondary analysis software application such as:

- **Fragment analysis**—GeneMapper™ Software 5 (or later)
- **HID**—GeneMapper™ *ID-X* Software v1.2 (or later)



# Run calibrations and install checks

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■	Run a Sequencing install check .....	144
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## Section 7.1 Run spatial and spectral calibrations

### Run a spatial calibration

#### Spatial calibration overview

The software uses images collected during the spatial calibration to establish a relationship between the signal emitted by each capillary and the position where that signal falls on, and is detected by, the CCD camera.

#### When to perform a spatial calibration

Perform a spatial calibration after you:

- Remove or replace the capillary array.
- Replace the capillary array when it expires.

---

**Note:** When the instrument reads the information from a newly installed capillary array, you are required to run a spatial calibration and a spectral calibration before you can run plates.

---

- Open the detector door or move the detection cell.
- Move the instrument.

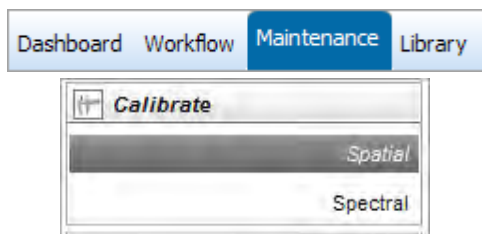
#### Perform a spatial calibration

---

**IMPORTANT!** Do not open the instrument door during a spatial calibration run. Doing so will stop the run and require you to restart the software.

---

1. In the **Dashboard**, preheat the oven if you will be selecting the **Fill** option for the calibration (fill the array with polymer).
2. Click the **Maintenance** menu, then select **Calibration ▶ Spatial**.



---

**Note:** The screen does not display results unless you have previously performed a spatial calibration.

---

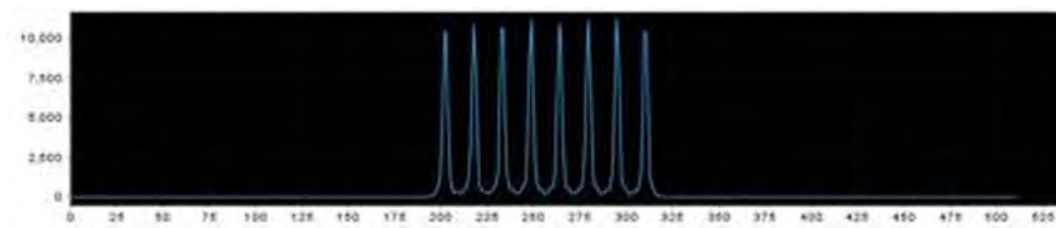
3. Select **No Fill**, or select **Fill** to fill the array with polymer before starting the calibration.
4. Select **Perform QC Checks**.

5. Click **Start Calibration**.

During the calibration, the software performs quality checks and calculates the following values:

Attribute	Calculation	Threshold
Average peak height	(sum of all peak heights) divided by (number of peaks)	<ul style="list-style-type: none"> <li>8-cap: 6,400 RFU</li> <li>24-cap: 3,000 RFU</li> </ul>
Individual peak height	Peak height	1,000 RFU
Uniformity (peak height similarity)	(standard deviation) divided by (average peak height)	0.2
Capillary spacing	max. spacing - min. spacing	2 pixels

The display updates as the run progresses.



- A signal optimization factor is calculated for each capillary using a fitted curve method. The fitted curve method minimizes background and reduces noise. The adjusted spatial intensity, not the spatial intensity displayed for the capillary, is used to calculate the signal optimization factor.

The signal optimization factors are applied during data collection to minimize optical variation effects and increase signal uniformity between capillaries.

- If any of the QC check calculations do not meet a threshold condition, a Spatial QC Check error message is displayed.

## Evaluate the spatial calibration profile

When the run is complete:

1. Evaluate the spatial calibration profile to ensure that you see:
  - One sharp peak for each capillary. Small shoulders are acceptable.
  - One marker (+) at the apex of every peak. No off-apex markers.
  - An even peak profile (all peaks about the same height).
2. If the results meet the criteria above, click **Accept Results**.  
If the results do not meet the criteria above, the **Accept** button is dimmed. Go to “Spatial calibration troubleshooting” on page 298.

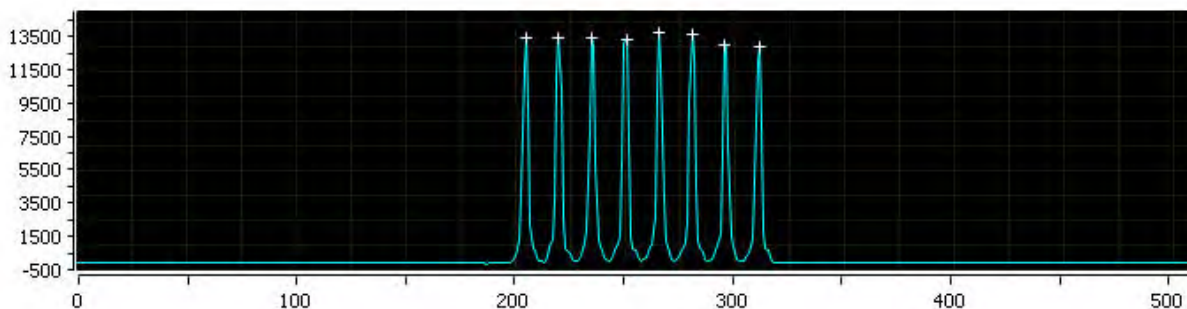
---

**IMPORTANT!** Do not log off or close the software before clicking Accept Results. Spatial calibration results are not saved until you click Accept Results.

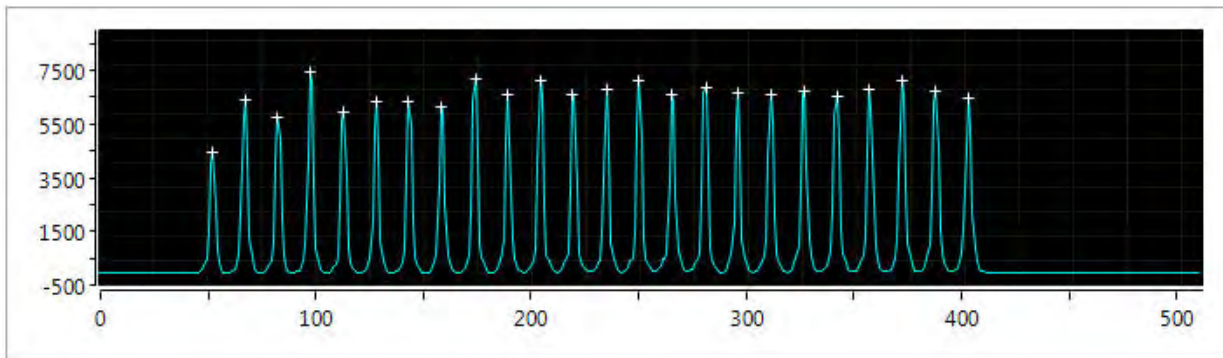
---

## Example spatial profiles

### 8-capillary spatial

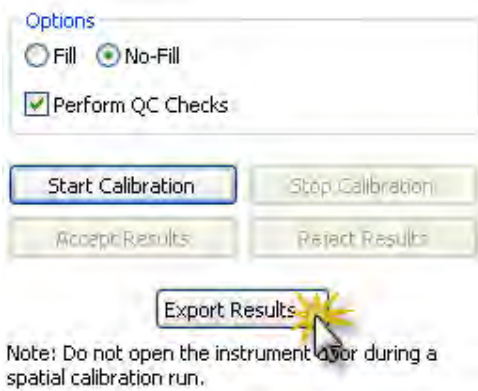


### 24-capillary spatial



## Export spatial calibration results

1. Click **Export Result**.



2. Enter an export file name.
3. Select the export file type, then click **Save**.



The export file contains the following results:



- **Capillary Number**
- **Position** (pixels)
- **Spacing**
- **Intensity**

## View and print a calibration report

---

**Note:** Spatial and spectral calibration reports include the date on which a capillary array is installed for the first time on the instrument. Install standard reports use the most recent install date if a capillary array was removed and re-installed on the instrument.

---



1. Click  **View Report**.
2. (Optional) In the **Report** screen, click toolbar options to manipulate the report. Place the mouse pointer over an item for a description of the item.
3. To print the report, click  **Print**.

## Save historical reports (PDF) for record keeping

---

**IMPORTANT!** Save a report electronically for record keeping. The software does not save historical results. Only the most recent results are maintained in the software.

---

1. Click  **View Report**.
2. Click  **Print**.
3. In the **Printer** dialog box, select a PDF printer.
4. Specify a name and location for the report.

## Run a spectral calibration

### Spectral calibration overview

A spectral calibration creates a de-convolution matrix that compensates for dye overlap (reduces raw data from the instrument) in the dye data stored in each sample file.

---

**IMPORTANT!** To calibrate a custom dye set using AnyDye, first create the dye set, then select the name of the custom dye set from the Dye Set list. The AnyDye selection in the Dye Set list contains default settings. It does not correspond to custom dye sets created with the AnyDye dye set template.

---

## When to perform a spectral calibration

Perform a spectral calibration when you:

- Use a dye set that you have not previously calibrated
- Replace the capillary array for maintenance purposes
- Replace the capillary array when it expires (the expiration date is indicated on the packaging and the RFID tag)

---

**Note:** When the instrument reads the information from a newly installed capillary array, you are required to run a spatial calibration and a spectral calibration before you can run plates.

---

- See a decrease in spectral separation (pull-up/pull-down in peaks) in the raw or analyzed data
- 

**Note:** For sequencing applications, you can skip this process, and run the Sequencing install check. If you select **Keep Spectral Calibration Data** in the Install Check, the software runs a spectral calibration for the dye set during a sequencing check and allows you to save the spectral calibration data. For information, see “Run an install check” on page 144.

---

## Estimated run time

**Note:** The run times listed below do not include the time for the oven to preheat to 60°C.

Application	Standard	Polymer type	Run time (min)
Sequencing	Sequencing standard	POP-6™ polymer	≤135
Sequencing	Sequencing standard	POP-7™ polymer	≤40
Fragment analysis	Matrix standard	Any polymer	≤75

## Prepare for spectral calibration

### Before you begin

If you have not already done so, perform a spatial calibration (see page 125).

### Prepare the instrument

1. In the **Dashboard**, check consumables status (see “Check consumables status” on page 37).  
Ensure that:

- Consumables are not expired
- Adequate injections remain for consumables

2. Ensure that buffer levels are at the fill lines (see “Check buffer fill levels” on page 39).

3. Set the oven temperature, then click **Start Pre-heat**.

Pre-heat the oven and detection cell while you prepare for a run (detection cell temperature is set by the software). Pre-heating helps mitigate subtle first-run migration rate effects. The pre-heat function automatically turns off after 2 hours.

We recommend that you pre-heat the oven for at least 30 minutes before you start a run if the instrument is cold.

Temperatures are displayed in red as they warm to the set-points. When temperatures are at the set-point they are displayed in green. Temperatures may fluctuate slightly when they reach the set-point as they stabilize.

4. Check the pump assembly for bubbles and run the **Remove Bubble wizard** if needed (see “Remove bubbles from the polymer pump” on page 268).

### Prepare the spectral calibration standard

Prepare the matrix or sequencing standard appropriate for your application as described in the product insert. See Appendix D, “Catalog numbers” for catalog numbers.


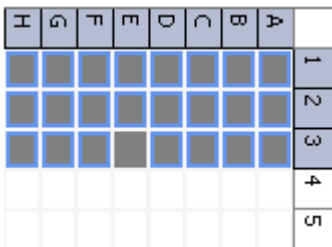
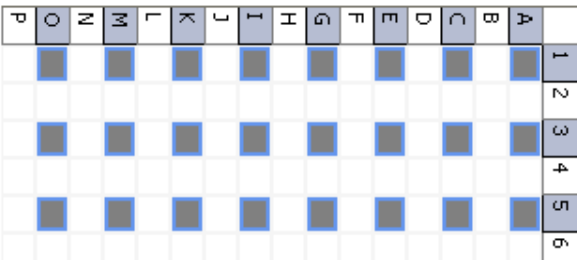
If peaks are offscale for G5, F, and E5 dye sets, dilute the matrix standard and repeat the calibration.

### Prepare the standard plate

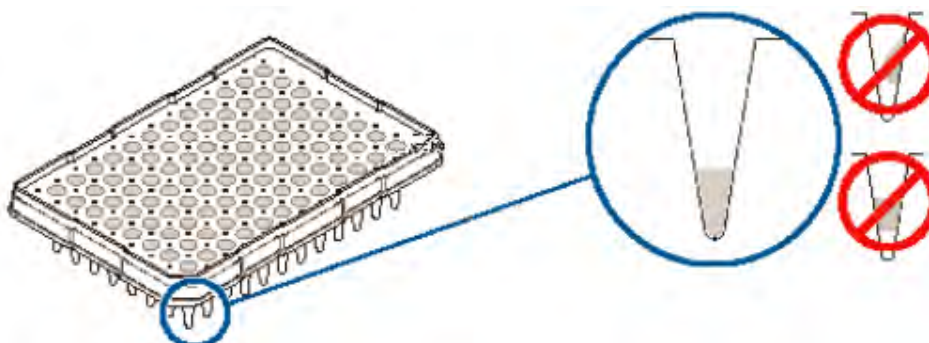
**IMPORTANT!** Do not use warped or damaged plates.

1. Load the standards in any injection position in the plate. The example below shows injection position 1, but you can specify the starting well for an injection position.

**IMPORTANT!** You do not create a plate in the software for the install check.

<p>8-capillary 96-well plate</p>	<p>A1 through H1</p> 
<p>24-capillary 96-well plate</p>	<p>A1 through H1, A2 through H2, and A3 through H3</p> 
<p>24-capillary 384-well plate</p> <p><b>Note:</b> 384-well plates are not supported on 8-capillary instruments.</p>	<p>Columns 1, 3, and 5 in rows A, C, E, G, I, K, M, O</p> 

2. Briefly centrifuge the plate that contains the standards.
3. Verify that each standard is positioned correctly in the bottom of its well.



---

**IMPORTANT!** If the contents of any well contain bubbles or are not located at the bottom of the well, briefly centrifuge the plate, remove the plate from the centrifuge, and verify that each standard is positioned correctly in the bottom of its well.

---

4. Store the plate on ice until you prepare the plate assembly and load the plate in the instrument.
5. Prepare the plate assembly as described in “Prepare the plate assembly” on page 70.

### Load the plate in the instrument

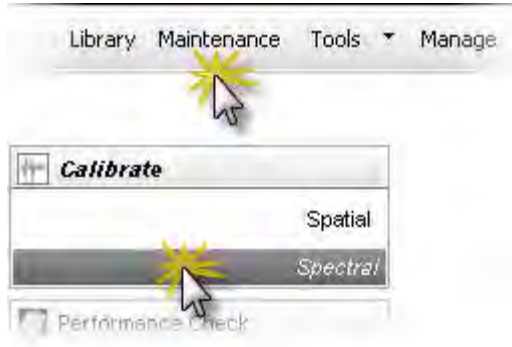
1. Click the Tray button on the front panel to move the autosampler to the front position, then open the instrument door.
2. Place the plate in the autosampler with the labels facing you (or the instrument door) and the notched corner of the plate in the notched corner of the autosampler.
3. Close the instrument door to initialize the instrument.

## Perform a spectral calibration

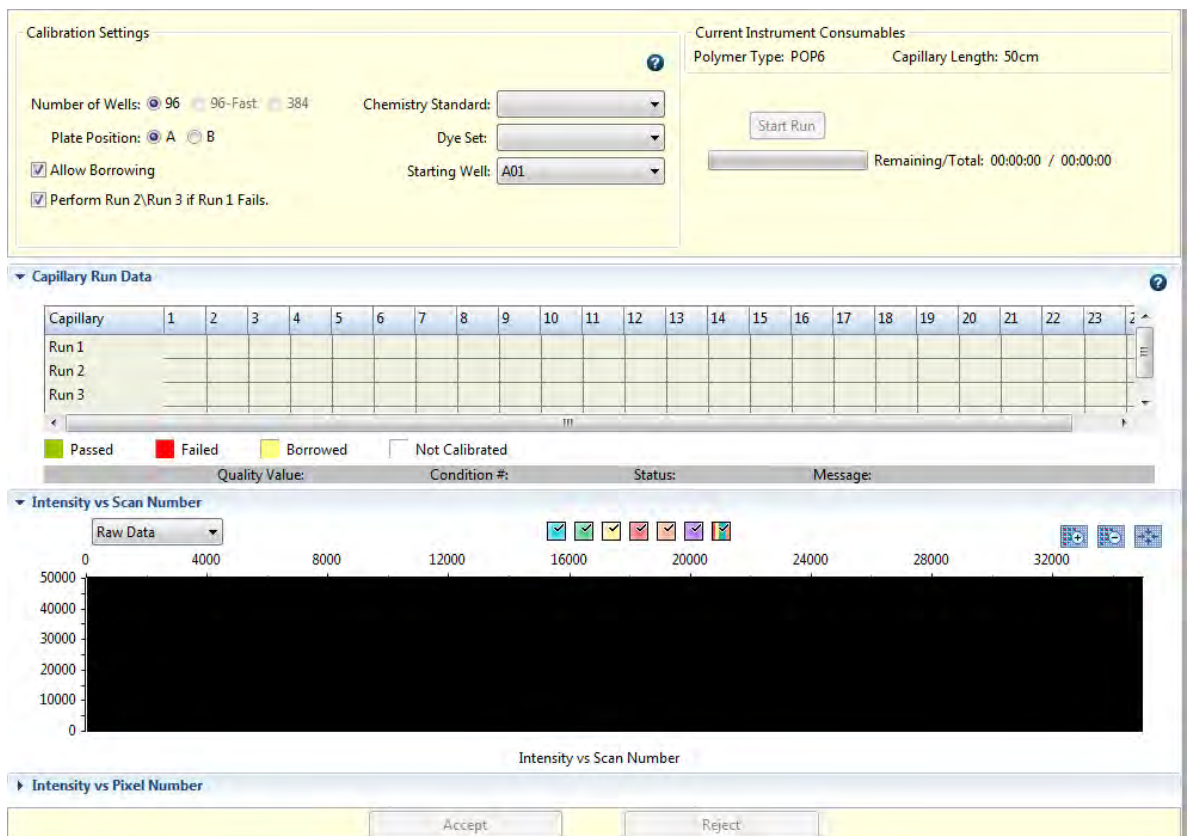
**IMPORTANT!** Do not change E-Signature settings during a spectral calibration.

**IMPORTANT!** If you change polymer type, spectral calibrations for the original polymer type are not retained.

1. Access the **Spectral Calibration** screen.



**Note:** The screen does not display results until you perform a spectral calibration. To view previous calibration data, click **History View**.



2. Select the number of wells, standard, and dye set.
3. Select the plate position for the plate loaded in the instrument.

---

**Note:** You do not create a plate in the software for the calibration.

---

4. Specify the starting well for the injection position in which you loaded the standard in the plate.
5. For **Chemistry Standard** and **Dye Set**, select:

---

**Note:** For the BigDye™ Direct DNA PCR Amplification/ Clean-up/Cycle Sequencing kit, use dye set Z.

---

Chemistry standard	Dye set	Application
Sequencing standard v1.1	E	Sequencing
BigDye™ Terminator v1.1 matrix standard	E	Sequencing
Sequencing standard v3.1	Z	Sequencing
BigDye™ Terminator v3.1 matrix standard	Z	Sequencing
DS-32 Matrix Standard Kit (Dye Set F)	F	Fragment analysis
DS-02 Matrix Standard Kit (Dye Set E5)	E5	Fragment analysis
DS-30 Matrix Standard Kit (Dye Set D)	D	Fragment analysis
DS-33 Matrix Standard (Dye Set G5)	G5	Fragment analysis
DS-36 Matrix Standard Kit (Dye set J6, 6-dye)	J6	Fragment analysis
DS-37 Matrix Standard Kit (Dye set J6-T, 6-dye)	J6-T	Fragment analysis
Custom	AnyDye	Fragment analysis

---

**IMPORTANT!** The E-signature function creates a record when a spectral calibration is performed, but does not record the dye set calibrated. To include the dye set calibrated in the E-signature record, enter the dye set in the E-Sig Comments field.

---

6. (Optional) Select **Allow Borrowing**. Selecting this option instructs the software to automatically replace information from failed capillaries with information from an adjacent passing capillary with the highest Quality value. For more information, see “What you see during a spectral calibration” on page 138.

7. Click **Start Run**. The following occurs:

- A **Progress Information** message with a dimmed **Cancel** button is displayed. The message is displayed for several minutes while the instrument checks system components. You cannot cancel the calibration during this initialization period. When the initialization is complete, the **Progress Information** message automatically closes. The **Abort** button is displayed at the top of the screen.
- If you used the default setting "**Perform run 2 and 3 if run 1 fails**", the instrument sets up three injections (see "What you see during a spectral calibration" on page 138 for information on the number of injections performed).
- The **Capillary Run Data** display updates after each injection is complete.
- The status bar updates during Run 1.

---

**IMPORTANT!** The status bar does not update during Run 2 or Run 3.

---

- Passing and failing capillaries are shown in green and red respectively. Borrowed capillaries are shown in yellow with an arrow indicating the adjacent capillary from which results were borrowed.

To display the result for each capillary (spectral data, **Quality Value**, and **Condition Number**) below the run results table, click a capillary in the table.

**Note:** The results displayed when you click a borrowed capillary are the passing results borrowed from the adjacent capillary. To determine the reason that a capillary fails, view the spectral calibration report. See "View and print a calibration report" on page 129.

Capillary	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
Run 1	Failed	Passed	Passed	Passed	Passed	Passed	Passed	Passed	Passed	Passed	Passed	Passed	Passed	Passed	Failed
Run 2															
Run 3															
Overall	Borrowed	Passed	Passed	Passed	Passed	Passed	Passed	Passed	Passed	Passed	Passed	Passed	Passed	Passed	Passed

■ Passed   
 ■ Failed   
 ■ Borrowed   
 ■ Not Calibrated

Capillary 1 - Run 1    Quality Value: 0.999513    Condition #: 3.47569    Status: Passed

For all spectral calibration injections (even capillaries that are green in the **Overall** row), evaluate the data as described in the next section.

## Spectral Quality Values and Condition Numbers

### Spectral Quality Value

A spectral Quality Value reflects the confidence that the individual dye emission signals can be separated from the overall measured fluorescence signal. It is a measure of the consistency between the final matrix and the data from which it was computed. A Quality Value of 1.0 indicates high consistency, providing an ideal matrix with no detected pull-up/pull-down peaks.

In rare cases, a high Quality Value can be computed for a poor matrix. This can happen if the matrix standard contains artifacts, leading to the creation of one or more extra peaks. The extra peaks cause the true dye peak to be missed by the algorithm, and can lead to a higher Quality Value than would be computed with the correct peak. Therefore, it is important to visually inspect the spectral calibration profile for each capillary.

### Condition Number

A Condition Number indicates the amount of overlap between the dye peaks in the fluorescence emission spectra of the dyes in the dye set.

If there is no overlap in a dye set, the Condition Number is 1.0 (ideal conditions), the lowest possible value. The condition number increases with increasing peak overlap.

The ranges that the software uses to determine if a capillary passes or fails are:

Dye set	Quality Value minimum	Condition Number maximum
AnyDye	0.8 (default)	20.0 (default)
D	0.95	8.5
E	0.95	5.5
E5	0.95	6.0
F	0.95	8.5
G5	0.95	13.5
J6 or J6-T	0.95	8.0
Z	0.95	5.5



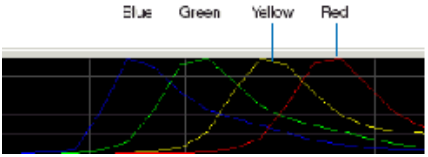
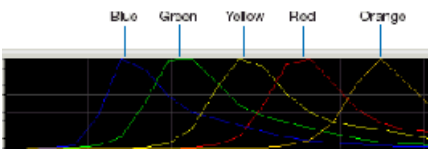
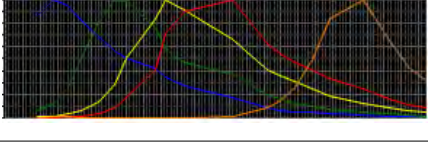
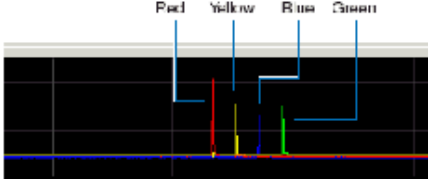
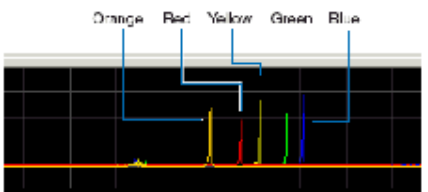
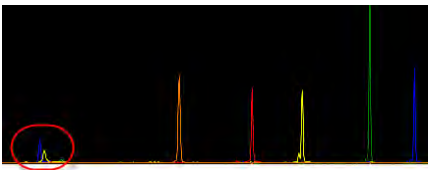
## Evaluate the spectral calibration data

**IMPORTANT!** Do not accept a spectral calibration until you examine the data for all capillaries.

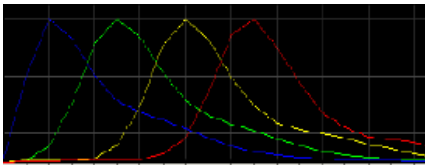
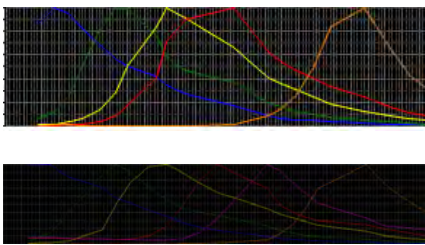
When a spectral calibration completes successfully, the **Overall** row displays green, red, or yellow results.

For each capillary:

1. Click a capillary to display the spectral and raw data for a capillary.
2. Check that the data meet the following criteria:





Attribute	Acceptance criteria	Example
Order of the peaks in the spectral profile (intensity vs pixel) from left to right	4-dye: blue-green-yellow-red	
	5-dye: blue-green-yellow-red-orange	
	6-dye: blue-green-yellow-red-purple-orange	
Order of the peaks in the raw data profile from left to right	Sequencing (matrix standard only): 4-dye: red-yellow-blue-green	
Order of the peaks in the raw data profile from left to right	Fragment analysis: <ul style="list-style-type: none"> <li>• 4-dye: red-yellow-green-blue</li> <li>• 5-dye: orange-red-yellow-green-blue</li> </ul>	
Extraneous peaks in the raw data profile (intensity vs scan)	None <b>Note:</b> The E5 profile may include extraneous peaks outside the matrix peak region, which can be ignored.	E5: 

(continued)

Attribute	Acceptance criteria	Example
Peak morphology in the spectral profile (intensity vs pixel)	<ul style="list-style-type: none"> <li>No gross overlaps, dips, or other irregularities</li> <li>Peaks are separate and distinct</li> <li>Peak apexes are separate and distinct (the tails will overlap)</li> </ul>	
	<p><b>Note:</b> The peak morphology of G5 (shown to the right, top), F, and J6 (shown to the right, bottom) may not be as rounded and symmetrical as the peak morphology for other dye sets (shown above) due to the effect of variable binning (a feature that reduces signal variation between dyes of different fluorescent efficiencies).</p>	

- As needed, zoom on the spectral profile traces to determine if the data meet the criteria (see “Zoom on data” on page 118).
- If the data for all capillaries meet the criteria above, click **Accept Results**.
- If any capillary data does not meeting the criteria above, click **Reject Results**, then go to “Spectral calibration troubleshooting” on page 299.

### Zoom on data

- Place the pointer *above the top* of the plot or *to the left* of the plot at the start of the area you want to zoom, then click to turn the pointer to .
- With the  still *above* the plot or *to the left* of the plot, click-drag to the end of the area you want to zoom. Do not drag the  inside the plot area. Doing so changes  back to a pointer and does not zoom as expected.

You can also click zoom and fit buttons to zoom   .

### What you see during a spectral calibration

A spectral calibration can run up to three injections. The number of injections performed depends on:

- The number of capillaries that pass or fail during an injection
- Whether you select the Allow Borrowing option

---

**Note:** The first time you perform a spectral calibration (for each dye set) after installing a new capillary array, you may notice pull-down peaks (or mirror image peaks). While the run is in progress, these pull-down peaks will eventually correct themselves. Once the run completes the electropherogram, the pull-down peaks disappear.

---

## Capillary information sharing

A spectral calibration can share capillary information:

- **Between injections** – If a capillary in an injection does not meet the spectral Quality Value and Condition Number limits shown on page 105, the software automatically uses the information from that capillary in a different injection.
- **Within an injection** – If a capillary in an injection does not meet the spectral Quality Value and Condition Number limits shown on page 105 and the Allow Borrowing option is selected, the software can also use the information from a capillary to the left or the right of that capillary, if the values are higher than those for that capillary in a different injection.

### Spectral calibration with Borrowing disabled

When Borrowing is *disabled*, all capillaries must pass (meet the spectral Quality Value and Condition Number limits) for the calibration to pass.

Allow Borrowing

Injection 1	<ul style="list-style-type: none"> <li>• The software evaluates the Quality Value and Condition Number of all capillaries.</li> <li>• If all capillaries pass, the calibration is complete, and injections 2 and 3 are not performed.</li> <li>• If any capillaries fail, injection 2 is performed.</li> </ul>
Injection 2	<ul style="list-style-type: none"> <li>• The software evaluates the Quality Value for each capillary across injections 1 and 2 and uses the information from the capillary with the highest Quality Value.</li> <li>• If all capillaries now pass, the calibration is complete and injection 3 is not performed.</li> <li>• If the same capillary fails in both injection 1 and 2, injection 3 is performed.</li> </ul>
Injection 3	<ul style="list-style-type: none"> <li>• The software evaluates the Quality Value for each capillary across injections 1, 2, and 3 and the information from the capillary with the highest Quality Value.</li> <li>• If all capillaries now pass, the calibration passes.</li> <li>• If the same capillary fails in injection 1, 2, or 3, the calibration fails.</li> </ul>

### Spectral calibration with Borrowing enabled

When Borrowing is *enabled*, all capillaries have to pass (meet the spectral Quality Value and Condition Number limits) within the borrowing limits:

Allow Borrowing

- 8-capillary instruments – One adjacent-capillary borrowing event allowed
- 24-capillary instruments – Up to three adjacent-capillary borrowing events allowed (the number of allowed borrowing events can be decreased in Preferences).

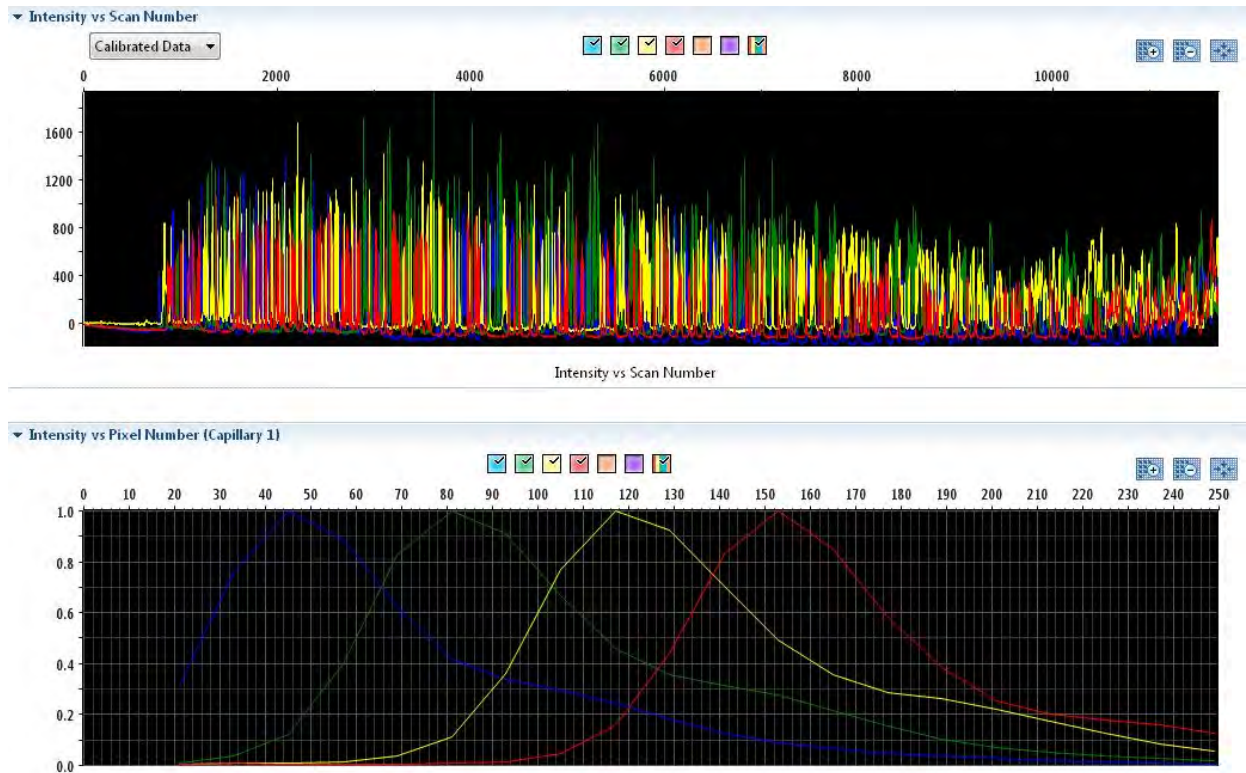
The software identifies a borrowed capillary with an arrow pointing from the capillary from which the data is borrowed.



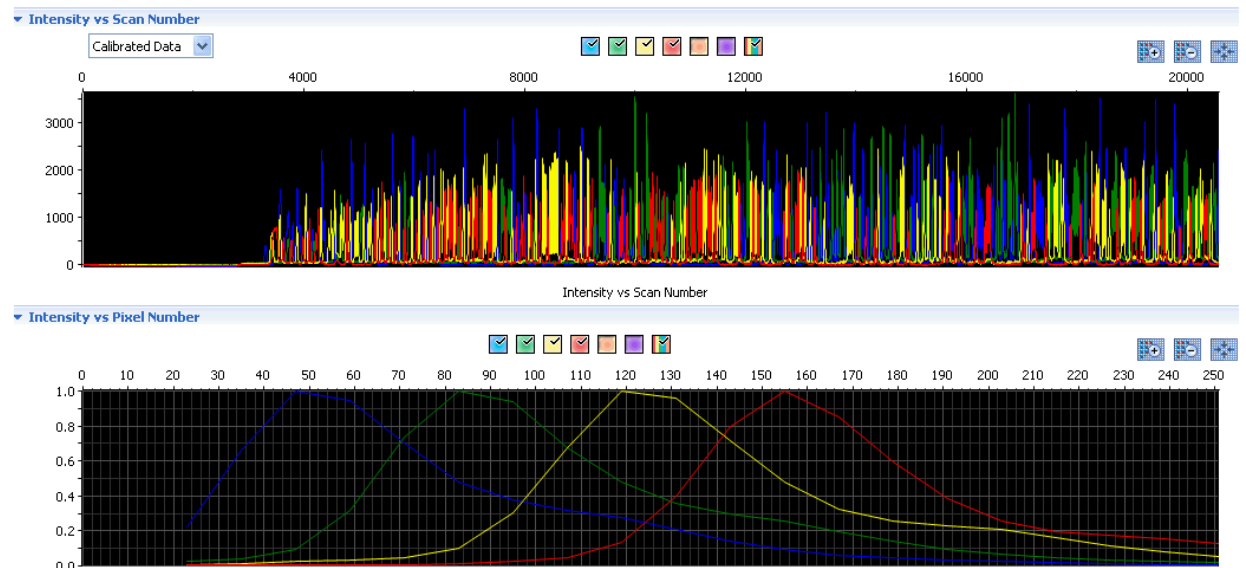
Injection 1	<ul style="list-style-type: none"> <li>• The software evaluates the Quality Value and Condition Number of all capillaries.</li> <li>• If all capillaries pass, the calibration is complete, and injections 2 and 3 are not performed.</li> <li>• If any capillaries fail, the software borrows from an adjacent capillary.</li> <li>• If, after borrowing, &gt;1 or &gt; 3 capillaries fail, injection 2 is performed.</li> </ul>
Injection 2	<ul style="list-style-type: none"> <li>• The software evaluates the quality values between adjacent capillaries in injection 2 and for each capillary across injections 1 and 2 and uses the information with the highest Quality Value for each capillary.</li> <li>• If all capillaries pass, the calibration is complete and injection 3 is not performed.</li> <li>• If, after borrowing, &gt;1 or &gt; 3 capillaries from injection 1 or 2 do not pass, injection 3 is performed.</li> </ul>
Injection 3	<ul style="list-style-type: none"> <li>• The software evaluates the quality values between adjacent capillaries in injection 3 and for each capillary across injections 1, 2, and 3, then uses the information with the highest Quality Value for each capillary.</li> <li>• If all capillaries now pass, the calibration passes.</li> <li>• If after borrowing, &gt;1 or &gt; 3 capillaries from injection 1, 2, or 3 do not pass, the calibration fails.</li> </ul>

## Example spectral calibration data

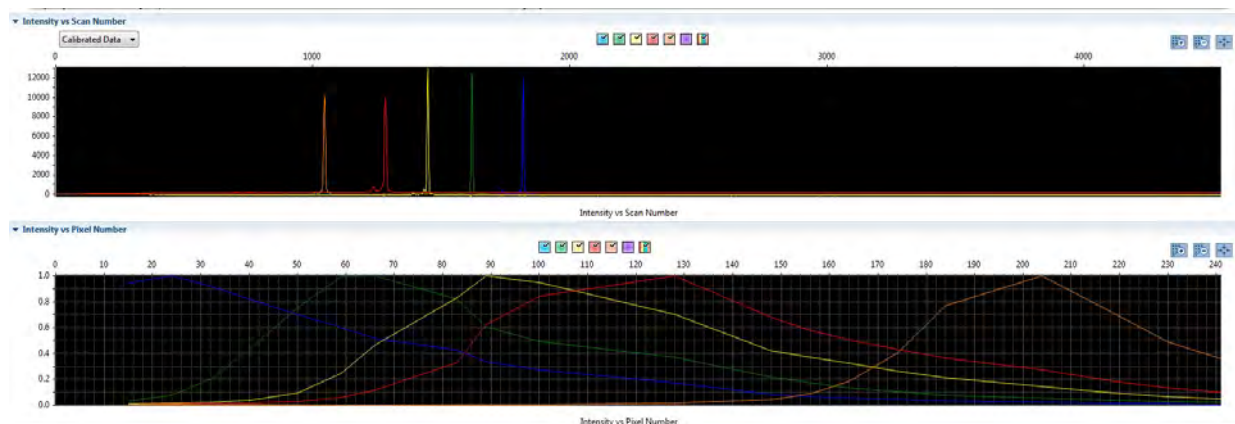
### Dye Set E created from Sequencing Standard



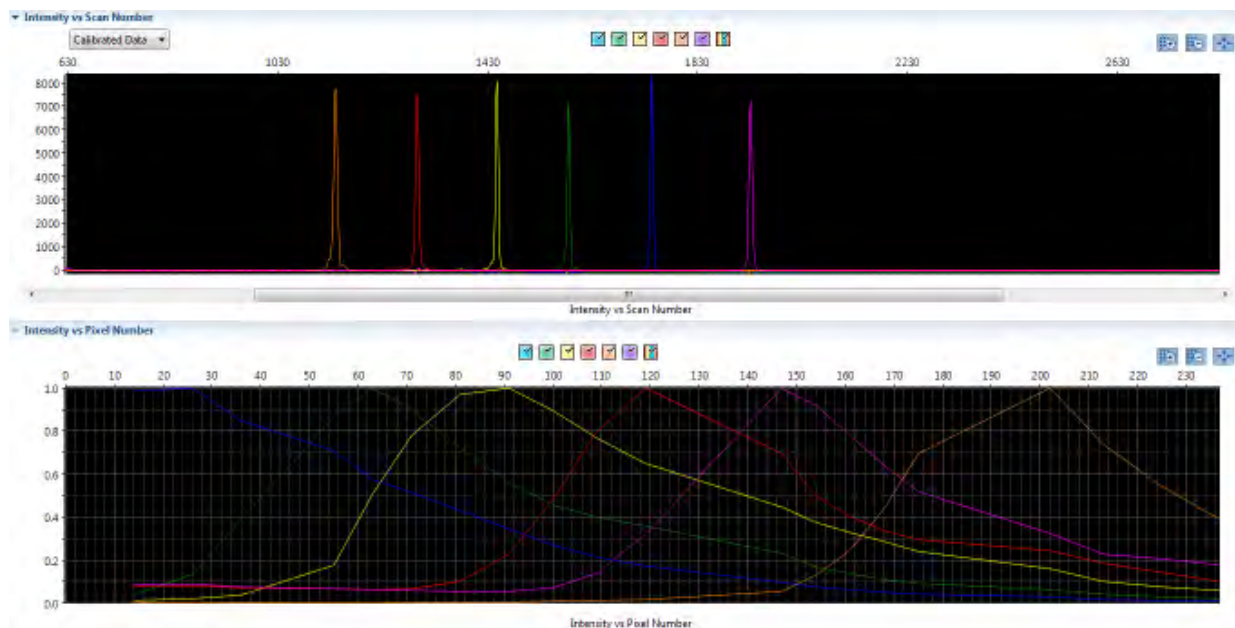
### Dye Set Z created from Sequencing Standard



## Dye Set G5 created from Matrix Standard Set DS-33




## Dye Set J6 created from Matrix Standard Set DS-36



## Export spectral calibration results

To export spectral calibration results:

1. Click  **Export Spectral Calibration Results**.
2. Specify an export file name and location, then click **Save**.

The export file contains the following results:

- **Capillary Number**
- **Condition Number**
- **Scan Number**





- **Borrowed From Capillary**
- **Quality Value**
- **Peak Height**
- **Reason For Failure**
- **Run From Injection**

## View and print a calibration report

---

**Note:** Spatial and spectral calibration reports include the date on which a capillary array is installed for the first time on the instrument. Install standard reports use the most recent install date if a capillary array was removed and re-installed on the instrument.

---



1. Click  **View Report**.
2. (Optional) In the **Report** screen, click toolbar options to manipulate the report. Place the mouse pointer over an item for a description of the item.
3. To print the report, click  **Print**.

## Save historical reports (PDF) for record keeping

---

**IMPORTANT!** Save a report electronically for record keeping. The software does not save historical results. Only the most recent results are maintained in the software.

---

1. Click  **View Report**.
2. Click  **Print**.
3. In the **Printer** dialog box, select a PDF printer.
4. Specify a name and location for the report.

## View the spectral calibration history

Only the most recent spectral calibration for each dye set is maintained in the software.

Select **History View**, then select a dye set to view the associated calibration history.



## Section 7.2 Run an install check

### Run a Sequencing install check

#### When to perform a sequencing install check

If an install check is not performed when your instrument is installed, you must perform an install check before you can run plates.

We recommend that you run an install check monthly to verify that the instrument meets specifications.

The sequencing install check has an option to include and save the spectral calibration. If you select this option and you accept the sequencing install standard results, you do not need to run a separate spectral calibration (described in “Run a Sequencing install check” on page 144) for the dye set.

#### Estimated run time

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**Note:** The run times listed below do not include the time for the oven to preheat to 60°C.

---

- General sequencing (BDTv3.1): ~1 hour
- MicroSeq ID: 2 hours
- BDTv1.1POP6: ~2.5 hours

#### Prepare for the sequencing install check

##### Before you begin

If you will not save the spectral calibration from the sequencing install run, perform a spectral calibration (see “Perform a spectral calibration” on page 133).

##### Prepare the instrument

1. In the **Dashboard**, check consumables status (see “Check consumables status” on page 37).  
Ensure that:
  - Consumables are not expired
  - Adequate injections remain for consumables
2. Ensure that buffer levels are at the fill lines (see “Check buffer fill levels” on page 39).
3. Set the oven temperature, then click **Start Pre-heat**.

Pre-heat the oven and detection cell while you prepare for a run (detection cell temperature is set by the software). Pre-heating helps mitigate subtle first-run migration rate effects. The pre-heat function automatically turns off after 2 hours.

We recommend that you pre-heat the oven for at least 30 minutes before you start a run if the instrument is cold.



Temperatures are displayed in red as they warm to the set-points. When temperatures are at the set-point they are displayed in green. Temperatures may fluctuate slightly when they reach the set-point as they stabilize.

4. Check the pump assembly for bubbles and run the **Remove Bubble wizard** if needed (see “Remove bubbles from the polymer pump” on page 268).

### Prepare the sequencing install check standard

Prepare the BigDye™ Terminator v1.1 or v3.1 Sequencing Standard as described in the product insert. See Appendix D, “Catalog numbers” for catalog numbers.

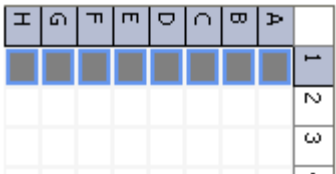
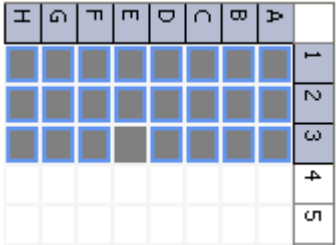
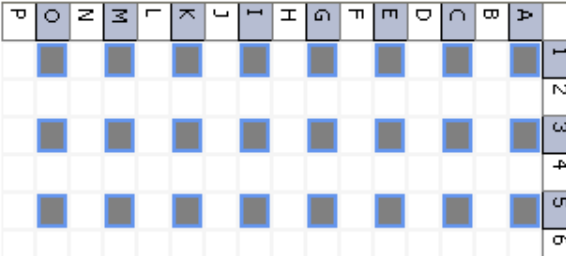
**Note:** If you are using the BigDye™ Direct DNA PCR Amplification/Clean-up/Cycle Sequencing kit and you will use the sequencing install data for spectral calibration, use the v3.1 Sequencing Standard.

### Prepare the standard plate

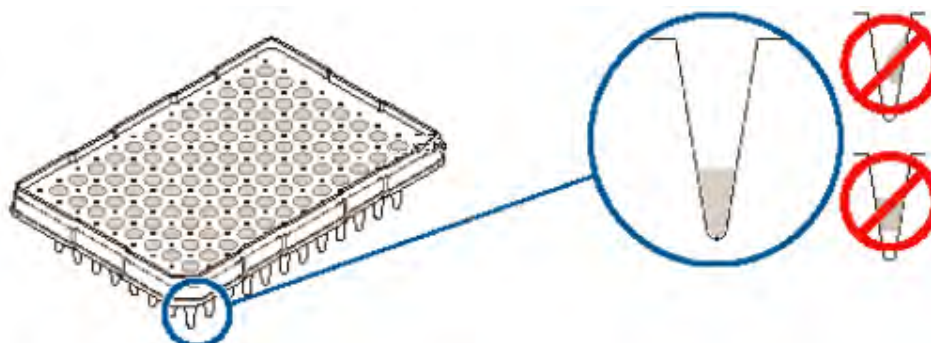
**IMPORTANT!** Do not use warped or damaged plates.

1. Load the standards in any injection position in the plate. The example below shows injection position 1, but you can specify the starting well for an injection position.

**IMPORTANT!** You do not create a plate in the software for the install check.

<p>8-capillary 96-well plate</p>	<p>A1 through H1</p> 
<p>24-capillary 96-well plate</p>	<p>A1 through H1, A2 through H2, and A3 through H3</p> 
<p>24-capillary 384-well plate</p> <p><b>Note:</b> 384-well plates are not supported on 8-capillary instruments.</p>	<p>Columns 1, 3, and 5 in rows A, C, E, G, I, K, M, O</p> 

2. Briefly centrifuge the plate that contains the standards.
3. Verify that each standard is positioned correctly in the bottom of its well.




---

**IMPORTANT!** If the contents of any well contain bubbles or are not located at the bottom of the well, briefly centrifuge the plate, remove the plate from the centrifuge, and verify that each standard is positioned correctly in the bottom of its well.

---

4. Store the plate on ice until you prepare the plate assembly and load the plate in the instrument.
5. Prepare the plate assembly as described in “Prepare the plate assembly” on page 70.

### Load the plate in the instrument

1. Click the Tray button on the front panel to move the autosampler to the front position, then open the instrument door.
2. Place the plate in the autosampler with the labels facing you (or the instrument door) and the notched corner of the plate in the notched corner of the autosampler.
3. Close the instrument door to initialize the instrument.

### Perform a sequencing install check

1. Access the **Sequencing Install Standard** screen.



2. Select the chemistry type.

---

**Note:** BDTv3.1 with POP-6™ polymer is not available for the install check (it can be used for application runs). If your application uses BDTv3.1 with POP-6™ polymer, select BDTv.1 for the sequencing install check, then perform a separate spectral calibration using the Z dye set. Do not select **Keep Spectral Calibration Data**.

---

3. Select the number of wells and plate position in the instrument.

---

**Note:** You do not create a plate in the software for the install check.

---

4. Specify the starting well for the injection position in which you loaded the standard in the plate.

---

**Note:** If you navigate away from the **Install Standard** screen after you start the install check, the starting well may be reset to A01. This is a display issue only; the starting well you specify is used for the install check.

---

5. (Optional) If you have not already run a spectral calibration, select **Keep Spectral Calibration Data** to save the sequencing install standard run (if it passes) as a spectral calibration.

---

**Note:** The spectral calibration record will only be saved if the **Keep Spectral Calibration Data** option is checked on the screen. If you uncheck the option, create a separate spectral calibration from the **Maintenance** menu.

---



## What you see during a sequencing install check

The instrument performs one run, then evaluates:

- Spectral data, if you specified to keep spectral data
- Sequence data

The **Capillary Run Data** display (Figure 14) is updated after the run is complete:

- The spectral calibration status is displayed in the first row of the run results table. Passing and failing capillaries in the install check run are shown in green and red respectively for the CRL (contiguous read length) criteria. Borrowed capillaries (spectral only) are shown in yellow with an arrow indicating the adjacent capillary from which results were borrowed. The spectral result for each capillary is displayed below the run results table.
- The sequencing install standard status is displayed in the third row of the run results table (CRL Pass/Fail).
- The **Quality Value** and **Condition Number** for each capillary is displayed below the table.

**Note:** The values shown in this figure are examples only.

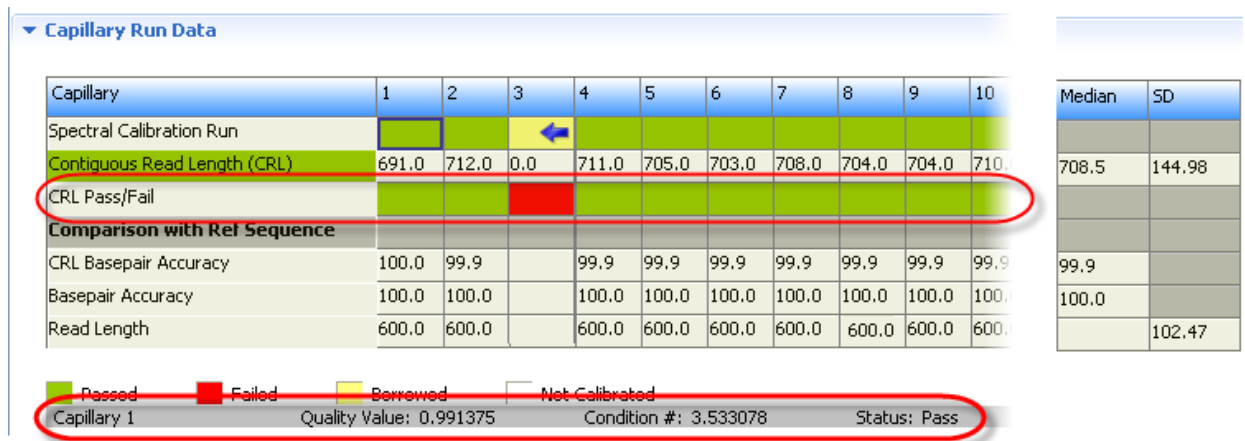


Figure 14 Capillary Run Data

## Pass/fail criteria for the optional spectral calibration

The software evaluates the Quality Value and Condition Number for each capillary (for more information, see “Spectral Quality Values and Condition Numbers” on page 136).

Borrowing is automatically enabled. 1 borrowing event is allowed for 8-capillary instruments. Up to 3 borrowing events are allowed for 24-capillary instruments. For more information, see “Spectral calibration with Borrowing enabled” on page 139. The number of borrowing events can be decreased (see “System preferences” on page 42).

Thresholds used by the software for pass/fail are listed in the following table:

Dye set	Quality Value minimum	Condition Number maximum
E	0.95	5.5
Z	0.95	5.5

## Pass/fail criteria for the sequencing install check

The software calculates the **Contiguous Read Length** for each capillary. Capillaries that are below the threshold fail. The remaining results that the software displays are for information only.

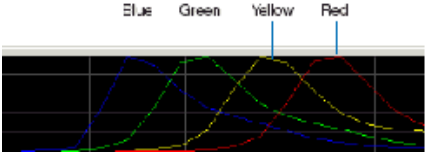
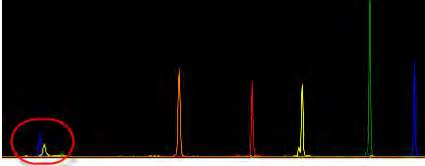
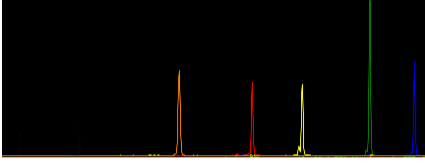
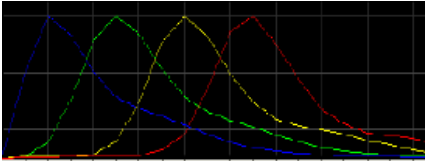
Result	Description
<b>Contiguous Read Length (CRL)</b>	<p>The longest uninterrupted segment of basecalls with an average Quality Value (QV) <math>\geq 20</math>.</p> <p>In addition to evaluating the QV of a basecall, the software considers the QV of adjacent basecalls within a 21-bp moving window to determine a contiguous read length based on quality values: the software starts from the 5' end and calculates the average QV across a moving window size of 21, sliding 1 bp at a time, to the 3' end. The resulting longest contiguous segment is determined as the CRL.</p>
<b>CRL Pass/Fail</b>	<ul style="list-style-type: none"> <li>• <b>BDTv1.1</b>—Capillaries with a CRL &lt;600 bp fail.</li> <li>• <b>BDTv3.1 (General Sequencing)</b>—Capillaries with a CRL &lt;500 bp fail.</li> <li>• <b>MicroSEQ™ ID</b> – Capillaries with a CRL &lt;600 bp fail.</li> </ul>
<b>For information only</b> — The alignment of the base-called sample sequence with the known reference of the sequencing install standard is used to calculate the following results.	
<b>CRL Basepair Accuracy</b>	CRL <b>Basepair Accuracy</b> is determined by basepair comparison between the base-called sample sequence and the known reference sequence of the sequencing install standard within the contiguous read length region calculated (as described in the CRL definition above).
<b>Read Length</b>	<p>The length of read (in bases) at which base calling accuracy is <math>\geq 98.5\%</math>.</p> <p>The Read Length is measured only within the following regions:</p> <ul style="list-style-type: none"> <li>• BDTv1.1: 20–619 bp (maximum value is 600)</li> <li>• BDTv3.1 (General Sequencing): 40–539 bp (maximum value is 500)</li> <li>• MicroSEQ™ ID: 20–619 bp (maximum value is 600)</li> </ul> <p>The <b>Read Length</b> value is derived from basecall accuracy, and not from quality values.</p>
<b>Basepair Accuracy (Read Length Accuracy)</b>	<b>Basepair Accuracy</b> calculates the percent of accurate basecalls in the known reference sequence within the <b>Read Length</b> of the sequencing install standard.
<b>CRL Median and SD</b>	Median and standard deviation determined for all capillaries.

## Evaluate sequencing install standard data

When a sequencing install standard run completes successfully, the **CRL Pass/Fail** row displays green or red results.

For each capillary:

1. Click a capillary to display the spectral and raw data profiles for a capillary.
2. Check that the data meet the following criteria:

Attribute	Acceptance Criteria	Example
Order of the peaks in the spectral profile (intensity vs pixel) from left to right	4-dye: blue-green-yellow-red	
Extraneous peaks in the raw data profile (intensity vs scan)	None <b>Note:</b> The E5 profile may include extraneous peaks outside the matrix peak region, which can be ignored.	E5: 
Extraneous peaks in the raw data profile (intensity vs scan)	None	
Peak morphology in the spectral profile (intensity vs pixel)	<ul style="list-style-type: none"> <li>• No gross overlaps, dips, or other irregularities</li> <li>• Peaks separate and distinct</li> <li>• Peak apexes are separate and distinct (the tails will overlap)</li> </ul>	

3. (Optional) Review the CRL **Basepair Accuracy** to determine discrepancies from the reference sequence.

If you observe large discrepancies (for example, 5–10 contiguous miscalled bases in the middle of a sequence), review the data. If you see a raw data peak larger than the adjacent peaks with baseline pull-up in all 4-dye color channels, it may indicate the presence of a bubble. Check the pump, run the **Remove Bubbles wizard** (see “Remove bubbles from the polymer pump” on page 268), then repeat the run as needed.

4. If the data for the required number of capillaries meets the criteria above (at least 7 capillaries for 8-capillary instruments, at least 22 capillaries for 24-capillary instruments), click **Accept Results**.







## View and print an install check report

---

**Note:** Ensure that all dyes are selected before viewing the report. The report may contain incomplete data if all dyes are not selected.

---

Note the following:


- Install check reports include the most recent install date if a capillary array was removed, then re-installed on the instrument. Spatial and spectral calibration reports include the date on which a capillary array is installed on the instrument for the first time.
- The sorting in the **Install Standard** screen is not applied to the report.
- You can generate a report for a failed install check run before you click **Reject Results**.

1. Click  **View Report**.

---

**Note:** The **Date Performed** field reflects the date that the install check was accepted, not the date it was run.

---



2. (Optional) In the **Report** screen, click toolbar options to manipulate the report. Place the mouse pointer over an item for a description of the item.
3. To print the report, click  **Print**.
4. To save the report electronically (PDF), print the report and select a PDF printer.

## Save historical reports (PDF) for record keeping

---

**IMPORTANT!** Save a report electronically for record keeping. The software does not save historical results. Only the most recent results are maintained in the software.

---

1. Click  **View Report**.
2. Click  **Print**.
3. In the **Printer** dialog box, select a PDF printer.
4. Specify a name and location for the report.

## Run a fragment/HID install check

### When to perform a fragment/HID install check

If an install check is not performed when your instrument is installed, you must perform an install check before you can run plates.

We recommend that you run an install check monthly to verify that the instrument meets specifications.

## Estimated run time

---

**Note:** The run times listed below do not include the time for the oven to preheat to 60°C.

---

- **Fragment install check** (POP-7™ Polymer, 50-cm capillary array)—≤ 90 minutes
- **HID install check** (POP-4™ Polymer, 36-cm capillary array)—≤ 30 minutes

## Prepare for the fragment/HID install check

### Before you begin

If you will not save the spectral calibration from the sequencing install run, perform a spectral calibration (see “Perform a spectral calibration” on page 133).

### Prepare the instrument

1. In the **Dashboard**, check consumables status (see “Check consumables status” on page 37). Ensure that:
  - Consumables are not expired
  - Adequate injections remain for consumables
2. Ensure that buffer levels are at the fill lines (see “Check buffer fill levels” on page 39).
3. Set the oven temperature, then click **Start Pre-heat**.

Pre-heat the oven and detection cell while you prepare for a run (detection cell temperature is set by the software). Pre-heating helps mitigate subtle first-run migration rate effects. The pre-heat function automatically turns off after 2 hours.

We recommend that you pre-heat the oven for at least 30 minutes before you start a run if the instrument is cold.

Temperatures are displayed in red as they warm to the set-points. When temperatures are at the set-point they are displayed in green. Temperatures may fluctuate slightly when they reach the set-point as they stabilize.
4. Check the pump assembly for bubbles and run the **Remove Bubble wizard** if needed (see “Remove bubbles from the polymer pump” on page 268).

### Prepare the fragment/HID install check standard

Prepare the standard as described in the product insert. See Appendix D, “Catalog numbers” for catalog numbers.


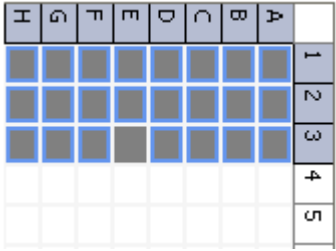
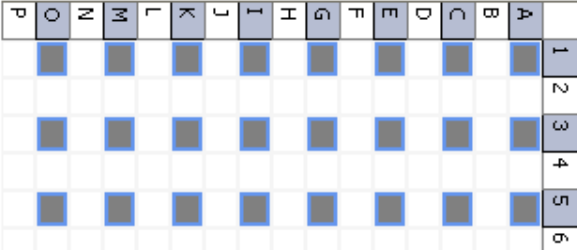
- Fragment analysis: DS-33 GeneScan™ Installation Standards with GeneScan™ 600 LIZ™ Size Standard v2.0
- HID: AmpFℓSTR™ Identifiler™ Allelic Ladder (For HID install check)

## Prepare the standard plate

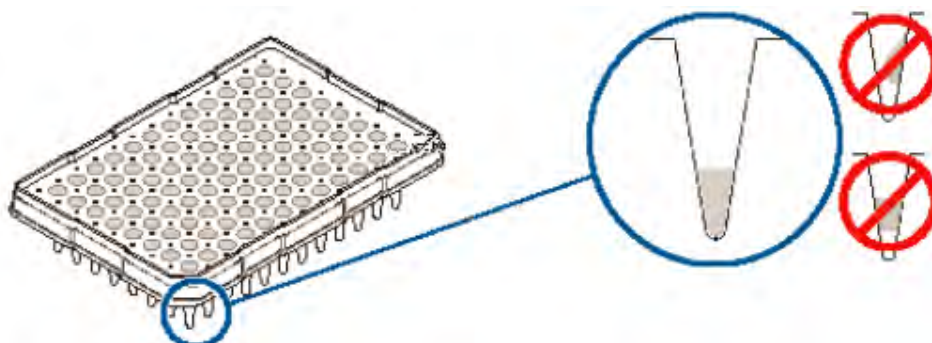
**IMPORTANT!** Do not use warped or damaged plates.

1. Load the standards in any injection position in the plate. The example below shows injection position 1, but you can specify the starting well for an injection position.

**IMPORTANT!** You do not create a plate in the software for the install check.

<p>8-capillary 96-well plate</p>	<p>A1 through H1</p> 
<p>24-capillary 96-well plate</p>	<p>A1 through H1, A2 through H2, and A3 through H3</p> 
<p>24-capillary 384-well plate</p> <p><b>Note:</b> 384-well plates are not supported on 8-capillary instruments.</p>	<p>Columns 1, 3, and 5 in rows A, C, E, G, I, K, M, O</p> 

2. Briefly centrifuge the plate that contains the standards.
3. Verify that each standard is positioned correctly in the bottom of its well.



---

**IMPORTANT!** If the contents of any well contain bubbles or are not located at the bottom of the well, briefly centrifuge the plate, remove the plate from the centrifuge, and verify that each standard is positioned correctly in the bottom of its well.

---

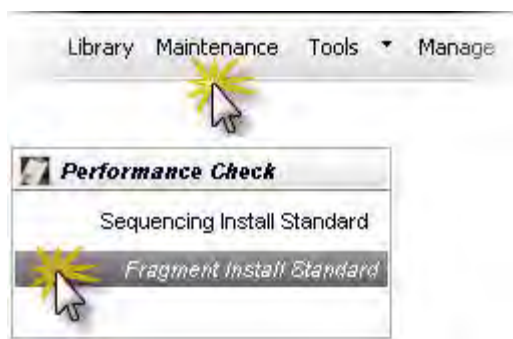
4. Store the plate on ice until you prepare the plate assembly and load the plate in the instrument.
5. Prepare the plate assembly as described in “Prepare the plate assembly” on page 70.

### Load the plate in the instrument

1. Click the Tray button on the front panel to move the autosampler to the front position, then open the instrument door.
2. Place the plate in the autosampler with the labels facing you (or the instrument door) and the notched corner of the plate in the notched corner of the autosampler.
3. Close the instrument door to initialize the instrument.

### Perform the fragment/HID install check

1. Access the **Fragment Install Standard** or **HID Install Standard** screen.

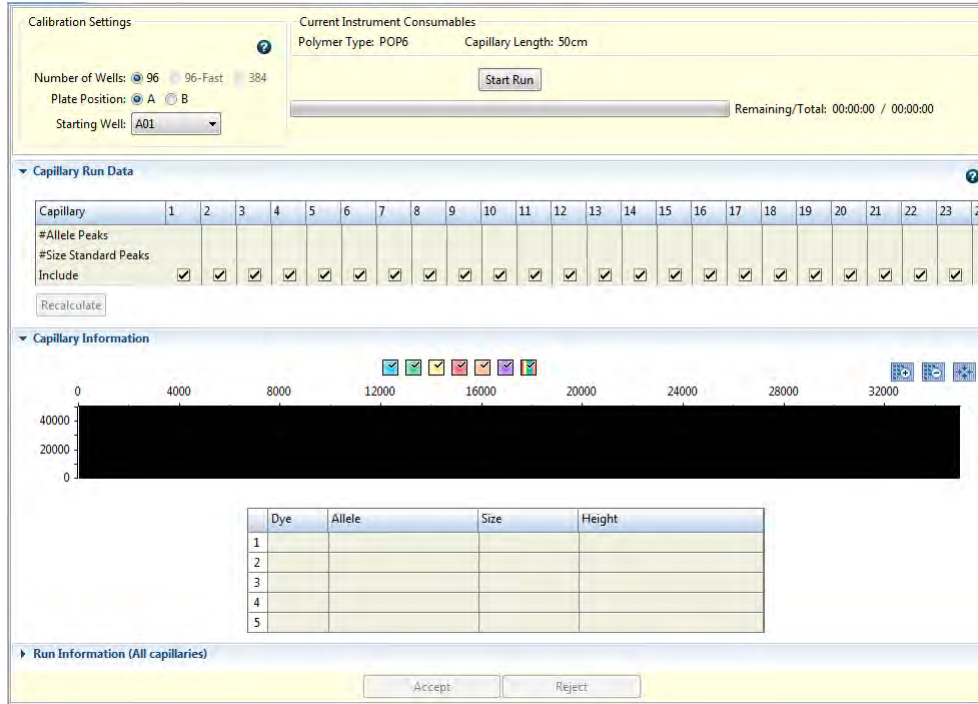


2. Select the plate type (number of wells).
3. Select the plate position in the instrument.

---

**Note:** You do not create a plate in the software for the install check.

---



- Specify the starting well for the injection position in which you loaded the standard in the plate.

---

**Note:** If you navigate away from the **Install Standard** screen after you start the install check, the starting well may be reset to A01. This is a display issue only; the starting well you specify is used for the install check.

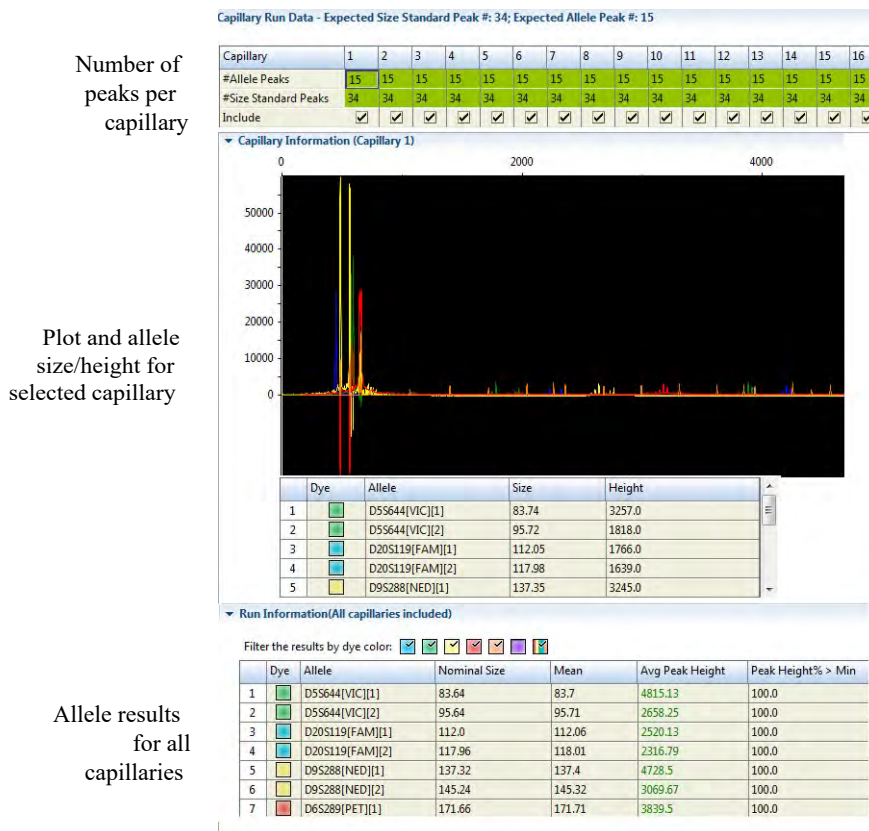
---

- Click **Start Run**.

## What you see during a fragment install check

The instrument performs one run and indicates the number of observed allele and size standard peaks.

The **Capillary Run Data** display is updated after the run is complete. The number of observed size standard and allele peaks is shown. Results for each allele are shown at the bottom of the screen in the **Run Information** table.



## Pass/fail criteria for the fragment/HID install check

The software evaluates peaks in the data for each capillary. To be identified as a possible allele, peaks must be within the following ranges (nominal allele size, or reference bin size, is hard-coded):

Fragment analysis	HID analysis
All markers between $\pm 0.4$ bp and $\pm 0.5$ bp of nominal size for the allele	<ul style="list-style-type: none"> <li>All markers except TH01: <math>\pm 0.7</math> bp of nominal size for the allele</li> <li>TH01:               <ul style="list-style-type: none"> <li>Seven markers are <math>\pm 0.7</math> bp of nominal size for the allele</li> <li>Three markers are <math>\pm 0.5</math> bp of nominal size for the allele</li> </ul> </li> </ul>

For all peaks that are within the nominal size range, the software calculates the **Average Peak Height** and the **Sizing Precision**. Peaks that meet the following thresholds pass.

Result	Description	Threshold
Min Peak Height	Minimum of peak heights for observed allele peaks of the included capillaries.	<ul style="list-style-type: none"> <li>Fragment: &gt;175 RFU</li> <li>HID: &gt;400 RFU</li> </ul>
Sizing Precision	Standard deviation of the observed allele fragment sizes	<0.15 for expected alleles
Pass/Fail	Alleles with a sizing precision and minimum peak height that do not meet thresholds fail.	
For information only		
Nominal Size	Expected allele fragment peak size (bp).	
Mean	Average fragment size for the observed allele peaks.	
Peak Height % >Min	Percentage of observed allele peaks with a peak height above the minimum threshold.	
Sizing Accuracy	Difference between the expected allele size and the mean allele size.	

## Evaluate fragment install standard data

1. Examine the number of size standard and allele peaks found for each capillary.

▼ Capillary Run Data - Expected Size Standard Peak #: 34; Expected Allele Peak #: 15

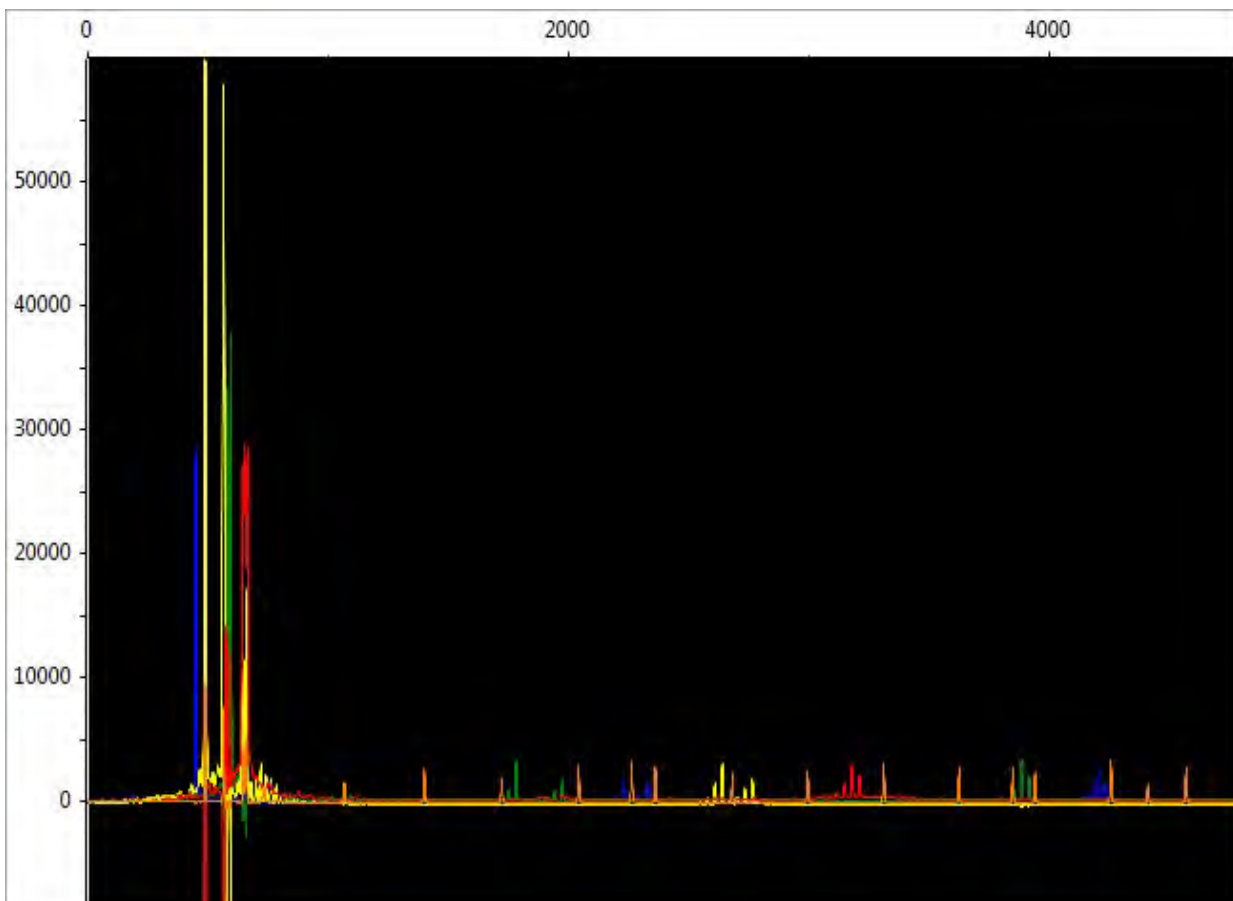
Capillary	1	2	3	4	5	6	7	8	9	10	11	12	13	14
#Allele Peaks	15	15	15	15	15	15	15	15	15	15	15	15	15	15
#Size Standard Peaks	34	34	34	34	34	34	34	34	34	34	34	34	34	34
Include	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>

2. If all capillaries pass, click **Accept Results**.

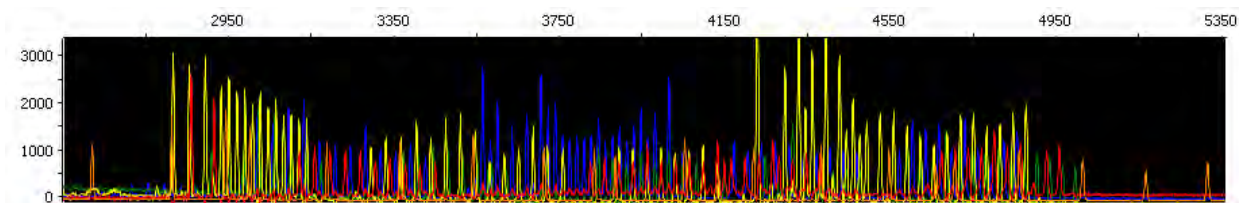
If any capillaries fail, the **Accept Results** button is disabled. Evaluate the raw data for failed capillaries. You can deselect 1 failed capillary for 8-capillary instruments or 2 failed capillaries for 24-capillary instruments to recalculate results and then click **Accept**.



## Example fragment install standard results



## Example HID install standard results



## View previously run install standards

Select **History View**, then select an install standard to view the associated install check information.



## View and print an install check report

---

**Note:** Ensure that all dyes are selected before viewing the report. The report may contain incomplete data if all dyes are not selected.

---

Note the following:


- Install check reports include the most recent install date if a capillary array was removed, then re-installed on the instrument. Spatial and spectral calibration reports include the date on which a capillary array is installed on the instrument for the first time.
- The sorting in the **Install Standard** screen is not applied to the report.
- You can generate a report for a failed install check run before you click **Reject Results**.

1. Click  **View Report**.

---

**Note:** The **Date Performed** field reflects the date that the install check was accepted, not the date it was run.

---



2. (Optional) In the **Report** screen, click toolbar options to manipulate the report. Place the mouse pointer over an item for a description of the item.
3. To print the report, click  **Print**.
4. To save the report electronically (PDF), print the report and select a PDF printer.

## Save historical reports (PDF) for record keeping

---

**IMPORTANT!** Save a report electronically for record keeping. The software does not save historical results. Only the most recent results are maintained in the software.

---

1. Click  **View Report**.
2. Click  **Print**.
3. In the **Printer** dialog box, select a PDF printer.
4. Specify a name and location for the report.



# Manage library resources

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## Overview of libraries

The **Library** workflow contains the following libraries:




- Items that you select when you set up a run:
  - **Plates**—Contains factory-provided plate templates that you can use to create plates for each run.
  - **Assays**—Contains factory-provided assay templates that you cannot modify. You can also create new assays.
  - **Optional Filename Conventions**—Contains factory-provided file name conventions that you cannot modify. You can also create new file name conventions.
  - **Optional Results Groups**—Contains factory-provided results groups that you cannot modify. You can also create new results groups.
- Items that you select when you create an assay:
  - Instrument protocols
  - Primary analysis protocols—Basecalling (sequencing), sizecalling (fragment analysis), QC (HID analysis)
- Items you select when you create instrument sizecalling and QC protocols:
  - Dye sets
  - Size standards

## Factory-provided template and locked items

The software libraries include factory-provided items that are optimized for different applications (for example, instrument protocols with specific run modules and primary analysis protocols with specific settings). You can use the factory-provided items directly. If the factory-provided items do not suit your needs, you can do one of the following:

- Duplicate and modify a factory-provided item, and save the item with a new name.
- Create a new item.

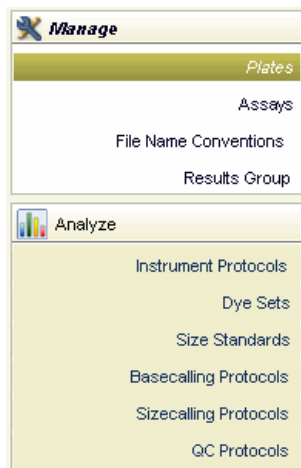
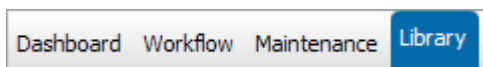
Entries in the library may be flagged with the following symbols:

-  Factory-provided. Cannot be edited or deleted.
-  Template.
-  Locked. If the SAE module is enabled on your system, a locked item can be unlocked and modified by the user who created it, the administrator, or another user with unlock permissions. For information, see Chapter 9, “Use Security, Audit, and E-Sig functions (SAE Module)” .

## General library procedures

### Access libraries

Click the **Library** tab to access the **Library** workflow.





You can click **Main Workflow**, or select **Dashboard** or any other menu item at any time to advance from the Library workflow.

## Create a new entry from a factory-provided template or locked entry

---

**IMPORTANT!** Auditing of an item depends on whether it is created directly from the library or from within another item (for example, you can create an assay directly from the library, or within a plate in the Assign Plate Contents screen). For more information on auditing, see “Review the object audit history” on page 232.

---


1. Select the factory-provided entry in the library.
2. Click  **Duplicate**.
3. Enter a name for the item.
4. Select the item, then click  **Edit**.
5. Modify parameters as needed (see the appropriate section for information).
6. Click **Save**.

## Delete a library entry

---

**IMPORTANT!** Auditing of an item depends on whether it is deleted directly from the library or from within another item (for example, you can delete an assay directly from the library, or within a plate in the Assign Plate Contents screen). For more information on auditing, see “Review the object audit history” on page 232.

---

**Note:** You cannot delete  or  factory-provided items.

---

Select an item, then click  **Delete**.

Deleting a library entry does not affect existing items that contain the entry. (When you select an item to include in a higher-level item, a copy of that item is included in the higher-level item. For example, when you select an instrument protocol to include in an assay, a copy of the instrument protocol is included in the assay. If you delete the instrument protocol, the copy of the instrument protocol in the assay remains intact.)

For information on how deleted items are tracked in auditing, see “Audit action” on page 233.

## Edit a library entry


---

**IMPORTANT!** Auditing of an item depends on whether it is edited directly from the library or from within another item (for example, you can edit an assay directly from the library, or within a plate in the **Assign Plate Contents** screen). For more information on auditing, see “Review the object audit history” on page 232.

---



**Note:** To edit a plate template, select the template from the main workflow. Go to **Define Plate Properties** ▶ **Open Plate** ▶ **Edit Existing Template**.

---

1. Select an item, then click  **Edit**.
2. Modify parameters as needed.
3. Click **Save**.

## Import and export a library entry

To import or export .xml files for use with other instruments that use the same version of the software:

- **Import**—Click  **Import**, then select the .xml file to import. If any items in the import file exist in the library, the software displays a message and gives you the option to replace or skip the item.
- **Export**—Select one or more entries, then click  **Export**, then specify a location for the export file. To select multiple entries, Shift-click to select contiguous entries, Ctrl-click to select non-contiguous entries.

---

**IMPORTANT!** You must save a plate before you export it.

---

## View audit and e-signature histories for library entries

---

**Note:** An administrator can also view audit and e-signature histories in the SAE module. For information, see Chapter 9, “Use Security, Audit, and E-Sig functions (SAE Module)”.

---

To view the audit or e-signature history for a library entry:

1. Select the item in the library.
2. Click  **View Audit History** or  **View E-Signature History** (active only if the selected item is enabled for e-sig).

---

**Note:** Factory-provided items do not list creation date in the audit history. If you duplicate a factory-provided item, the new item contains an audit history that starts with the duplication date listed as the creation date.

---

3. For more information, see “Display audit histories” on page 231.

## Sort and search library entries

### Sort by one or multiple columns

Double-click column headers to sort. To sort by multiple columns:

- Double-click a column header to sort the column.
- Alt+Shift-click another column header to sort another column.
- Alt+Shift-click a third column header to sort a third column.

Numbers in the column headers reflect sort order.



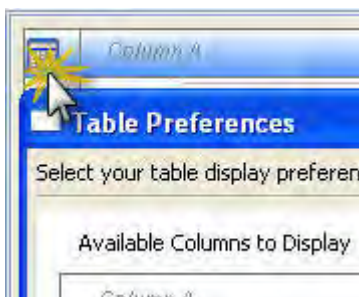
### Search

In each library, you can select a category to search, then enter the text to search for. The list of categories corresponds to the column headers in each library.

Click **Go** to search. Click **Clear** to remove the search criteria.

## Customize a table

Click the **Table Settings** button, then specify the columns to show or hide.



Click:

- **Apply**—To use the settings for this session only.
- **Save to Preferences**—To save for future use by all users. Preferences are saved for the logged-in user.
- **Restore Defaults**—To restore factory-default settings.

## Plates library

The **Plates** library contains all plates that have been saved in the software (plates that have been run and plates that have not yet been run).

## Plate overview

### Plate definition

A plate associates sample attributes (sample information and analysis information) with a well position. A plate defines how samples are analyzed during capillary electrophoresis and how sample files are named and stored after analysis.

When you create a plate, you specify:

- Plate type (sequencing, fragment, mixed, or HID)
- Number of wells, capillary length, and polymer type

When you set up a plate for a run, you add assays, optional file name conventions, and optional results groups to wells in the plate. If you add these items from the library, a *copy* of the items is added to the plate, and can be modified independently from the original items stored in the library. For information on how changes are tracked if auditing is enabled, see “Audit action” on page 233.

### Plate templates

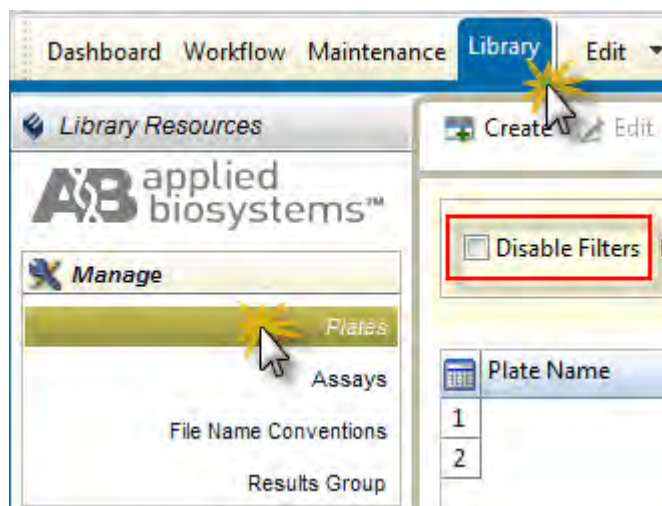
The Plates library includes templates that specify the appropriate application type, polymer, and capillary length. You can use these template to create new plates. To create your own templates, see “Create a plate template” on page 97.

Plate template names reflect the run module associated with the plate (a plate specifies an assay, an assay specifies an instrument protocol, and an instrument protocol specifies a run module which contains data collection settings). Appendix B, “Run modules and dye sets” lists the run time and size or base range collected for each run module.


## Create a new plate

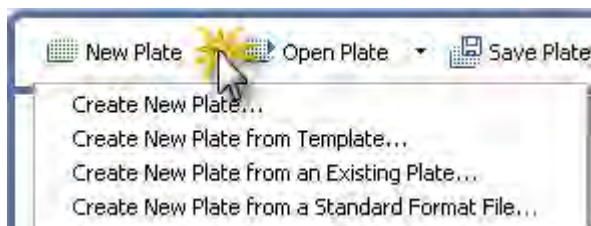
If you are running a stand-alone version of the software (a version that is not installed on the instrument computer), you can create plates, then export them for use on the instrument computer.


1. Access the **Plates** library.



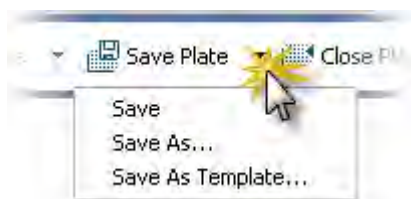
The list of items in the library may be filtered based on the library filtering user preference. Click **Disable Filters** to show all items in the list.

2. Click  **Create**. The software switches to the Workflow tab.
3. To create a new plate, specify settings (“Define plate properties” on page 168).



To create a new plate based on an existing plate, click  **New Plate**, then select an option. Select a plate, click **Open**, then specify settings.

4. Select a Save option.



## Define plate properties

Setting	Description
<b>Plate Details</b>	
<b>Name</b>	Plate name. Names must be unique.
<b>Number of Wells</b>	<ul style="list-style-type: none"> <li>• <b>96 well</b> —For standard 96-well plates standard reaction plates and 8-strip standard tubes with retainers.</li> <li>• <b>96 Fast tube</b>—For Fast 96-well plates and Fast 8-strip tubes with retainers.</li> <li>• <b>384 well</b>—For 384-well plates (24-capillary instruments only)</li> </ul>
<b>Plate Type</b>	Sequencing, Fragment, or Mixed (Sequencing and Fragment).
Capillary Length and Polymer	Capillary length and polymer type with which the plate will be used.
<b>Owner, Barcode, Description (optional)</b>	Optional text entries. You can use these entries to search for plates in the <b>Plates</b> library and in run logs ( <b>Tools ▶ View Run Logs</b> ).
<b>Autoanalysis</b>	Settings to communicate with secondary analysis software. For information, see the instructions provided with the secondary analysis software.



# Assays library

## Assay overview

An assay contains the instrument protocol (dye set and run module) and primary analysis protocol needed to collect data and basecall or sizecall a sample. Assays, File Name Conventions, and Results Groups may already be listed in the plate template when you create a plate from a template.

An assay contains:

- One or more instrument protocols appropriate for the sample type/dye set for which the assay will be used
- A primary analysis protocol that depends on your application:
  - **Sequencing**—Basecalling protocol
  - **Fragment**—Sizecalling protocol
  - **HID**—QC protocol

You must assign an assay to all named sample wells on a plate before you can link a plate and run it.


When you create an assay, you add one or more instrument protocols and a primary analysis protocol. If you add these items from the library, a *copy* of the items is added to the assay, and can be modified independently from the original items stored in the library. For information on how changes are tracked if auditing is enabled, see “Audit action” on page 233.

## Create a new assay

1. Access the Assays library.



The list of items in the library may be filtered based on the library filtering user preference. Click **Disable Filters** to show all items in the list.

2. Select an assay.
3. Click  **Edit**.

---

**Note:** You can also create an assay from the Assign Plate Contents screen.

---



The fields in the Edit Assay dialog box (Figure 15) are described in “Assay settings” on page 171.

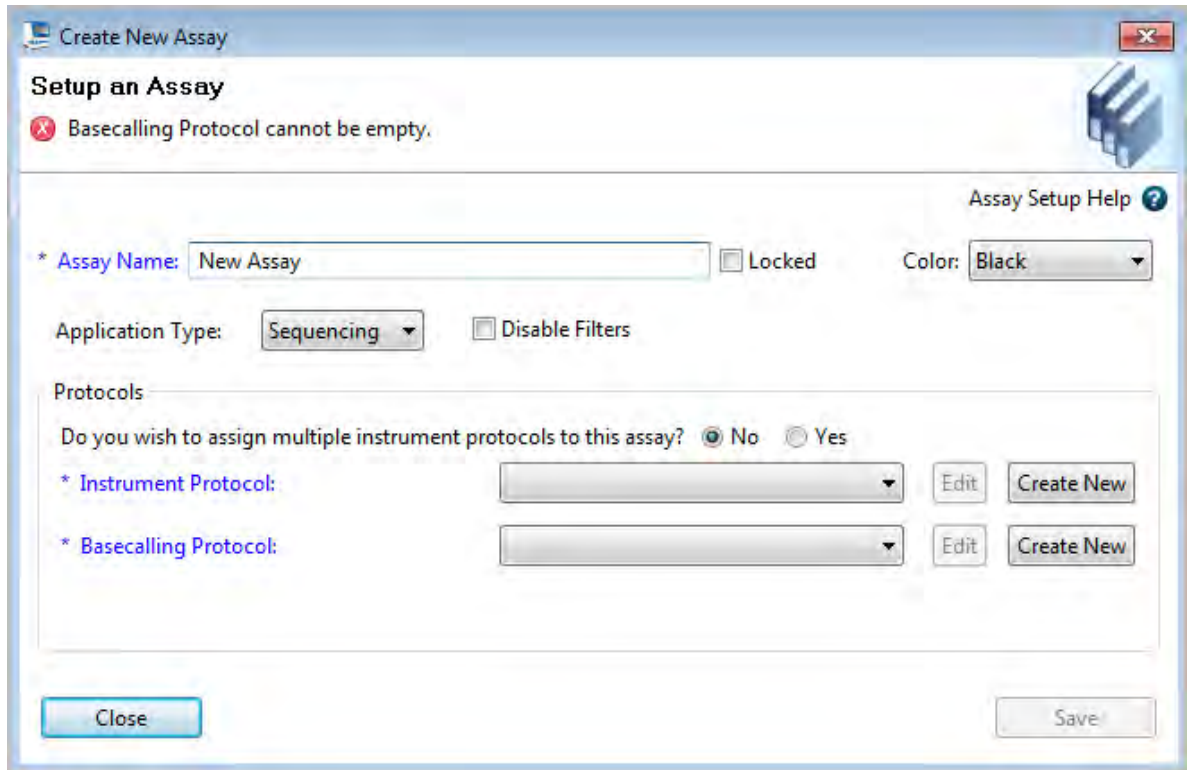
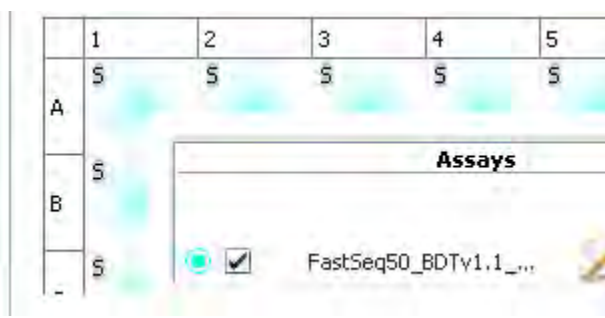
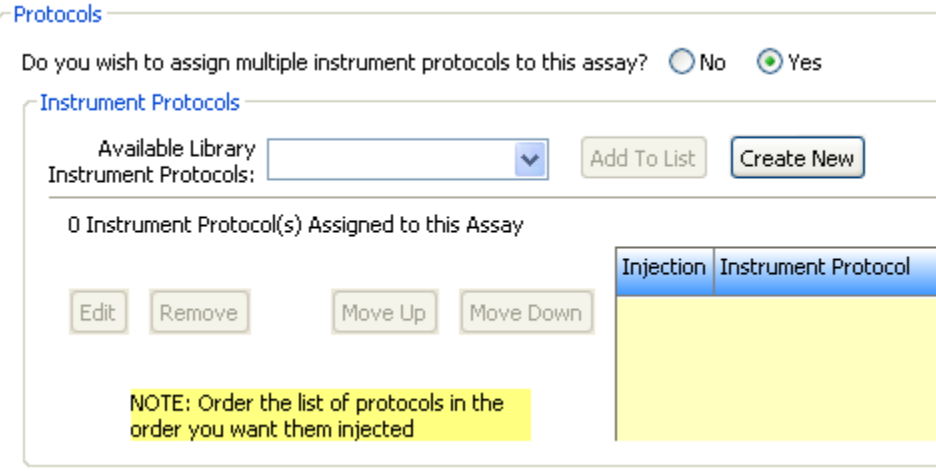


Figure 15 Create new assay

## Assay settings

Setting	Description
Assay Name	Name of the assay.
Locked	Prevents the item from being edited.
Color	Color code for the assay when it is displayed in the <b>Assign Plate Contents</b> screen (if <b>Assay Color</b> is selected for <b>Show In Wells</b> ). 
Application Type	Sequencing or Fragment.

(continued)

Setting	Description
<p><b>Do you wish to assign multiple instrument protocols to this assay?</b></p>	<p>When you select Yes, allows you to select or create additional instrument protocols for the assay. The software creates one injection for each instrument protocol specified in an assay.</p> 
<p><b>Instrument Protocol</b></p>	<p>Instrument protocol for data collection. For information, see “Instrument protocol settings” on page 190.</p>
<p><b>Basecalling Protocol (sequencing)</b></p>	<p>Protocol for basecalling, trimming, and quality determination. For information, see “Basecalling protocol—Analysis settings” on page 203.</p>
<p><b>Sizecalling Protocol (fragment analysis)</b></p>	<p>Protocol for primary analysis (peak detection and sizing) and quality determination. For information, see “Sizecalling protocol—Analysis settings” on page 208 .</p>
<p><b>QC Protocol (HID)</b></p>	<p>Protocol for primary analysis (peak detection and sizing) and quality determination. For information, see “QC protocols library (primary analysis—HID)” on page 211.</p>

# File Name Conventions library

## File name convention overview

A File Name Convention (FNC) specifies the naming convention for sample data files. It is an optional component in a plate.

If you do not specify a file name convention, data files are named in this format:

<sample name>\_<well>

The file extension is determined by the application you run:

- **Sequencing**—AB1 (you can also set Preferences to export additional file formats. See “Set preferences (optional)” on page 41.)
- **Fragment analysis**—FSA
- **HID**—HID

---

**Note:** The file location specified in a file name convention is used only if a results group is not specified for a well.

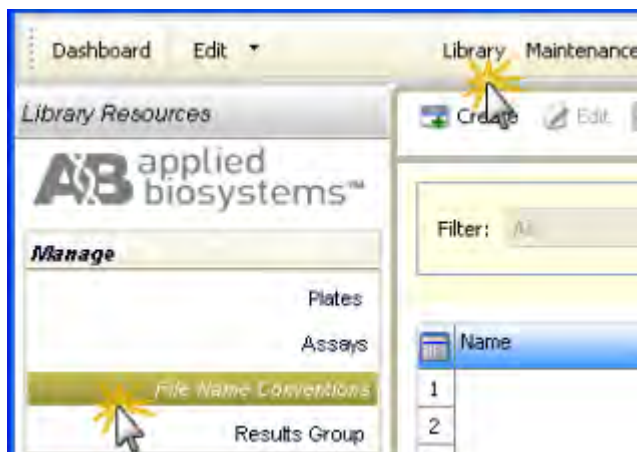
---

When you set up a plate for a run, you can optionally add file name conventions to the plate. If you add this item from the library, a *copy* of the item is added to the plate, and can be modified independently from the original item stored in the library. For information on how changes are tracked if auditing is enabled, see “Audit action” on page 233.

## Create a new file name convention

If factory-provided file name conventions do not suit your needs, you can create new file name conventions:

1. Access the **File Name Conventions** library.



2. Click  **Create**.

---

**Note:** You can also create a file name convention from the **Assign Plate Contents** screen.

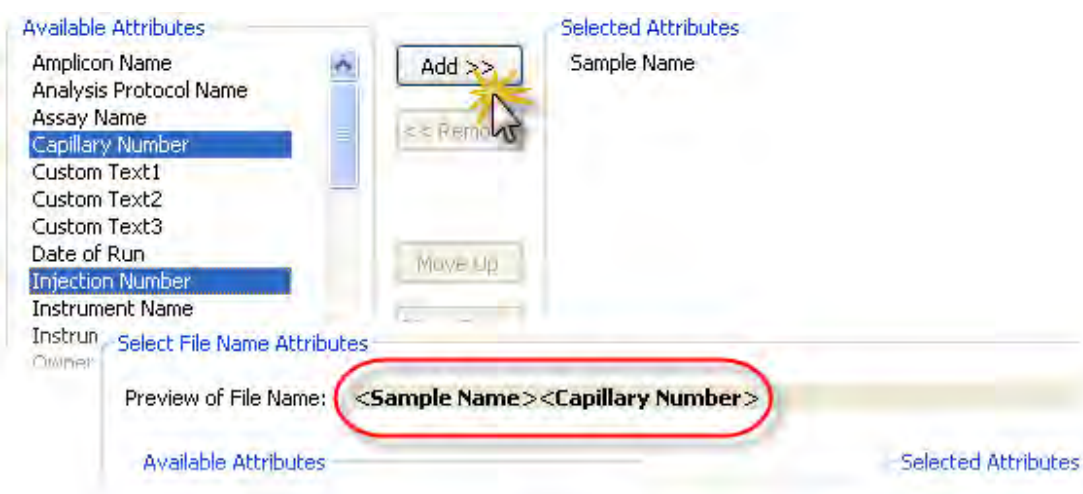
---



3. In the **Create New File Name Conventions** dialog box (Figure 16), select attributes and delimiters (“File name convention settings” on page 176).

**IMPORTANT!** Enter only alpha-numeric characters in the software. Special characters may not be correctly displayed in some software screens, may cause problems with plate, file, folder, user account, and/or library item names, and may interfere with starting a run and/or importing and exporting library items.

As you select attributes, the software displays a preview of the file name.



4. To add delimiters between items in the **Selected Attributes** list:
  - a. **Ctrl-click** or **Shift-click** to select two or more attributes.
  - b. Select a delimiter.
  - c. Select the **Add between attributes** check box.
  - d. Click **Add**.
5. Save the file name convention:
  - If you are creating the file name convention from the Library, click **Save**.
  - If you are creating the file name convention from the Assign Plate Contents screen, click **Apply to Plate** or **Save to Library**.



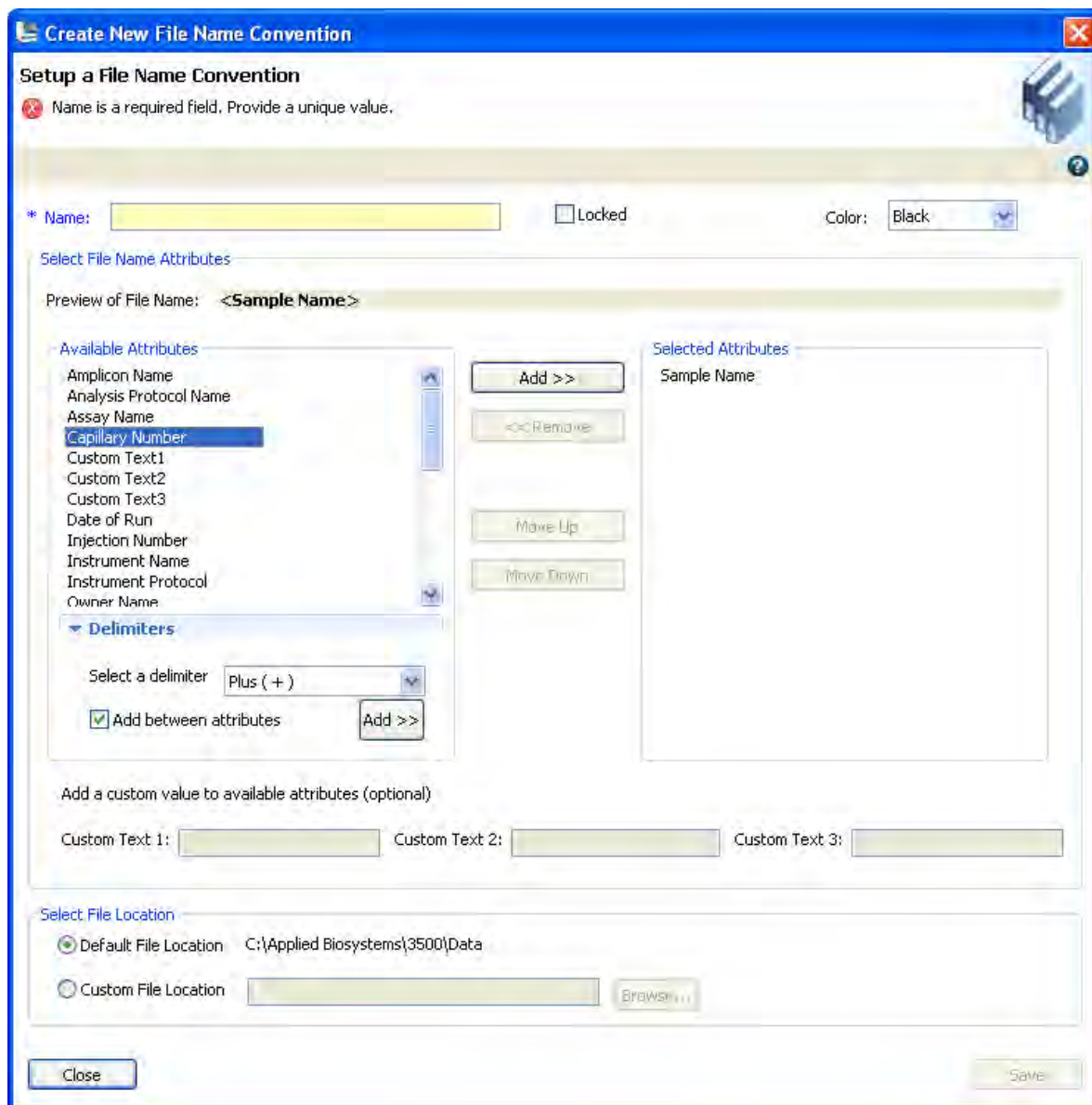


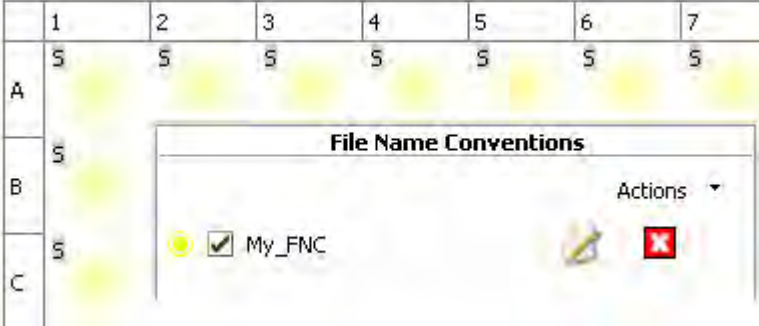
Figure 16 Create new File Name convention

## File name convention settings

Setting	Description
Name	Name of the file name convention. Names must be unique.
Locked	When enabled, allows the entry to be unlocked and modified only by the user who created it, the administrator, or another user with unlock permissions.



(continued)

Setting	Description
Color	<p>Color code for the file name convention when it is displayed in the Assign Plate Contents screen (if File Name Convention Color is selected for Show In Wells).</p> 
Preview of name	<p>Interactively displays the attributes you select.</p>
Available attributes	<ul style="list-style-type: none"> <li>• Amplicon Name (from Customize Sample Info in sequencing assays)</li> <li>• Analysis Protocol Name (primary analysis protocol)</li> <li>• Assay Name</li> <li>• Capillary Number</li> <li>• Custom Text fields (≤3)</li> <li>• Date of Run</li> <li>• Injection Number</li> <li>• Instrument Name</li> <li>• Instrument Protocol</li> <li>• Owner Name (plate owner)</li> <li>• Plate Name</li> <li>• Polymer Type</li> <li>• Run name</li> <li>• Sample Type</li> <li>• Specimen Name (from Customize Sample Info in sequencing assays)</li> <li>• Time of Run (run start time)</li> <li>• Unique Time Stamp Integer - (numeric string in milliseconds that does not correspond to the current time)</li> <li>• User-defined Fields (up to 5; specified in “Assign plate contents” on page 61)</li> <li>• User Name (available only when security is enabled in the SAE module)</li> <li>• Well Position</li> </ul>
	<p><b>IMPORTANT!</b> The maximum allowed length of a file name, including the path, is 240 characters. The software warns you if your selections will possibly exceed the maximum, but allows you to save the file name convention. However, you will see a pre-check validation error when you start a run if the file name will exceed 240 characters.</p>
Delimiters	<p>Symbols you can include in the file name: Dash (-), Dot (.), Underscore (_), Plus (+), Dollar (\$).</p>
Custom text	<p>Text to display for the custom text attribute fields.</p>
File location	<p>The file location in the file name convention is used only if no results group is specified for a well. The Results Group file location overrides the File Name Convention file location.</p>

# Results Group library

## Results Group overview

A Results Group is used to name, sort, and customize the folders in which sample data files are stored. It is an optional component in a plate.

---

**Note:** The file location specified in a results group overrides the file location in the file name convention specified for a well.

---

When you set up a plate for a run, you can optionally add results groups to wells in the plate. If you add this item from the library, a *copy* of the item is added to the plate, and can be modified independently from the original item stored in the library. For information on how changes are tracked if auditing is enabled, see “Audit action” on page 233.

## Allelic ladder location (HID analysis)

To accurately genotype samples, the GeneMapper™ *ID-X* Software requires at least one allelic ladder sample per run folder. (Multiple allelic ladder samples in a single run folder can also be used for analysis.)

We recommend that you run one allelic ladder for a set of 24 samples:

- **8-capillary instruments**—One allelic ladder per 3 injections
- **24-capillary instruments**—One allelic ladder per 1 injection

---

**Note:** Run HID validation studies to determine the required number of allelic ladders for your application.

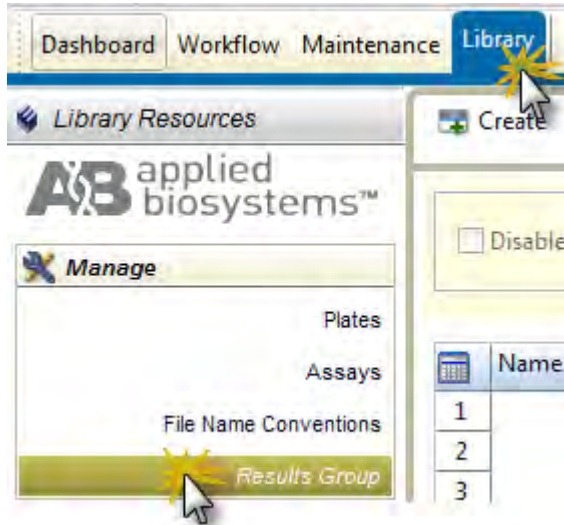
---

See “Results Group example 3: store one allelic ladder per run folder (8-capillary instruments)” on page 188 for a results group example that places three injections in each run folder for 8-capillary instruments.

## Create a new Results Group

If factory-provided results groups do not suit your needs, you can create new results groups:

1. Access the **Results Group** library.

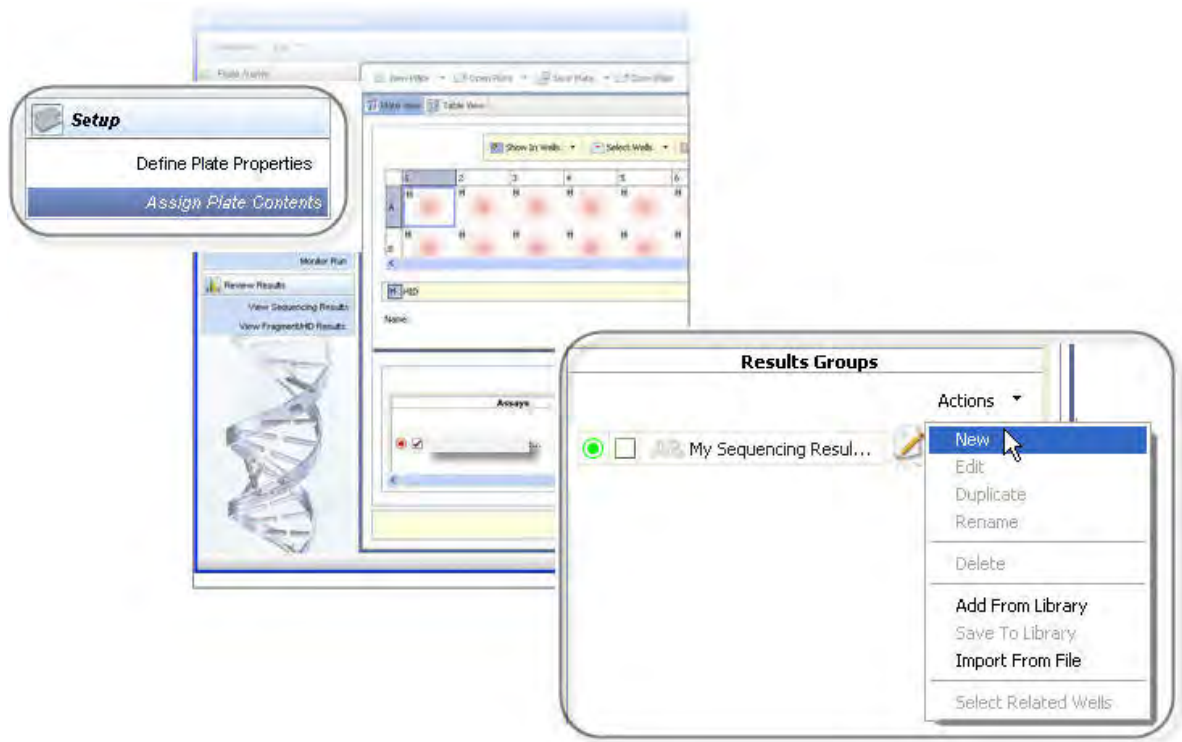


2. Click  **Create**.

---

**Note:** You can also create a results group from the **Assign Plate Contents** screen.

---



3. In the **Create Results Group** dialog box (Figure 17 on page ), select attributes and delimiters (“Results group settings” on page 182).

As you select attributes, the software displays a preview of the results group name.



4. To add delimiters between items in the **Selected Attributes** list:
  - a. **Ctrl-click** or **Shift-click** to select two or more attributes.
  - b. Select a delimiter.
  - c. Select the **Add between attributes** check box.
  - d. Click **Add**.
5. Save the results group:
  - If you are creating the results group from the Library, click **Save**.
  - If you are creating the results group from the Assign Plate Contents screen, click **Apply to Plate** or **Save to Library**.

The Results Group file location overrides the **File Name Convention** file location.

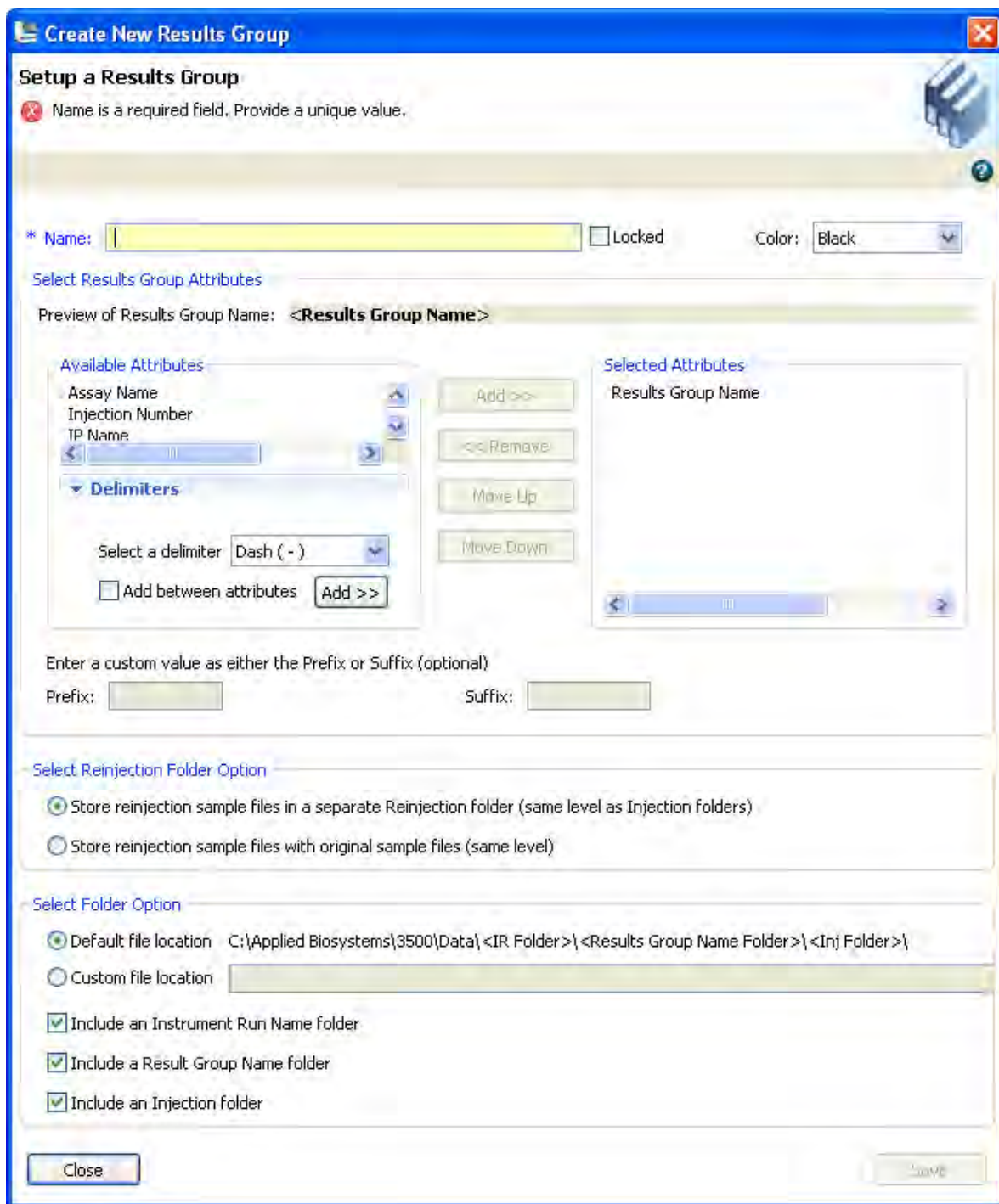
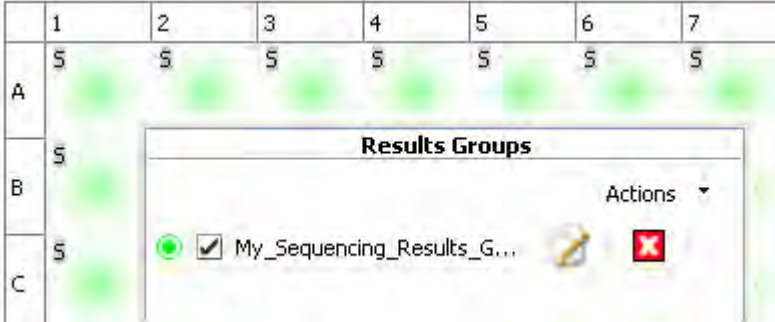


Figure 17 Create New Results Group

## Results group settings

Setting	Description
<b>Name</b>	Name of the results group. Names must be unique.  The Results Group Name is a required attribute, you cannot remove this attribute from the Selected Attribute list.
<b>Locked</b>	When enabled, allows the entry to be unlocked and modified only by the user who created it, the administrator, or another user with unlock permissions.
<b>Color</b>	Color code for the results group when it is displayed in the <b>Assign Plate Contents</b> screen (if <b>Results Group Color</b> is selected for <b>Show In Wells</b> ).  
<b>Preview of name</b>	Interactively displays the attributes you select.
<b>Available attributes</b>	<ul style="list-style-type: none"> <li>• <b>Results Group Name</b> (required)</li> <li>• <b>Assay Name</b></li> <li>• <b>Injection Number</b></li> <li>• <b>IP Name</b> (instrument protocol)</li> <li>• <b>Logged-in User Name</b> (available only when security is enabled in the SAE module)</li> <li>• <b>PA Protocol Name</b> (primary analysis=basecalling protocol)</li> <li>• <b>Plate Name</b></li> <li>• <b>Prefix</b></li> <li>• <b>Start Instrument Run Date/time Stamp</b></li> <li>• <b>Suffix</b></li> </ul>
<b>Delimiters</b>	Symbols you can include in the results group name: Dash (-), Dot (.), Underscore (_), Plus (+), Dollar (\$).
<b>Prefix/suffix text</b>	Text to display for the prefix or suffix text attribute fields.
<b>Select re-injection folder option</b>	<ul style="list-style-type: none"> <li>• Store reinjection sample files in a separate reinjection folder (same level as injection folders).</li> <li>• Store reinjection sample files with original sample files (same level).</li> </ul>



(continued)

Setting	Description
Select folder option	<p>Location:</p> <ul style="list-style-type: none"> <li>Default file location (specified in Preferences ► User ► Run Setup)</li> <li>Custom location</li> </ul> <p>Sub-folder options:</p> <ul style="list-style-type: none"> <li>Include an instrument run name folder (run name can be user-defined in the Load Plates for Run screen)</li> <li>Include a results group name folder</li> <li>Include an injection folder</li> </ul>

## Results group example 1: store files by plate name

Two default, factory-provided, results groups are provided that store sample data files by plate name:

- Figure 18 shows the factory-provided PN\_Injfolder\_RG results group and the folders created when it is used. This results group creates a folder for each injection.
- Figure 19 shows the factory-provided PN\_RG results group and the folders created when it is used. This results group does not create a folder for each injection. All samples for a plate are stored in the same folder. If you include two plates in a run, a separate folder is created for each plate.

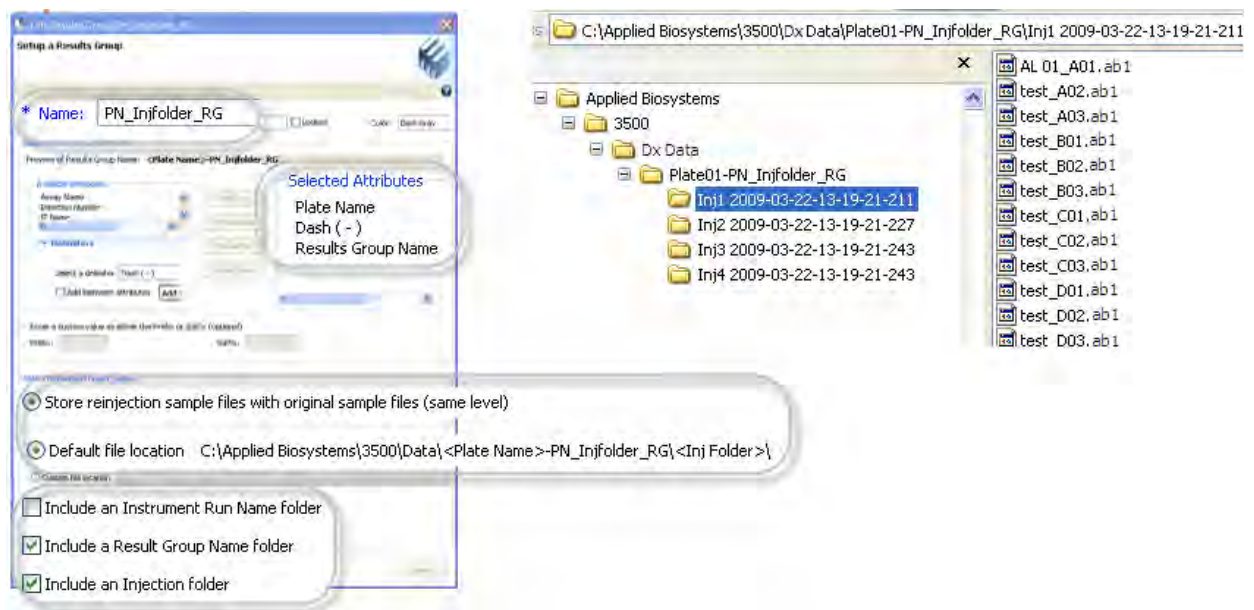


Figure 18 PN\_Injfolder\_RG results group

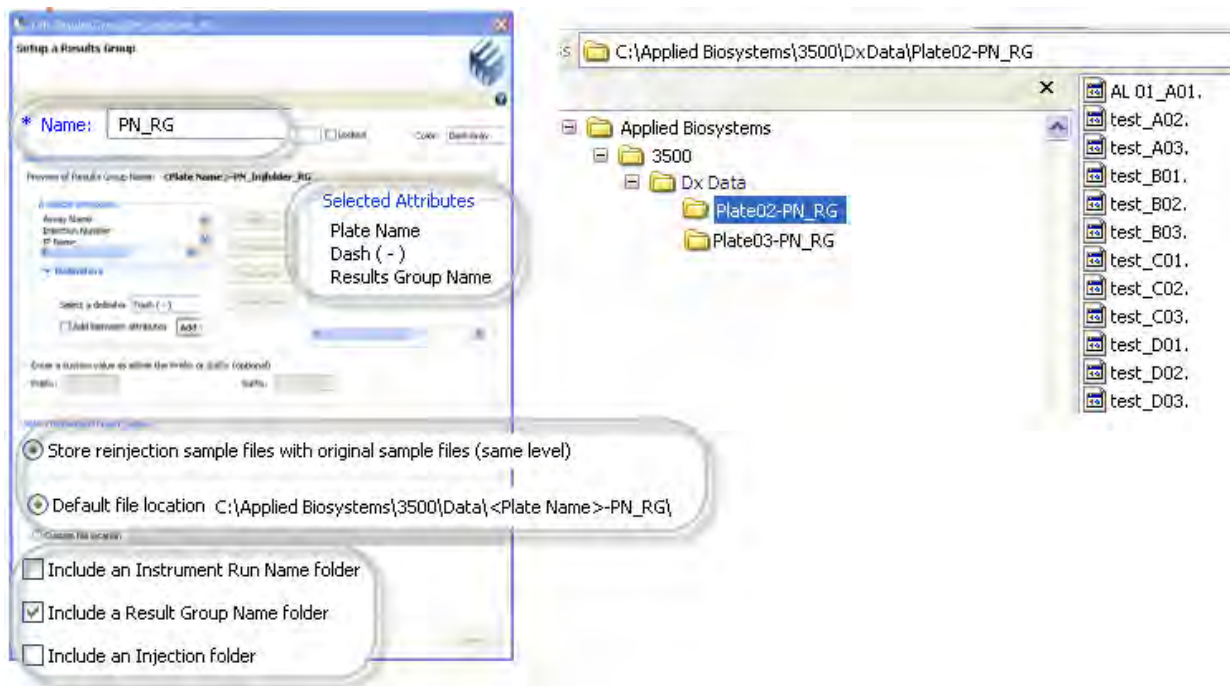


Figure 19 PN\_RG results group



## Results Group example 2: store re-injections in separate folders

Figure 20 shows an example results group that specifies a sample file storage location of:

C:\Example\instrument run (IR) folder\result group name folder[results group name+start instrument run date/time stamp+logged in user name]\injection name or re-injection name folder.

The numbers in the figure relate the elements in the results group with the elements in the file hierarchy created by a run that uses this results group (see Figure 23).

The screenshot shows the configuration for a Results Group named "RG Example".

- \* Name:** RG Example (Callout 3)
- Selected Attributes:**
  - Results Group Name (Callout 3)
  - Plus ( + )
  - Start Instrument Run Date/Time Stamp
  - Plus ( + )
  - Logged in User Name
- Select Reinjection Folder Option:**
  - Store reinjection sample files in a separate Reinjection folder (same level as Injection folders) (Callout 4)
  - Store reinjection sample files with original sample files (same level)
- Select Folder Option:**
  - Default file location C:\Applied Biosystems\3500\Data\
  - Custom file location C:\Example (Callout 1)
  - Include an Instrument Run Name folder (Callout 2)
  - Include a Result Group Name folder (Callout 3)
  - Include an Injection folder (Callout 4)

Figure 20 Results group example

Figure 21 shows the injection list for a run that specifies duplicate and re-injections.

The numbers in the figure relate the elements in the injection list with the elements in the file hierarchy created by this run (see Figure 23).

Connection Status: Connected  
Run Name: Run 2009-02-05-14-59-56-703

User Name: Administrator  
Run Status: Running

**Injection List Details**  
7 injections created - 7 in Plate A - 0 in Plate B

Injection	Type	Assay	Instrument Protocol	Plate	Analysis	Flags
1	(duplicate and re-injections)	IF+Norm_POP4_xl	HID36_POP4xl_G5	Plate 01	✓	
2		IF+Norm_POP4_xl	HID36_POP4xl_G5	Plate 01	✓	
3		IF+Norm_POP4_xl	HID36_POP4xl_G5	Plate 01	✓	
4		IF+Norm_POP4_xl	HID36_POP4xl_G5	Plate 01	✓	
5		IF+Norm_POP4_xl	HID36_POP4xl_G5	Plate 01	✓	
6		IF+Norm_POP4_xl	HID36_POP4xl_G5	Plate 01	✓	
7		IF+Norm_POP4_xl	HID36_POP4xl_G5	Plate 01		

Figure 21 Injection list example

Figure 22 shows an example file name convention that specifies a sample name syntax of:

sample name.(primary) analysis protocol name.unique time stamp integer

The numbers in the figure relate the elements in the file name convention with the files created by a run that uses file name convention (see Figure 23).

\* Name:   Locked

Select File Name Attributes

Preview of File Name: <Sample Name>.<Analysis Protocol Name>.<Unique Time Stamp Integer>

<p>Available Attributes</p> <ul style="list-style-type: none"> <li>Amplicon Name</li> <li>Assay Name</li> <li>Capillary Number</li> <li>Custom Text1</li> <li>Custom Text2</li> <li>Custom Text3</li> <li>Date of Run</li> </ul>	<input type="button" value="Add &gt;&gt;"/>  <input type="button" value="&lt;&lt; Remove"/>	<p>Selected Attributes</p> <ul style="list-style-type: none"> <li>Sample Name</li> <li>Dot ( . )</li> <li>Analysis Protocol Name</li> <li>Dot ( . )</li> <li>Unique Time Stamp Integer</li> </ul>
--	---	---

Figure 22 File name convention example

Figure 23 shows the folders and files generated by the results group, file name convention, run name, and injections shown in Figure 20, Figure 21, and Figure 22.

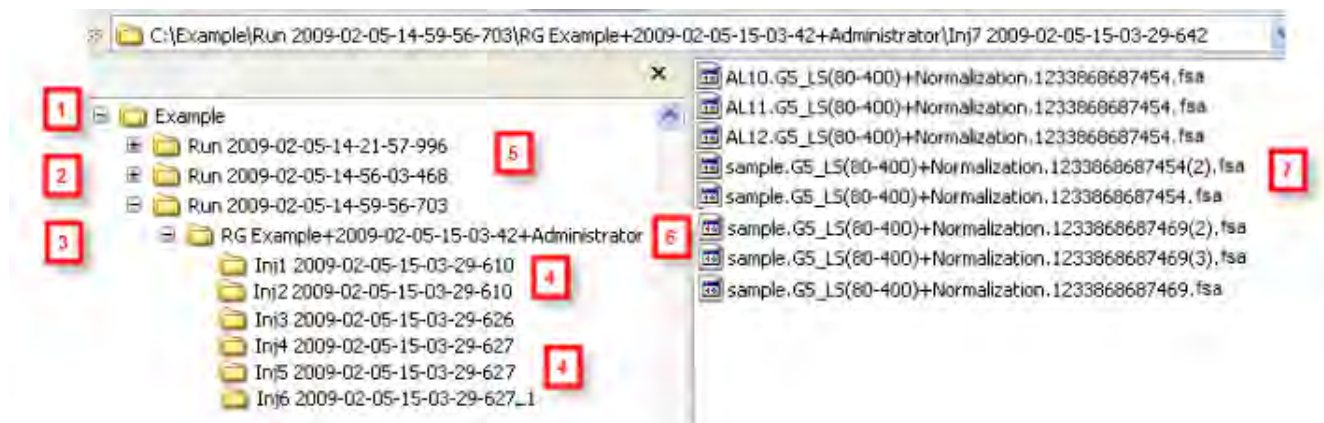


Figure 23 Folder hierarchy and file naming example

1	File location from results group <input type="radio"/> Custom file location <input type="radio"/> C:\Example
2	Instrument Run Name folder from results group <input checked="" type="checkbox"/> Include an Instrument Run Name folder
3	Results group Name folder from results group <input checked="" type="checkbox"/> Include a Result Group Name folder
4	Injection folder from results group <input checked="" type="checkbox"/> Include an Injection folder <ul style="list-style-type: none"> <li>• Duplicate injections (📄) have the same base folder name as the original injection. In the example above, the following injections are duplicates: 1 and 2, 4 and 5.</li> <li>• Re-injections (📄) have the same base folder name as the original injection, and are indicated with <code>_n</code> where <code>n</code> is the number of re-injections. In the example above, Injection 6 is a re-injection of Injection 5.</li> </ul>
5	Run name (default or user-defined) from injection list Run Name: Run 2009-02-05-14-59-56-703
6	Results group name syntax from results group <b>RG Example + &lt;Start Instrument Run Date/Time Stamp&gt; + &lt;Logged in User Name&gt;</b>
7	File name syntax from file name convention <b>&lt;Sample Name&gt;. &lt;Analysis Protocol Name&gt;. &lt;Unique Time Stamp Integer&gt;</b>

## Results Group example 3: store one allelic ladder per run folder (8-capillary instruments)

We recommend that you run one allelic ladder for each set of 24 samples (see “Allelic ladder location (HID analysis)” on page 178).

To store one allelic ladder per run folder on an 8-capillary instrument, create one results group for each set of three injections on the plate. Each results group specifies a results group name folder. Because you assign one results group to a set of three injections, all 24 sample data files, including the allelic ladder, are stored in the same results group folder.

The example below shows one results group; for a full 96-well plate, create three more with the same settings, but different names, for example, Injection 4 through 6, Injection 7 through 9, and Injection 10 through 12.

**Create New Results Group**

\* Name:   Locked

Select Results Group Attributes

Preview of Results Group Name: **Injection 1 - 3**

Available Attributes: IP Name, Logged in User Name, PA Protocol Name

Selected Attributes: Results Group Name

Select Reinjection Folder Option

Store reinjection sample files in a separate Reinjection Folder (same level as Injection folder)

Store reinjection sample files with original sample files (same level)

Select Folder Option

Default file location C:\Applied Biosystems\3500\Data\<IR Folder>\Injection 1 - 3\

Custom file location

Include an Instrument Run Name folder

Include a Result Group Name folder

Include an Injection folder

Close Save

# Instrument protocol library

## Instrument protocol overview

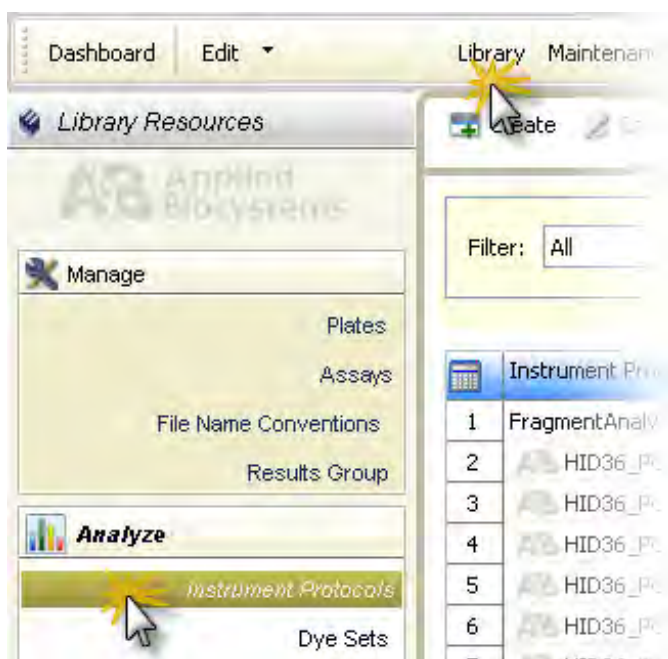
An instrument protocol contains the parameters that control the instrument during data acquisition. An instrument protocol is a required element of an assay for all applications.

When you create an assay, you add one or more instrument protocols to the assay. If you add these items from the library, a *copy* of the items is added to the assay, and can be modified independently from the original items stored in the library. For information on how changes are tracked if auditing is enabled, see “Audit action” on page 233.

## Create a new instrument protocol

If factory-provided instrument protocols do not suit your needs, you can create new instrument protocols:

1. Access the Instrument Protocols library.



2. Click  **Create**.

- In the Create New Instrument Protocol dialog box (Figure 24), select an application type: Sequencing, Fragment, or HID. The run module selection list is filtered based on the application you select.

Figure 24 Create New Instrument Protocol

**Note:** Normalization parameters circled in red are displayed for fragment analysis and HID applications only.

- Specify settings (“Instrument protocol settings” on page 190).
- Save the assay:
  - If you are creating the assay from the Library, click **Save**.
  - If you are creating the assay from the Assign Plate Contents screen, click **Apply to Plate** or **Save to Library**.

## Instrument protocol settings



Setting	Description
Application Type	<ul style="list-style-type: none"> <li>Sequencing</li> <li>Fragment analysis</li> <li>HID</li> </ul>

(continued)

Setting	Description
Capillary Length, Polymer, Dye set	Capillary length, polymer type, and dye set with which the protocol will be used
Run module	Factory-provided modules that specify instrument control parameters. For more information, see Appendix B, “Run modules and dye sets”.
Protocol name	Name of the protocol. Names must be unique.
Locked	When SAE is enabled, allows the entry to be unlocked and modified only by the user who created it, the administrator, or another user with unlock permissions. Useful when your system includes the SAE module (described in Chapter 9, “Use Security, Audit, and E-Sig functions (SAE Module)”.
Description	Optional text entry.
Oven temperature (°C)	Temperature setting for main oven throughout run.
Run voltage (kVolts)	Final sample electrophoresis separation run voltage.
Prerun voltage (kVolts)	Pre run voltage setting before sample injection.
Injection voltage (kVolts)	Injection voltage setting for sample injection.
Run time (sec)	Length of time data is collected after voltage is ramped up to the run voltage and the run starts.
PreRun time (sec)	Prerun voltage time.
Injection time (sec)	Sample injection time.
Data delay (sec)	Time from the start of separation to the start of sample data collection.
<i>Advanced options - Do not change unless advised otherwise by Thermo Fisher Scientific support personnel</i>	
Voltage tolerance (kVolts)	Maximum allowed voltage variation.
Voltage # of Steps (nk)	Number of voltage ramp steps to reach Run Voltage.
Voltage step interval (sec)	Dwell time at each voltage ramp step.
First read out time (ms)	The interval of time for a data point to be produced. First ReadOut time should be equal to Second ReadOut time.
Second read out time (ms)	The interval of time for a data point to be produced. Second ReadOut time should be equal to First ReadOut time.
<b>Fragment and HID protocols only:</b> Normalization parameters - Leave at default settings (for information on how these parameters are used, see “Review normalized data” on page 117).	



(continued)

Setting	Description
Normalization Target	<p>The expected average RFU for the subset of peaks in the GS600 LIZ™ v2 size standard used for normalization.</p> <p>The default value for each run module has been experimentally determined based on the average peak height of selected peaks in the GS600 size standard with a specific injection time.</p> <p><b>IMPORTANT!</b> If you change the injection time in an instrument protocol, adjust the Normalization Target proportionately. For example, for an instrument protocol with an injection time of 10 seconds and a Normalization Target of 2000: if you change the injection time to 15 seconds (50% increase), change the Normalization Target to 3000 (50% increase).</p>
Normalization Factor Thresholds	<p>The passing range for Normalization Factor (default range is 0.3 to 3.0).</p> <p><b>IMPORTANT!</b> Increasing the factor threshold above 3.0 may cause amplification of noise.</p> <p>If the calculated Normalization Factor is outside the Normalization Factor range, the software multiplies the peak heights of the sample by the low or high Normalization Factor threshold setting (for example, if the Normalization Factor range is 0.3 to 3.0 and the calculated Normalization Factor is 5, the software applies a Normalization Factor of 3.0).</p>
Normalization Factor	<p>Average peak height of the subset of peaks in the GS600 LIZ™ v2 size standard used for normalization divided by the Normalization Target. Samples are flagged with  in results if Normalization Factor is within threshold range, or with  if it is out of threshold range.</p>

## Dye sets library

### Dye set overview

A dye set defines the following for an instrument protocol:

- Dye color(s)
- Order of the dye peaks in the standard
- Spectral analysis parameters

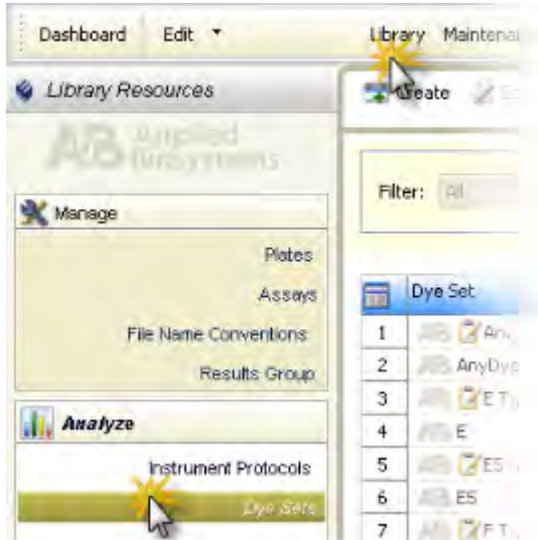
When you create an instrument protocol, you add a dye set to the protocol. If you add this item from the library, a copy of the item is added to the assay, and can be modified independently from the original item stored in the library. For information on how changes are tracked if auditing is enabled, see “Audit action” on page 233.



## Create a new dye set

If factory-provided dye sets do not suit your needs, you can create new dye sets:

1. Access the Dye Sets library.



2. Click  **Create**.

- In the Create New Dye Set dialog box (Figure 25), specify settings (“Dye set settings” on page 195).

**Create New Dye Set**

**Setup a Dye Set**

✘ Dye Set Name is a required field. Provide a unique value.

\* Dye Set Name   Locked

\* Chemistry

\* Dye Set Template

**Arrange Dyes**

Dye Selection	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
Reduced Selection	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
Calibration Peak Order	5	4	3	2	1

**Parameters**

The parameters will be used for instruments configured with 50cm capillary array and polymer POP7

Matrix Condition Number Upper Limit

Locate Start Point \* After Scan  \* Before Scan

\* Limit Scans To

Sensitivity

\* Minimum Quality Score

**Notes**

Applied Biosystems

Figure 25 Create New Dye Set

- Click **Save**.

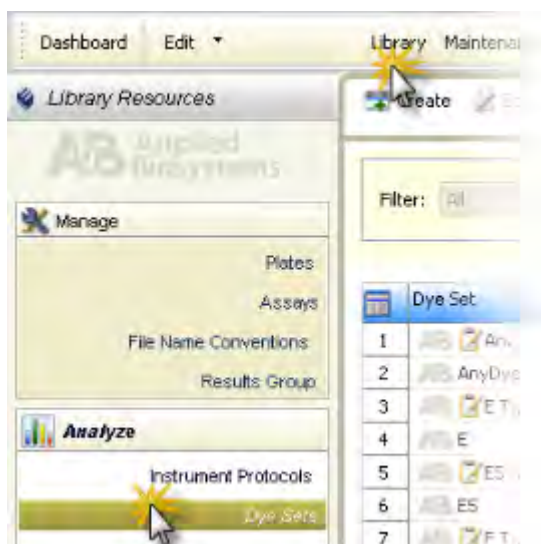
## Dye set settings

Setting	Description
Dye Set Name	Name of the dye set. Names must be unique.
Locked	When enabled, allows the entry to be unlocked and modified only by the user who created it, the administrator, or another user with unlock permissions. Useful when your system includes the SAE module (described in Chapter 9, “Use Security, Audit, and E-Sig functions (SAE Module)”).
Chemistry	The standard for which you are creating the dye set: Sequencing Standard or Matrix standard
Dye Set Template	Factory-provided template upon which to base the dye set.  The Any Dye template can be used for applications that do not use all of the dye colors contained in the matrix standard kits used for spectral calibration. For information, see “Create a new dye set using the AnyDye template” on page 195.
Arrange Dyes	Displays the dyes and the peak order for the dye set template selected. Editable only for AnyDye template: <ul style="list-style-type: none"> <li>• <b>Dye Selection</b>—Specifies the dyes to use for calibration</li> <li>• <b>Reduced Selection</b>—Specifies the dyes used in the samples.</li> </ul> For example, if you use the 5 dye kit and have samples with only blue peaks, you can “reduce” or deconvolute with blue and orange (size standard) dyes only.
Parameters	Specifies the Quality Value, Condition Number, Scan, and Sensitivity requirements for the dye set.
Notes	Optional text entry.

## Create a new dye set using the AnyDye template

If factory-provided dye sets do not suit your needs, you can create new dye sets:

1. Access the Dye Sets library.



2. Click  **Create**.

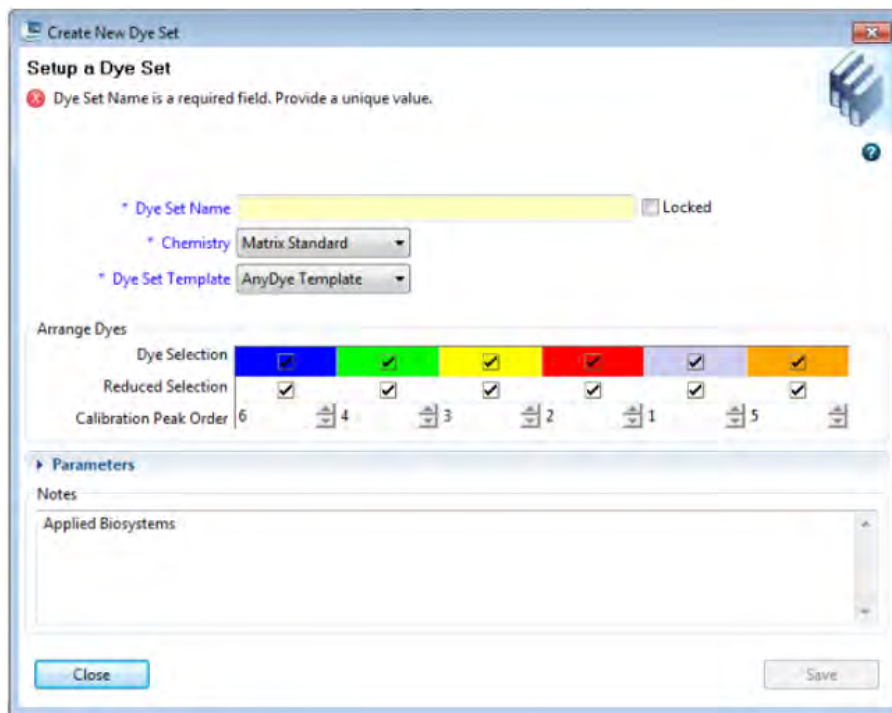


Figure 26 Create New Dye Set using the AnyDye template

3. Enter a dye set name.
4. Select a chemistry and the **AnyDye** dye set template.
5. Select the dye colors that are present in your dye set by selecting or deselecting the checkboxes in the **Dye Selection** row.

An internal ID number is assigned to each selected dye color based on the emission wavelength, from the shortest to the longest wavelength.

---

**IMPORTANT!** *The internal ID numbers are not displayed in the software.*

---

Figure 27 illustrates that the internal ID numbers change based on the dyes that are selected (from left to right). The internal ID numbers are shown in parentheses in the examples below for illustrative purposes.



Figure 27 Internal ID examples—IDs that correspond to dye colors are determined by the dyes that are selected (the internal ID numbers shown in the example are not shown in the software)

- ① **Example 1**—With all dyes selected, the internal ID numbers that are assigned to dye colors are: Blue (1), Green (2), Yellow (3), Red (4), Purple (5), Orange (6).
- ② **Example 2**—With the Purple dye *deselected*, the internal ID numbers that are assigned to dye colors are: Blue (1), Green (2), Yellow (3), Red (4), Orange (5)—the internal ID of the Orange dye changes to 5.
- ③ **Example 3**—With the Blue, Yellow, and Purple dyes *deselected*, the internal ID numbers that are assigned to dye colors are: Green (1), Red (2), Orange (3)—the internal ID of Green changes to 1, Red changes to 2, and Orange changes to 3.

6. Specify the migration order of the dyes in the **Calibration Peak Order** row.

Because the software does not allow you to set the migration order by color, you must enter the internal ID numbers associated with the dyes as determined in the previous step.

**IMPORTANT!** The Calibration Peak Order fields do not correspond to the dye colors displayed above the Calibration Peak Order fields.

Figure 28 through Figure 30 show examples of how to set migration order for the selected dyes. The internal ID numbers are shown in parentheses in the examples below for illustrative purposes.

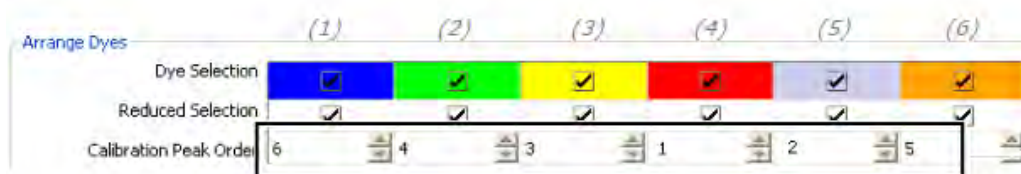


Figure 28 Example 1—For migration order of Orange, Red, Yellow, Blue, Green, Purple, specify Calibration Peak Order of 6 (Orange), 4 (Red), 3 (Yellow), 1 (Blue), 2 (Green), 5 (Purple).

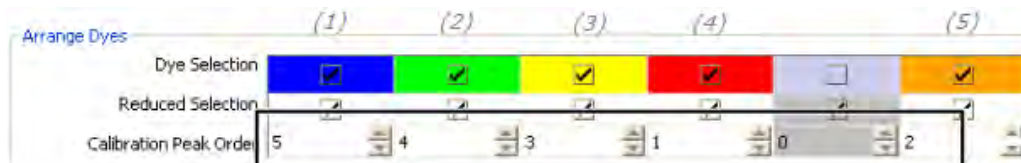


Figure 29 Example 2—For migration order of Orange, Red, Yellow, Blue, Green, specify Calibration Peak Order of 5 (Orange), 4 (Red), 3 (Yellow), 1 (Blue), 2 (Green).

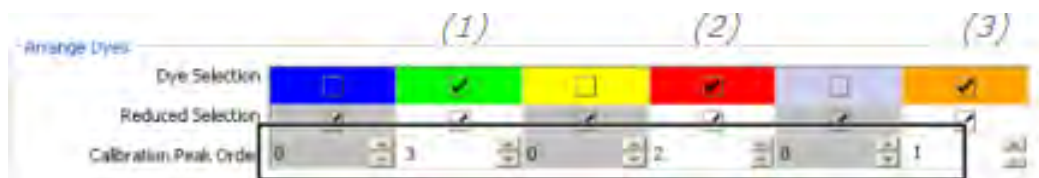


Figure 30 Example 3—For migration order of Orange, Red, Green, specify Calibration Peak Order of 3 (Orange), 2 (Red), 1 (Green).

**Note:** The Reduced Selection row contains checkmarks to indicate that the dye will be used for calibration. If a dye is not selected in the Dye Selection row, it is unselected in the Reduced Selection row and is not used for calibration.

7. (Optional) Expand the **Parameters** section, then specify remaining settings.
8. Click **Save**.

## Size standards library

### Size standard overview

A size standard defines the sizes of known fragments. It is used to generate a standard curve. The standard curve is used to determine the sizing of unknown samples.

When you create a sizecalling (fragment) or QC (HID) protocol, you add a size standard to the protocol. If you add this item from the library, a *copy* of the item is added to the protocol, and can be modified independently from the original items stored in the library. For information on how changes are tracked if auditing is enabled, see “Audit action” on page 233.

### Normalization size standards provided

The library contains factory-provided normalized size standards that you can use to normalize fragment analysis and HID data:

- Fragment analysis:
  - GS600LIZ+Normalization
  - GS600(60-600)LIZ+Normalization—For applications that have primer peaks that obscure the 20 and 40-mer peaks of the GS600 size standard.
- HID:
  - GS600(80-400)LIZ+Normalization

Normalization corrects for instrument, capillary, and injection variability. For each sample, the software calculates a normalization factor based on a threshold setting. The normalization factor is used as a multiplier to adjust the peak height of the sample peaks relative to the GS600 LIZ™ v2.0 size standard peaks.

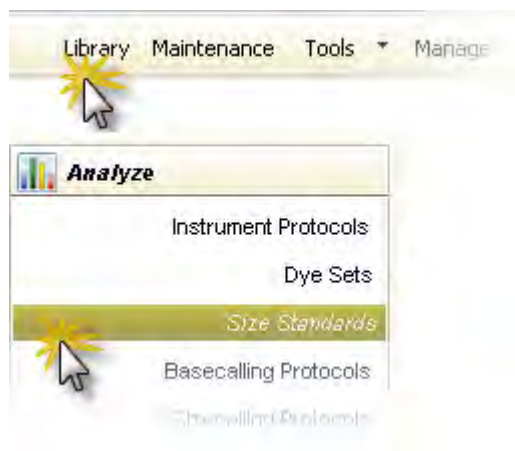
**IMPORTANT!** Normalization is not applied to samples with failing sizing quality. Select a size standard definition file appropriate for your application that accurately sizes samples. For example, if your application includes small fragments that may be obscured by primer peaks, or large fragments that may not be present due to slower migration rates, specify a size standard definition file that eliminates these fragments from sizing.


For more information, see “Review normalized data” on page 117.

## Create a new size standard

If factory-provided size standards do not suit your needs, you can create new size standards:

1. Access the Size Standards library.



2. Click  **Create**.
3. In the Create New Size Standard dialog box (Figure 31), enter a size standard name.
4. (Optional):
  - Select the **Locked** check box.  
When enabled, allows the entry to be unlocked and modified only by the user who created it, the administrator, or another user with unlock permissions. Useful when your system includes the SAE module (for more information, see Chapter 9, “Use Security, Audit, and E-Sig functions (SAE Module)”).
  - Enter a description.
5. Select a dye color.
6. Enter sizes in the list on the left. Separate sizes with a comma, space, or return.

7. Click **Add Sizes**.
8. Click **Save**.

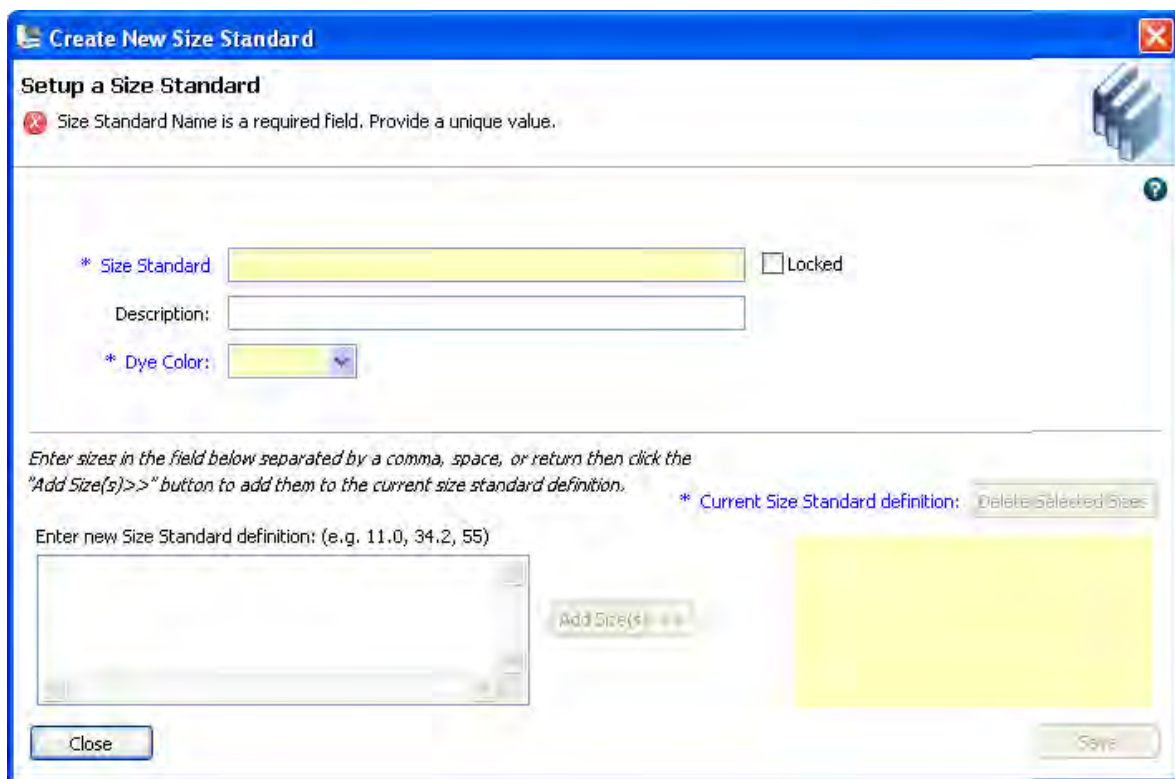



Figure 31 Create New Size Standard

## Modify a factory-provided normalization size standard

1. Select a factory-provided normalization size standard (indicated in the name with "+Normalization.").
2. Click  **Duplicate**.
3. Edit the copy of the normalized size standard. The size standard peaks used to normalize the data are displayed in gray and are not editable.
4. Click **Save**.



# Basecalling protocols library (primary analysis—sequencing)

## Basecalling protocol overview

A basecalling protocol is the required primary analysis protocol for sequencing applications.

A basecalling protocol defines the settings used by the sequencing basecallers to assign base calls to each detected peak and assign a quality value:

- Analysis settings
- Ranges for the sequencing quality flags displayed in View Results


When you create a sequencing assay, you add a basecalling protocol to the assay. If you add this item from the library, a copy of the item is added to the assay, and can be modified independently from the original item stored in the library. For information on how changes are tracked if auditing is enabled, see “Audit action” on page 233.

## Create a new basecalling protocol

If factory-provided basecalling protocols do not suit your needs, you can create new basecalling protocols:

1. Access the Basecalling Protocols library.



2. Click  **Create**.
3. In the Analysis Settings tab of the Create New Basecalling Protocol dialog box (Figure 32), specify settings “Basecalling protocol—Analysis settings” on page 203.

- Click **QV Settings**. In the QV Settings tab of the Create New Basecalling Protocol dialog box (Figure 33), specify settings (see “Basecalling protocol—QV settings” on page 205).

QV settings are quality value ranges used in the following screens:

- **Monitor Run screen**—The state of the QV flag:
  - If all three values are in the pass range, the QV flag in Monitor Run is set to ■ (green).
  - If any values are in the suspect range, the QV flag in Monitor Run is set to ▲ (yellow).
  - If any values are in the fail range, the QV flag in Monitor Run is set to ● (red).
- **View Sequencing Results ▶ Metric Analysis Results table**—The pass/check/fail status for Trace Score Quality, CRL Quality, and QV20+ Quality results.

- Click **Save**.



Figure 32 Create New Basecalling Protocol—Analysis Settings

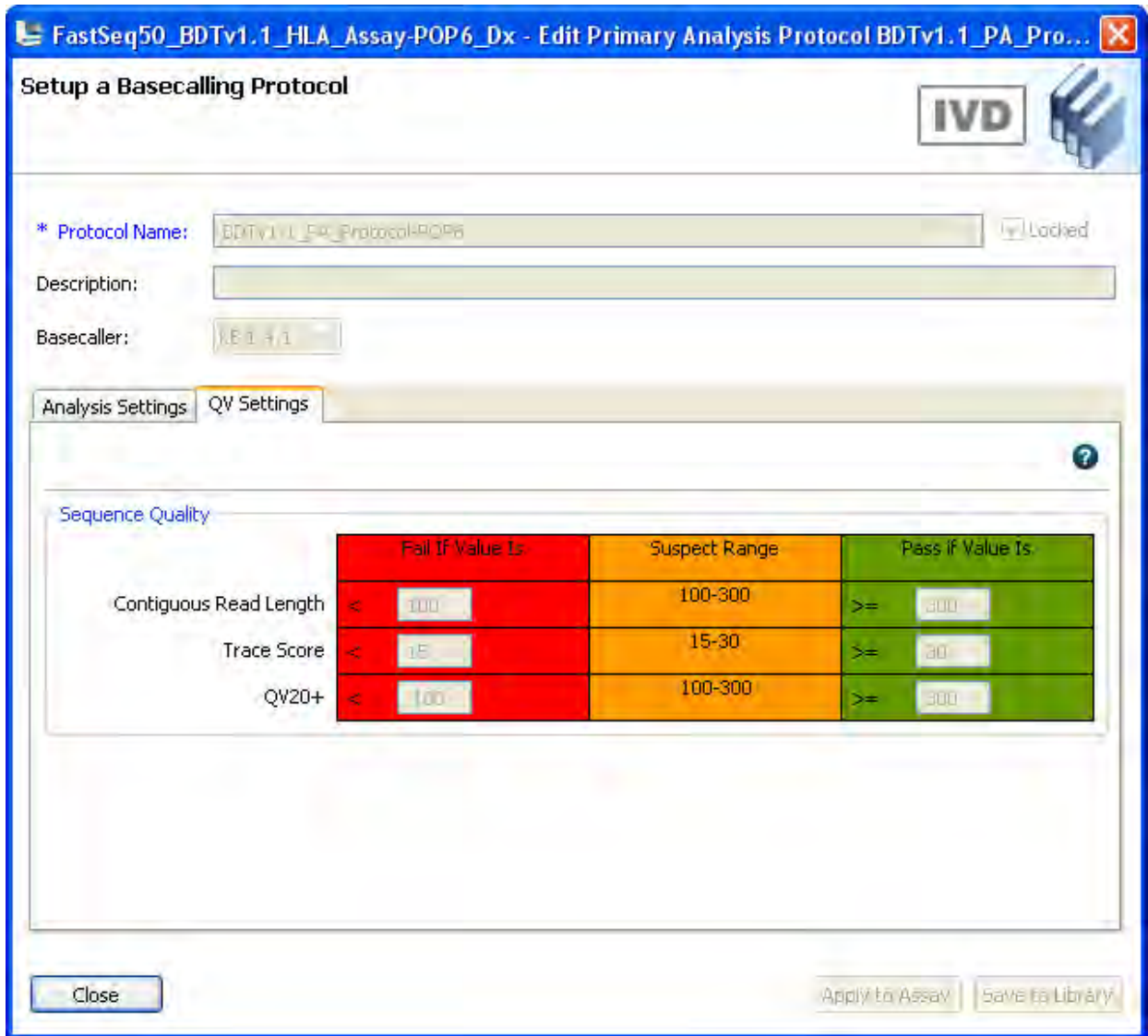
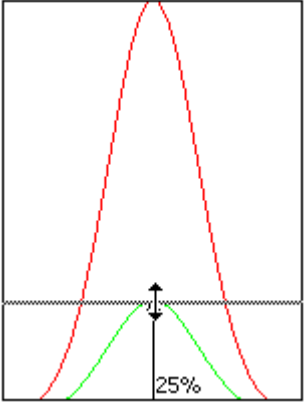


Figure 33 Create New Basecalling Protocol—QV Settings

## Basecalling protocol—Analysis settings

Setting	Description
<b>Name</b>	Name of the protocol. Names must be unique.
<b>Locked</b>	When SAE is enabled, allows the entry to be unlocked and modified only by the user who created it, the administrator, or another user with unlock permissions. Useful when your system includes the SAE module (described in Chapter 9, “Use Security, Audit, and E-Sig functions (SAE Module)”).
<b>Description</b>	Optional text entry.

(continued)

Setting	Description
<b>Basecaller</b>	Basecalling algorithm used to identify bases.  <b>Note:</b> The basecaller version listed in the basecalling protocol is a 3-digit number. The version listed in sequencing results is a 4-digit number. The fourth digit is an internal number used by the software.
<b>Mobility file</b>	Compensates for mobility differences between dyes used to label the DNA.
<b>Quality Threshold</b>	<ul style="list-style-type: none"> <li>• Basecall Assignment (ambiguous bases):               <ul style="list-style-type: none"> <li>– Do not assign Ns to basecalls</li> <li>– Assign Ns to basecalls with <math>QV &lt; 15</math>—Bases with a QV less than the threshold display N instead of the base letter</li> </ul> </li> <li>• Ending base—Last base on which to perform basecalling:               <ul style="list-style-type: none"> <li>• At PCR Stop</li> <li>• After X number of Bases</li> <li>• After X number of Ns in X number of Bases</li> <li>• After X number of Ns</li> </ul> </li> </ul> <b>Note:</b> If you have PCR products with sequences that end while data is still being collected, select the <b>At PCR Stop</b> check box.
<b>Mixed bases threshold</b>	When enabled, determines the secondary peak height ratio where the secondary peak is considered a potential mixed base. Reaching the threshold is a necessary but not sufficient condition for the basecalling algorithm to call a mixed base.  Do not assign a mixed base when the secondary peak height is $\leq$ to <input type="text" value="25"/> %  

(continued)

Setting	Description
<b>Analyzed Data Scaling</b>	<p>Determines scaling of the processed traces. This parameter does not affect the accuracy of the basecalling.</p> <ul style="list-style-type: none"> <li>• <b>True Profile</b>—The processed traces are scaled uniformly so that the average height of peaks in the region of strongest signal is about equal to a fixed value. The profile of the processed traces will be very similar to that of the raw traces.</li> <li>• <b>Flat Profile</b>—The processed traces are scaled semi-locally so that the average height of peaks in any region is about equal to a fixed value. The profile of the processed traces will be flat on an intermediate scale (&gt; about 40 bases).</li> </ul>
<b>Clear range methods</b>	<ul style="list-style-type: none"> <li>• <b>Use clear range minimum and maximum</b>—Specifies the first and last base in the range to consider, or trims the specified number of bases from the 3' end.</li> <li>• <b>Use quality values</b>—Sets a window with a specified number of allowed low-quality bases by removing bases until there are &lt; X number of bases per Z number of bases with QV &lt; Y.</li> <li>• <b>Use identification of N cells</b>—Sets a window with a specified number of allowed ambiguous base calls (Ns) by removing bases until there are &lt; X number of Ns per Y number of bases.</li> </ul>

## Basecalling protocol—QV settings

Setting	Description
<b>Contiguous Read Length</b>	<p>The longest uninterrupted segment of basecalls with an average Quality Value (QV) <math>\geq 20</math>.</p> <p>In addition to evaluating the QV of a basecall, the software considers the QV of adjacent basecalls within a 21-bp moving window to determine a contiguous read length based on quality values: the software starts from the 5' end and calculates the average QV across a moving window size of 21, sliding 1 bp at a time, to the 3' end. The resulting longest contiguous segment is determined as the CRL.</p>
<b>Trace Score</b>	<p>The average basecall Quality Value (QV) of basecalls in the clear range sequence of a trace.</p> <p>The <i>clear range</i> is the region of the sequence that remains after excluding the low-quality or error-prone sequence at the 5' and 3' ends. The clear range is calculated by the KB Basecaller using QVs.</p>
<b>QV20+</b>	<p>The total number of bases in the entire trace with Quality Value <math>\geq 20</math>.</p>

## Sizecalling protocols library (primary analysis—fragment)

### Sizecalling protocol overview

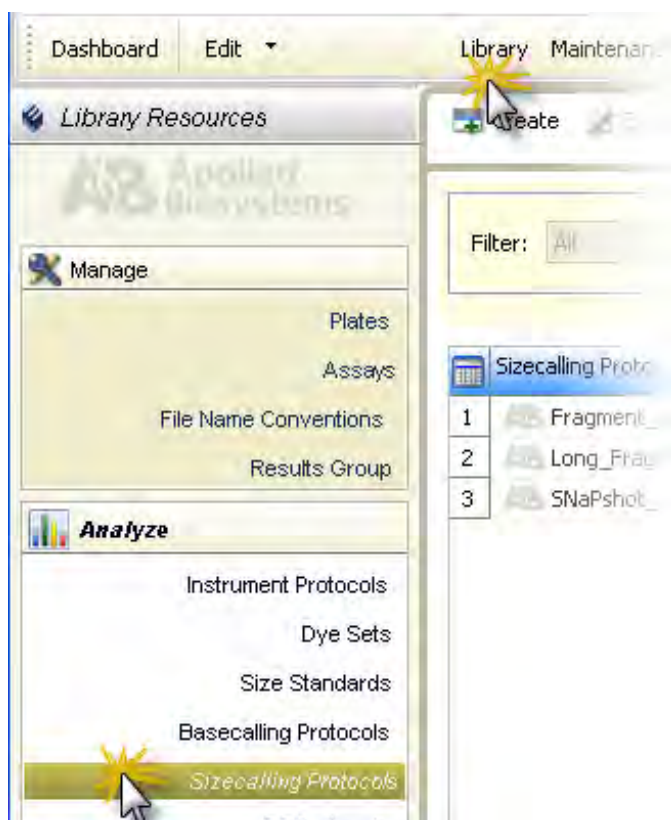
A sizecalling protocol is the required primary analysis protocol for fragment applications.


A sizecalling protocol defines peak detection, sizing, and quality values.

When you create a fragment assay, you add a sizecalling protocol to the assay. If you add this item from the library, a copy of the item is added to the assay, and can be modified independently from the original item stored in the library. For information on how changes are tracked if auditing is enabled, see “Audit action” on page 233.

### Create a new sizecalling protocol


1. Access the Sizecalling Protocols library.



2. Click  **Create**.
3. In the Analysis Settings tab of the Create New Sizecalling Protocol dialog box (Figure 34), specify settings (see “Sizecalling protocol—Analysis settings” on page 208).
4. Click **QC Settings**. In the QC Settings tab of the Create New Sizecalling Protocol dialog box (Figure 35), specify settings (“Sizecalling protocol—QC settings” on page 211).



5. Click **Save**.

**IMPORTANT!** Normalization is not applied to samples with  Size Quality flags. Specify analysis settings that accurately detect and size the size standard, and QC settings with appropriate pass fail ranges. The software does not support re-analyzing data with new settings.

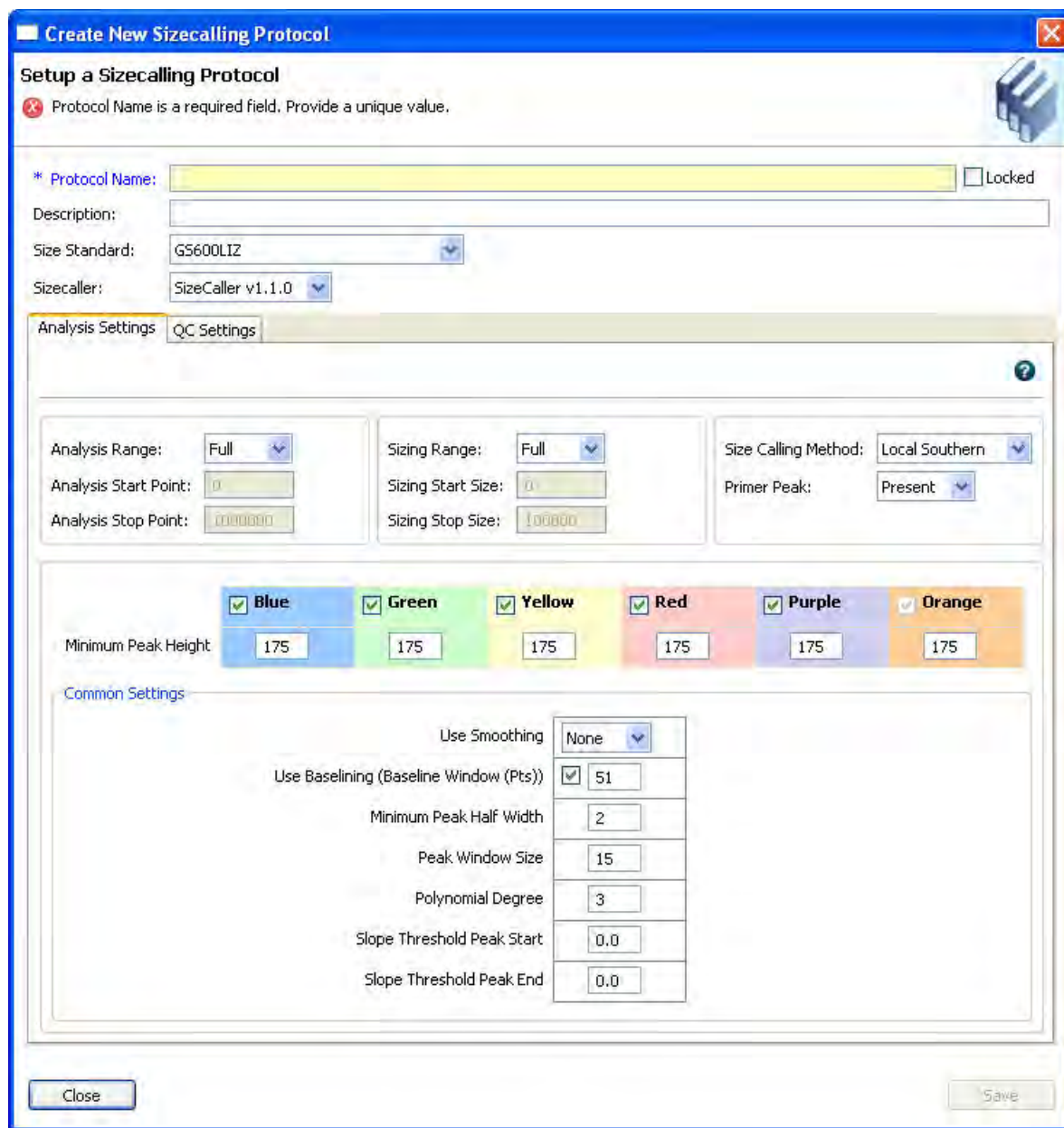


Figure 34 Create New Sizing Protocol—Analysis Settings

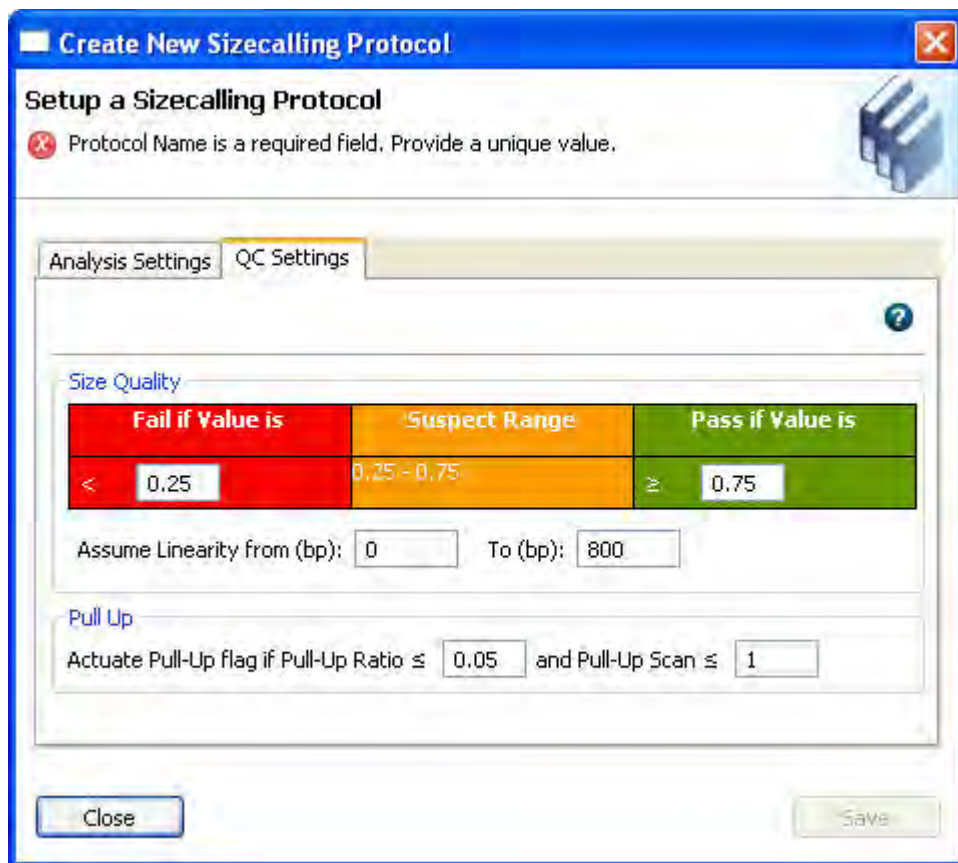


Figure 35 Create New Sizecalling Protocol—QC Settings

## Sizecalling protocol—Analysis settings

Setting	Description
Protocol Name	Name of the protocol. Names must be unique.
Description	Optional text entry.
Size standard	Size standard definition in the software that corresponds to the dye set used in the chemistry. To apply normalization, select a normalization size standard (see “Normalization size standards provided” on page 198).










(continued)

Setting	Description
<b>Analysis Range</b>	<p>The range (in data points) to analyze:</p> <ul style="list-style-type: none"> <li>• <b>Full Range</b> to analyze the entire scan region as collected by the genetic analysis instrument, including the primer peak.</li> <li>• <b>Partial Range</b> to analyze only data points within a specified range. Enter <b>Start Point</b> in data points after the primer peak and before the first required size standard peak. Enter a <b>Stop Point</b> after the last required size standard fragment. Start and Stop points may vary from instrument to instrument and platform to platform. Display raw data to determine the appropriate analysis range.</li> </ul> <p>Data points outside the specified analysis range are ignored.</p> <p><b>Note:</b> Ensure the Analysis Range contains all size standard fragments included in the Sizing Range specified below.</p>
<b>Sizing Range</b>	<p>The size range (in base pairs) appropriate for the kit you are using:</p> <ul style="list-style-type: none"> <li>• <b>All Sizes</b> for the software to analyze fragments of all sizes in the Analysis Range.</li> <li>• <b>Partial Sizes</b> for the software to analyze only fragments within a specified range. Enter a <b>Start Size</b> and a <b>Stop Size</b> appropriate for the size standard used.</li> </ul>
<b>Size Calling Method</b>	<ul style="list-style-type: none"> <li>• <b>Local Southern</b>—(default) Determines the fragment sizes using the reciprocal relationship between fragment length and electrophoretic mobility.</li> <li>• <b>3rd Order Least Squares</b>—Uses regression analysis to build a best-fit size calling curve.</li> <li>• <b>2nd Order Least Squares</b>—Uses regression analysis to build a best-fit size calling curve.</li> <li>• <b>Cubic Spline Interpolation</b>—Forces the sizing curve through all the known points of the selected size standard.</li> <li>• <b>Global Southern Method</b>—Compensates for standard fragments with anomalous electrophoretic mobility (similar to least squares methods).</li> </ul>
<b>Primer Peak</b>	<p>If the primer peaks in your application obscure peaks of interest, select <b>Present</b>. Selecting Present instructs the algorithm to ignore primer peaks. Primer peaks are still displayed in the trace.</p> <p><b>Note:</b> If this setting does not allow detection of the 20- and 40-mer peaks for samples that use the GS600 LIZ™ size standard, running samples with the GS600(60-600)LIZ+Normalization may allow detection of the peaks.</p>
<b>Peak Amplitude Thresholds</b>	<p>Specify the threshold (RFU) for peak detection for each dye color. Peaks below the threshold are not detected.</p> <p>For example, if you use the default values of 175, peaks with heights equal to or greater than 175 are detected. Peaks with heights below 175 are still displayed in the electropherogram plots but are not detected or labeled.</p> <p><b>Note:</b> Use the same peak amplitude thresholds in secondary analysis software.</p>

(continued)

Setting	Description
<b>Smoothing</b>	Select an option to smooth the outline of peaks and reduce the number of false peaks detected: <ul style="list-style-type: none"> <li>• <b>None</b> (default) to apply no smoothing. Best if the data display sharp, narrow peaks of interest.</li> <li>• <b>Light</b> to provide the best results for typical data. Light smoothing slightly reduces peak height.</li> <li>• <b>Heavy</b> for data with very sharp, narrow peaks of interest. Heavy smoothing can significantly reduce peak height.</li> </ul>
<b>Baseline Window</b>	Specify a window to adjust the baseline signals of all detected dye colors to the same level for an improved comparison of relative signal intensity. Note the following: <ul style="list-style-type: none"> <li>• A small baseline window relative to the width of a cluster, or grouping of peaks spatially close to each other, can result in shorter peak heights.</li> <li>• Larger baseline windows relative to the peaks being detected can create an elevated baseline, resulting in peaks that are elevated or not resolved to the baseline.</li> </ul>
<b>Min. Peak Half Width</b>	Specify the minimum full peak width at half maximum <b>Peak Height</b> required for peak detection. The range is 2 to 99 data points.
<b>Polynomial Degree</b>	Polynomial Degree cannot be greater than Peak Window Size. Adjust to affect the sensitivity of peak detection. You can adjust this parameter to detect a single base pair difference while minimizing the detection of shoulder effects and/or noise. The peak detector calculates the first derivative of a polynomial curve fitted to the data within a window that is centered on each data point in the analysis range. Using curves with larger polynomial degree values allows the curve to more closely approximate the signal and, therefore, captures more of the peak structure in the electropherogram.
<b>Peak Window Size</b>	Enter a window width in data points for peak detection sensitivity. If more than one peak apex is within the window, all are labeled as a single peak. Note the following: <ul style="list-style-type: none"> <li>• The maximum value is the number of data points between peaks.</li> <li>• The Peak Window Size setting is limited to odd numbers.</li> </ul> To increase peak detection sensitivity: Increase polynomial degree, decrease peak window size. To decrease peak detection sensitivity: Decrease polynomial degree, increase peak window size.
<b>Slope Thresholds Peak Start and End</b>	<ul style="list-style-type: none"> <li>• <b>Peak Start</b>—The peak starts when the first derivative (slope of the tangent) in the beginning of the peak signal before the inflection point becomes equal to or exceeds the “Peak Start” value. This threshold is set to 0 by default, which means that the peak will normally start at the leftmost point where the slope of the tangent is closest to 0° (horizontal line). A value other than 0 moves the peak start point toward its center. The value entered must be non-negative.</li> <li>• <b>Peak End</b>—The peak ends when the first derivative (slope of the tangent) in the end of the peak signal after the inflection point becomes equal to or exceeds the “Peak End” value. This value is set to 0 by default, which means that the peak will normally end at the rightmost point where the slope of the tangent is closest to 0° (horizontal line). A value other than 0 moves the peak end point toward its center. The value entered in this field must be non-positive.</li> </ul>

## Sizecalling protocol—QC settings

Setting	Description
Size Quality	<p>The <b>Pass Range</b> and the <b>Fail Range</b> for the SQ flag displayed in <b>View Fragment Results</b>.</p> <p>Results that are within the Pass range are flagged as  (Pass). Results that are within the Fail range are flagged as  (Fail). Results that are between the Pass and Fail ranges are flagged  (Check).</p> <p>For example, with a Pass Range of 0.75 to 1.0 and a Fail Range of 0.0 to 0.25, any result <math>\geq 0.75</math> is , any result <math>&lt; 0.25</math> is , and any result between <math>\geq 0.25</math> to <math>&lt; 0.75</math> is .</p> <p><b>How Size Quality is determined</b></p> <p>The Size Quality algorithm evaluates the similarity between the fragment pattern for the size standard dye specified in the size standard definition and the actual distribution of size standard peaks in the sample, calculates an interim SQ (a value between 0 and 1).</p>
Assume Linearity	<p>Defines the expected linear range. Useful in large fragment size standards where non-linearity might be expected.</p>
Pull-Up	<p>The pull-up ratio and tolerance for pull-up peak identification. A pull-up peak is identified when the peak height of the minor peak is:</p> <ul style="list-style-type: none"> <li><math>\leq X\%</math> (pull-up ratio) of the major peak <i>and</i></li> <li>Within <math>\pm Y</math> data point (pull-up scan) of the major peak</li> </ul> <p>When at least one peak is identified as a pull-up peak, the  (Check) flag is displayed for the Spectral Pull-Up quality flag in View Fragment Results.</p>

## QC protocols library (primary analysis—HID)

### QC protocol overview

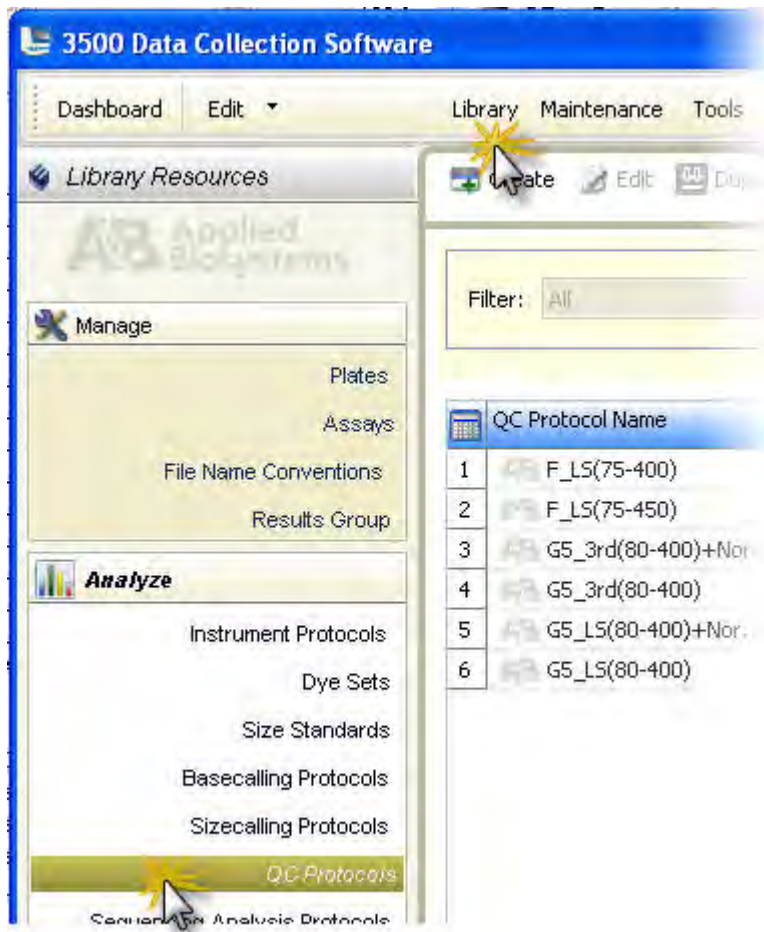
A QC protocol is the required primary analysis protocol for HID applications. A QC protocol defines peak detection, sizing, and quality values.

When you create an HID assay, you add a QC protocol to the assay. If you add this item from the library, a *copy* of the item is added to the assay, and can be modified independently from the original item stored in the library. For information on how changes are tracked if auditing is enabled, see “Audit action” on page 233.

## Create a new QC protocol

If factory-provided QC protocols do not suit your needs, you can create new QC protocols:


1. Access the QC Protocols library.



2. Click **Create**.
3. In the Analysis Settings tab of the Create New QC Protocol dialog box (Figure 36), specify settings (“QC protocol—Analysis settings” on page 214).
4. Click **QC Settings**. In the QC Settings tab of the Create New QC Protocol dialog box (Figure 37), specify settings (“QC protocol—QC settings” on page 217).

5. Click **Save**.

**IMPORTANT!** The default values in the QC protocol templates (other than peak amplitude threshold values) have been optimized for each kit. You must optimize and validate peak amplitude threshold values during internal HID validation. If you modify other settings, ensure that the size standard is accurately detected and sized with the new settings.

**IMPORTANT!** Normalization is not applied to samples with  Size Quality flags. The software does not support re-analyzing data with new settings.

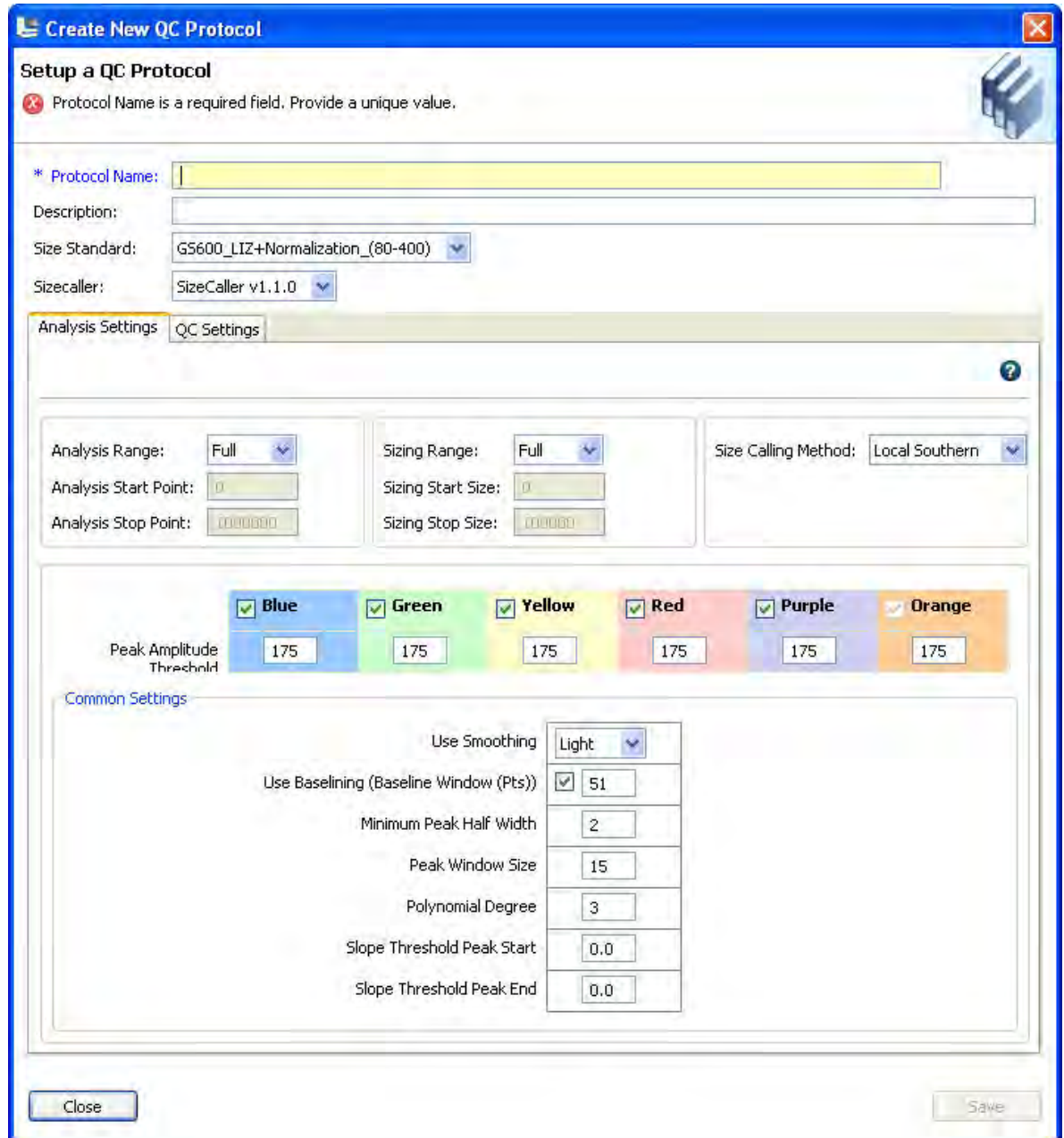


Figure 36 Create New QC Protocol—Analysis Settings

**Create New QC Protocol**

**Setup a QC Protocol**

Protocol Name is a required field. Provide a unique value.

\* Protocol Name:   Locked

Description:

Size Standard: GS600LIZ

Sizecaller: SizeCaller v1.1.0

Analysis Settings | **QC Settings**

Size Quality

Fail if Value is	Suspect Range	Pass if Value is
< 0.25	0.25 - 0.75	≥ 0.75

Broad Peak

Activate Broad Peak flag if value ≥ 1.5

Close Save


Figure 37 Create New QC Protocol—QC Settings

## QC protocol—Analysis settings

Setting	Description
Protocol Name	Name of the protocol. Names must be unique.
Description	Optional text entry.
Size standard	Size standard definition in the software that corresponds to the dye set used in the chemistry. To apply normalization, select a normalization size standard (see “Normalization size standards provided” on page 198).
Analysis Range	Select Full to collect data points for the entire scan region, including the primer peak. You can specify a limited analysis range in the GeneMapper™ ID-X Software. <b>Note:</b> If you select Partial, ensure that the Analysis Range contains all size standard fragments included in the Sizing Range specified below.



(continued)








Setting	Description
<b>Sizing Range</b>	Select <b>Partial</b> , then specify <b>80 to 400</b> to limit the fragment sizes evaluated for the size standard.  If you specify sizes outside this range, the Sizing Quality may fail.
<b>Size Calling Method</b>	Select the method to determine the molecular length of unknown fragments appropriate for the AmpFLSTR™ kit you use: <ul style="list-style-type: none"> <li>• <b>Local Southern</b>—(default) Determines the fragment sizes using the reciprocal relationship between fragment length and electrophoretic mobility. The unknown fragment is surrounded by two known-sized fragments above and one below, then two below and one above. The results are averaged and the size of the allele is determined.</li> <li>• <b>3rd Order Least Squares</b>—Uses regression analysis to build a best-fit size calling curve.</li> <li>• <b>2nd Order Least Squares</b>—Uses regression analysis to build a best-fit size calling curve.</li> <li>• <b>Cubic Spline Interpolation</b>—Forces the sizing curve through all the known points of the selected size standard.</li> <li>• <b>Global Southern Method</b>—Compensates for standard fragments with anomalous electrophoretic mobility (similar to least squares methods).</li> </ul>
<p><b>IMPORTANT!</b> If you modify peak detection settings, ensure that the size standard is accurately detected and sized with the new settings. Normalization is not applied to samples with  Size Quality flags. The software does not support re-analyzing data with new settings. For more information on peak detection parameters, see the <i>GeneMapper™ ID-X Software Reference Guide</i>.</p>	
<b>Use Smoothing</b>	Select an option to smooth the outline of peaks and reduce the number of false peaks detected: <ul style="list-style-type: none"> <li>• <b>None</b> to apply no smoothing. Best if the data display sharp, narrow peaks of interest.</li> <li>• <b>Light</b> (default) to provide the best results for typical data. Light smoothing slightly reduces peak height.</li> <li>• <b>Heavy</b> for data with very sharp, narrow peaks of interest. Heavy smoothing can significantly reduce peak height.</li> </ul>
<b>Use Baseline</b>	Specify a window to adjust the baseline signals of all detected dye colors to the same level for an improved comparison of relative signal intensity. Note the following: <ul style="list-style-type: none"> <li>• A small baseline window relative to the width of a cluster, or grouping of peaks spatially close to each other, can result in shorter peak heights.</li> <li>• Larger baseline windows relative to the peaks being detected can create an elevated baseline, resulting in peaks that are elevated or not resolved to the baseline.</li> </ul>

(continued)

Setting	Description
<b>Peak Amplitude Threshold</b>	<p><b>IMPORTANT!</b> Optimize these thresholds during internal HID validation.</p> <p>Specify the threshold (RFU) for peak detection for each dye color. Peaks below the threshold are not detected.</p> <p>For example, if you use the default values of 175, peaks with heights equal to or greater than 175 are detected. Peaks with heights below 175 are still displayed in the electropherogram plots but are not detected or labeled.</p> <p><b>Note:</b> Use the same peak amplitude thresholds in secondary analysis software.</p>
<b>Minimum Peak Half Width</b>	<p>Specify the smallest half peak width at full height for peak detection. The range is 2 to 99 data points.</p>
<b>Polynomial Degree</b>	<p>Adjust to affect the sensitivity of peak detection. You can adjust this parameter to detect a single base pair difference while minimizing the detection of shoulder effects and/or noise.</p> <p>The peak detector calculates the first derivative of a polynomial curve fitted to the data within a window that is centered on each data point in the analysis range.</p> <p>Using curves with larger polynomial degree values allows the curve to more closely approximate the signal and, therefore, captures more of the peak structure in the electropherogram.</p>
<b>Peak Window Size</b>	<p>Enter a window width in data points for peak detection sensitivity. If more than one peak apex is within the window, all are labeled as a single peak. Note the following:</p> <ul style="list-style-type: none"> <li>• The maximum value is the number of data points between peaks.</li> <li>• The Peak Window Size setting is limited to odd numbers.</li> </ul> <p>To increase peak detection sensitivity: Increase polynomial degree, decrease peak window size.</p> <p>To decrease peak detection sensitivity: Decrease polynomial degree, increase peak window size.</p>
<b>Slope Thresholds Peak Start</b>  <b>Slope Thresholds Peak End</b>	<p>Not recommended for use with AmpF<math>\ell</math>STR™ kit data.</p> <ul style="list-style-type: none"> <li>• <b>Peak Start</b>—The peak starts when the first derivative (slope of the tangent) in the beginning of the peak signal before the inflection point becomes equal to or exceeds the “Peak Start” value. This threshold is set to 0 by default, which means that the peak will normally start at the leftmost point where the slope of the tangent is closest to 0° (horizontal line). A value other than 0 moves the peak start point toward its center. The value entered must be non-negative.</li> <li>• <b>Peak End</b>—The peak ends when the first derivative (slope of the tangent) in the end of the peak signal after the inflection point becomes equal to or exceeds the “Peak End” value. This value is set to 0 by default, which means that the peak will normally end at the rightmost point where the slope of the tangent is closest to 0° (horizontal line). A value other than 0 moves the peak end point toward its center. The value entered in this field must be non-positive.</li> </ul>



## QC protocol—QC settings

Setting	Description
<b>Size Quality</b>	<p>Enter the Pass Range and the Fail Range for the SQ flag displayed in View HID Results.</p> <p>Results that are within the Pass range are flagged as  (Pass). Results that are within the Fail range are flagged as  (Fail). Results that are between the Pass and Fail ranges are flagged  (Check).</p> <p>For example, with a Pass Range of 0.75 to 1.0 and a Fail Range of 0.0 to 0.25, any result <math>\geq 0.75</math> is , any result <math>&lt; 0.25</math> is , and any result between <math>\geq 0.25</math> to <math>&lt; 0.75</math> is .</p> <p><b>How Size Quality is determined</b></p> <p>The Size Quality algorithm evaluates the similarity between the fragment pattern for the size standard dye specified in the size standard definition and the actual distribution of size standard peaks in the sample, calculates an interim SQ (a value between 0 and 1).</p> <p><b>Weighting</b></p> <p>The Broad Peak (BD) threshold specified in the QC Protocol - QC Settings tab affects the SQ. To determine the final SQ value, the software:</p> <ul style="list-style-type: none"> <li>• Evaluates size standard peak widths in the sample in the dye color specified in the size standard definition.</li> <li>• If the width of any size standard peak in the sizing range exceeds the broad peak threshold, applies a 0.5 weighting factor:</li> <li>• <math>\text{Interim SQ} \times (1 - 0.5)</math></li> </ul> <p><b>Note:</b> The GeneMapper™ ID-X Software allows you to set broad peak weighting. For more information, see the <i>GeneMapper™ ID-X Software Reference Guide</i>.</p>
<b>Broad Peak</b>	<p>Enter the maximum peak width (in base pairs).</p> <p>When a peak width is greater than the threshold, the  (Check) flag is displayed for the BD (Broad Peak) quality flag in View HID Results.</p>



# Use Security, Audit, and E-Sig functions (SAE Module)

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- Users ..... 246

## Administrators

### Administrators overview of system security auditing and electronic signature

This option is available if your system includes a license for the Security, Audit, and E-Signature module.

The Security, Audit, E-Signature module (SAE module) provides the following functionality:

- **System security**—Controls user access to the software. A default Administrator user account is provided, and additional user accounts and permissions can be user-defined.
- **Auditing**—Tracks changes made to library items, actions performed by users, and changes to the SAE settings. The software automatically audits some actions silently. You can select other items for auditing and specify the audit mode. Provides reports for audited library items, SAE changes, and actions.
- **Electronic signature (e-sig)**—Determines if users are permitted, prompted, or required to provide a user name and password when performing certain functions. Can be configured so that a predefined list of functions can be performed only if the data used for the functions is signed (for example, you can run a plate only if the calibration data for the system has been signed).

### Example applications

You can configure the SAE module in a variety of ways:

- Require multiple e-sigs.
- Require specific users or users with specific permissions to e-sign.
- Allow only certain users to approve reviewed samples.

## Configure the security system

### Access the Security screen

The **Security** screen allows you to control restrictions and security policies for all user accounts, and set up notifications when certain security events occur.

Access the Security screen.

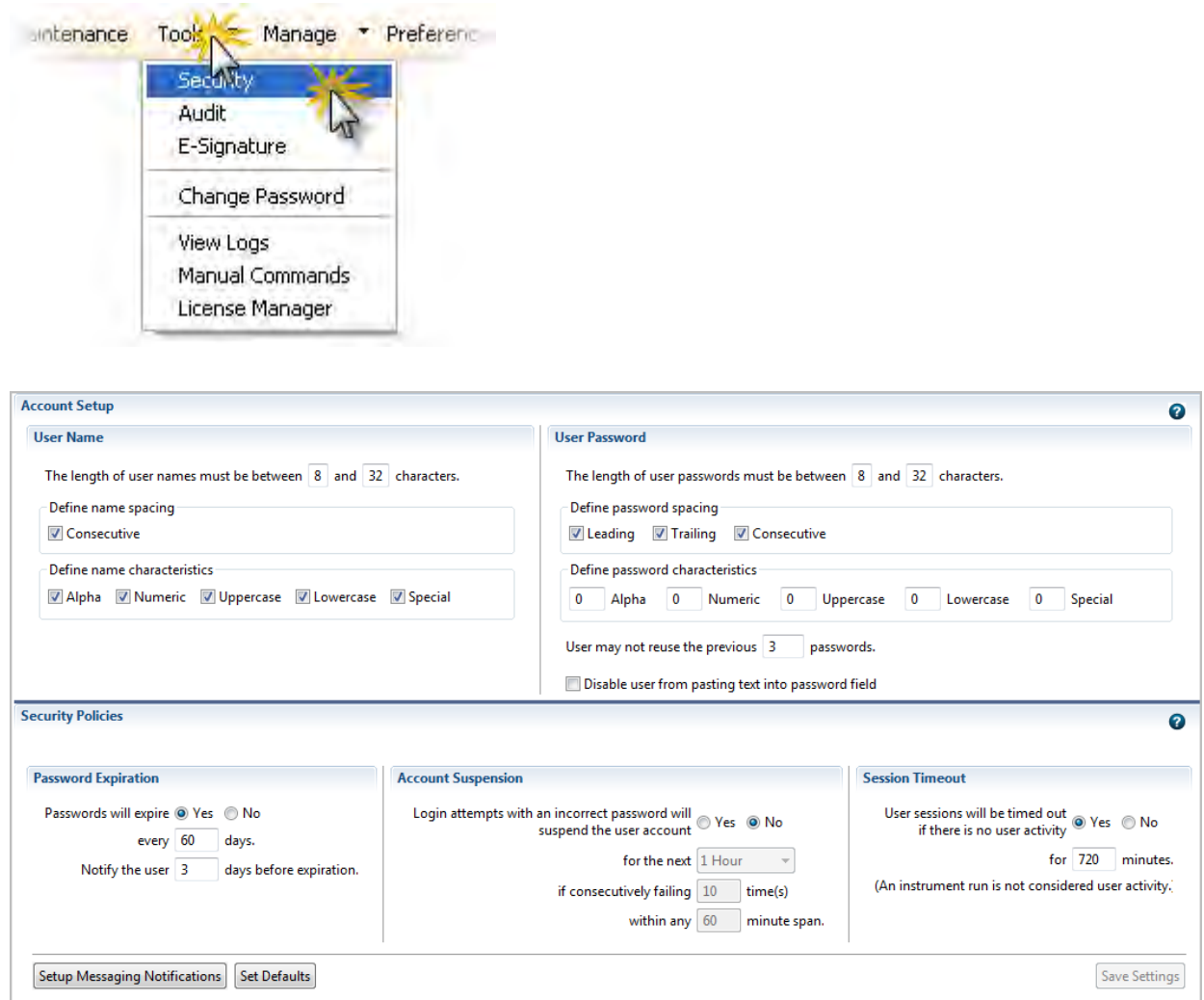
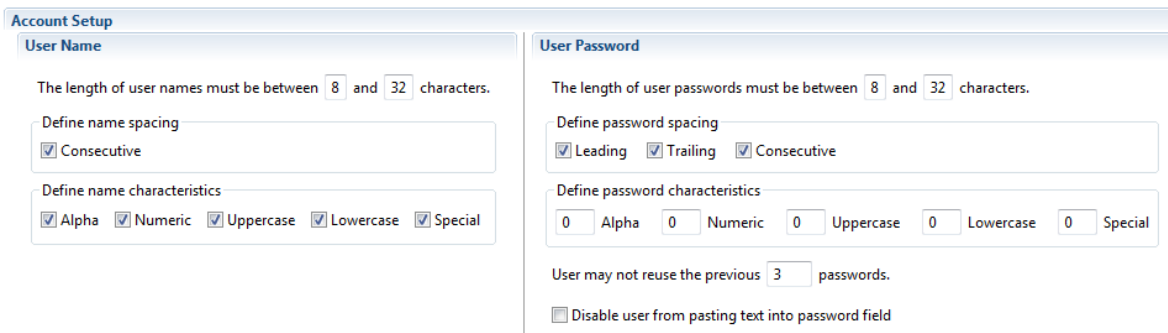


Figure 38 Security screen

## Set account setup and security policies

Security policies apply to all user accounts.

1. Under **Account Setup**, specify user name limits.



**Account Setup**

**User Name**

The length of user names must be between  and  characters.

Define name spacing

Consecutive

Define name characteristics

Alpha  Numeric  Uppercase  Lowercase  Special

**User Password**

The length of user passwords must be between  and  characters.

Define password spacing

Leading  Trailing  Consecutive

Define password characteristics

Alpha  Numeric  Uppercase  Lowercase  Special

User may not reuse the previous  passwords.

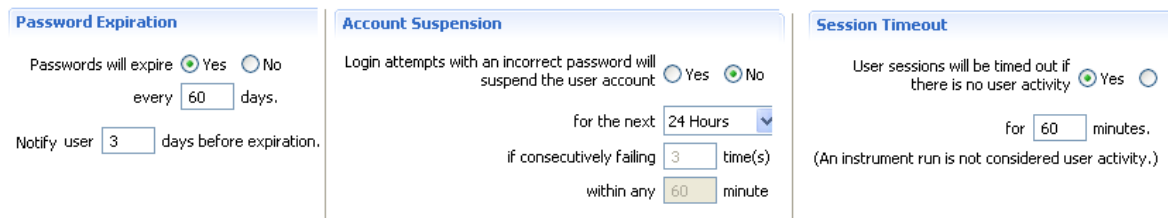
Disable user from pasting text into password field

---

**IMPORTANT!** The software allows spaces in user names (Define name spacing). Use spaces in user names with caution. For information, see “Spaces in user names” on page 221.

---

2. Specify the *allowed* characters in user names: spaces and alpha, numeric, upper/ lower case, and special characters (@, commas, periods, semicolons, dashes, underscores, and tildes).
3. Specify password limits and whether users can paste copied text into the password field.
4. Specify the *required* characters in passwords: spaces and alpha, numeric, upper/ lower case, and special characters (any non-space, non-alpha, or non-numeric characters).
5. Specify password reuse. You cannot disable the password reuse restriction.



**Password Expiration**

Passwords will expire  Yes  No  
every  days.

Notify user  days before expiration.

**Account Suspension**

Login attempts with an incorrect password will suspend the user account  Yes  No  
for the next  Hours  
if consecutively failing  time(s)  
within any  minute

**Session Timeout**

User sessions will be timed out if there is no user activity  Yes  No  
for  minutes.  
(An instrument run is not considered user activity.)

---

**Note:** Do not disable the **Account Suspension** feature.

---

6. Click **Setup Messaging Notification** to specify when and how to notify the administrator of certain security events. For information, see “Set up messaging notifications” on page 221.
7. Click **Save Settings**.  
The new settings are applied to the logged-in user the next time the user logs in.

## Spaces in user names

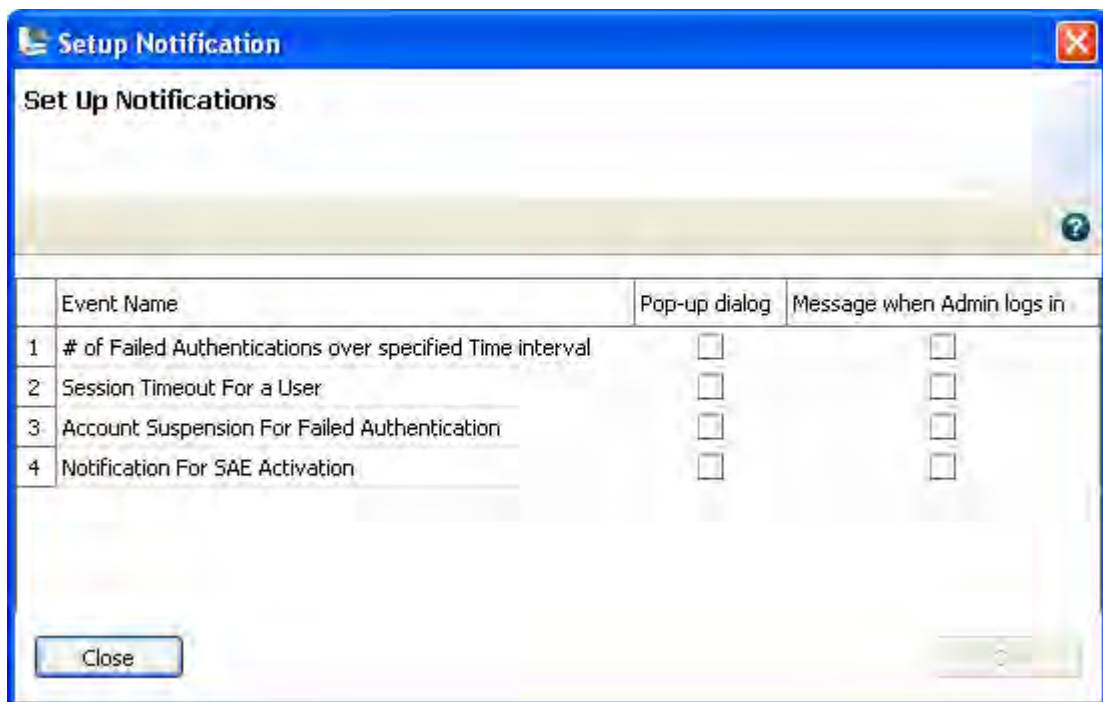
If you allow spaces in user names, be aware of the following issues:

- Leading and trailing spaces in user names are difficult to detect on the screen or in printed reports.
- The number of consecutive spaces in a user name is difficult to determine on the screen or in printed reports.

Spaces in user names may cause confusion when searching for an audit or e-sig record associated with a user name. To find a record associated with a user name, you must specify the user name exactly, including leading, consecutive, and trailing spaces.

## Set up messaging notifications

1. In the **Security** screen (Figure 38), click **Setup Messaging Notifications** to display the **Setup Notifications** dialog box.



2. Select the events for notification:
  - **Number (#) of failed authentications over specified time interval**—A user attempts to log in with an incorrect password. The message indicates the number of failed authentications.
  - **Session timeout for a user**—No activity occurred in a user account for the specified period of inactivity.
  - **Account suspension for failed authentication**—The user exceeds maximum number of allowed failed authentications (login attempts with an incorrect password).
  - **Notification for SAE activation** —Not supported.

## 3. Select the notification method:

- **Pop-up dialog**—The software immediately displays a pop-up message to the current user if an event is triggered by the current user. The message instructs the user to inform a system administrator of the event.
- **Message when Admin logs in**—If an event triggers notification, the next time any user with an Administrator role logs in, the software displays a list those events, indicating the time each event occurred and the user who triggered the event.

The Administrator has the option of acknowledging the event, which removes it from the notification list.

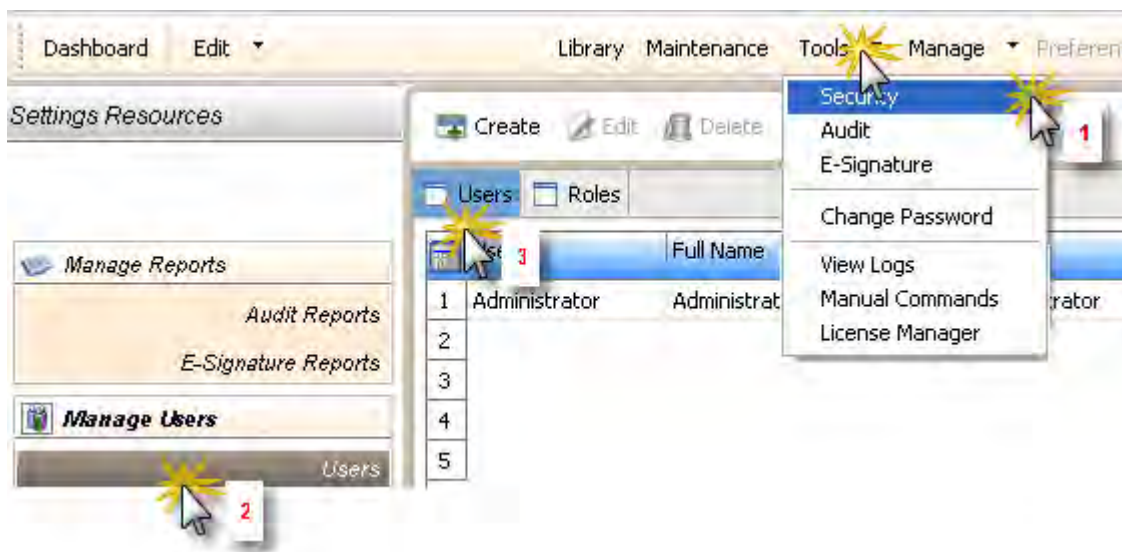
4. Click **OK**.

## Manage user accounts

### Create or edit a user account

The software includes a default Administrator user account with permissions (defined by the account user role) to perform all functions in the software.

### Create a user account

1. Access the **Users** screen.

2. Click  **Create** to display the **New User** dialog box.

3. Enter **User Name**, **Password**, **First Name**, MI (middle initial – *optional*) and **Last Name**. Click a field to display the field limits, which are specified in Security settings.

---

**Note:** First Name, MI (middle initial), and Last Name are used to create **User Full Name**, which is displayed as the name of the logged-in user.

---

**Note:** You cannot change the User Name after you save the user account.

---

4. Select **Pre-expired** to require the user account to specify a new password at first log in. The **Password Expires On** date is specified in Security settings.
5. Select the user role (described in “Create or edit a user role” on page 225) and the electronic signature state (determines if a user account has permission to electronically sign objects). Leave the status set to Active.

---

**Note:** The Dx User function is not supported.

---

6. (*Optional*) Enter email (for information only), phone, and comments.


7. Click **Save**.

If the **Save** button is dimmed, it indicates an invalid entry in a field. Click a field to display the limits for the field, then enter a valid entry.

The Users screen displays the following information for each user account:

- **User**
- **Full Name**
- **Dx User** (not supported in research use only mode.)
- **Role**
- **Status**
- **Password Expired** (true=yes, false=no)
- **Last Modified On**
- **Created Date**
- **Password Change Date** (by either user or administrator)
- **Email** (for records only)
- **Phone**
- **Comments**

### Edit a user account

1. In the Users screen, select a user account, then click  **Edit**.


---

**Note:** If you select multiple users, only Status and Role will be changed.

---


2. Edit settings as needed. You cannot edit the user name of an existing user.
3. Click **Save**.

### Activate a suspended user account

1. Select the user.
2. Click  **Edit**.
3. Change the status from **Suspended** to **Active**.

### Delete (inactivate) a user account

You cannot delete a user because user records are required for auditing. To disable a user account, inactivate it.

1. Select the user.
2. Click  **Edit**.
3. Change the status from **Active** to **Inactive**.
4. Click **Save**.

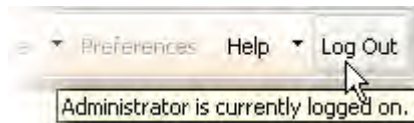


## Determine the name of the logged-in user

To display the full name of the logged-in user:

Place the mouse pointer on the **Logout** menu.

The full name of the logged-in user is also displayed in the **Load Plates for Run** screen and the **Monitor Run** screen.



## Create or edit a user role

User roles determine the permissions associated with a user account.

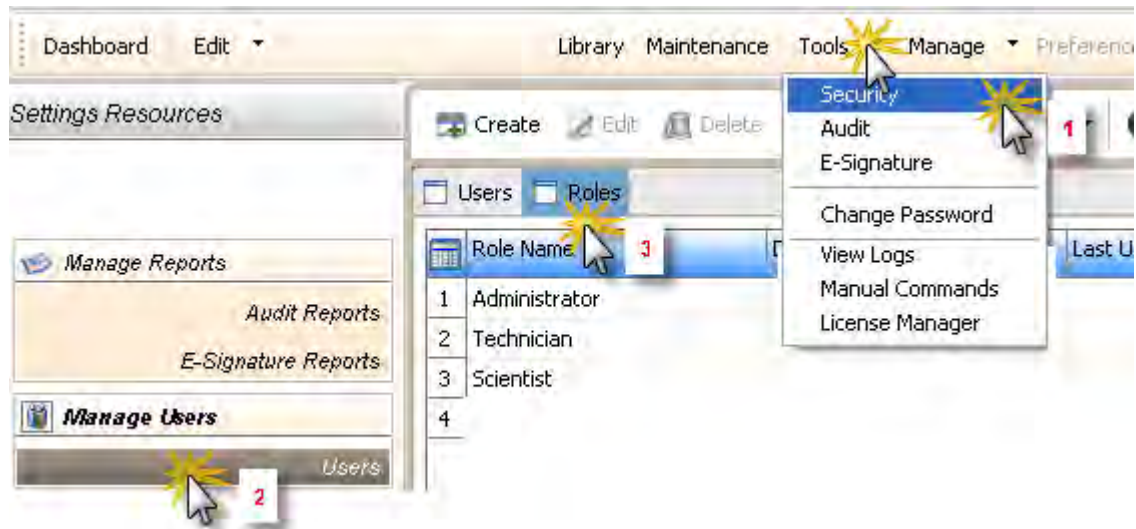
Three default user roles are included in the software. You can modify two of them, and can create your own roles with customized settings as needed:

- Administrator (cannot be edited or deleted)
- Scientist
- Technician

To determine the permissions for these roles or to edit these roles, select the role, then click **Edit**.

## Create a user role

1. Access the **Roles** screen.



2. Click **Create**.
3. Enter a role name and (*optional*) comment.

4. Select permissions (described below). To select all permissions in a category, select the checkbox next to the category.
5. Click **Save Role**.


### User role permissions

Category	Permissions
Setup	Create plate/plate template
Run	<ul style="list-style-type: none"> <li>• Start plate run</li> <li>• Edit default instrument run name</li> <li>• Manage injection list</li> <li>• Duplicate injection</li> <li>• Re-inject</li> </ul>
Primary Analysis	<ul style="list-style-type: none"> <li>• Edit sample (names)</li> <li>• Export sequencing results</li> </ul>
<ul style="list-style-type: none"> <li>• Assay</li> <li>• File name convention</li> <li>• Results group</li> <li>• Instrument protocol</li> <li>• PA protocol</li> <li>• QC protocol</li> <li>• Size standard</li> <li>• Dye sets</li> </ul>	<ul style="list-style-type: none"> <li>• Create</li> <li>• Edit</li> <li>• Delete</li> <li>• Import</li> <li>• Export</li> </ul>
Plates and templates	<ul style="list-style-type: none"> <li>• Edit</li> <li>• Delete</li> <li>• Import</li> <li>• Export</li> </ul>
Locking/Unlocking	<ul style="list-style-type: none"> <li>• Assays</li> <li>• File name convention</li> <li>• Results group</li> <li>• Instrument protocols</li> <li>• PA protocols</li> <li>• Size standards</li> <li>• Dye sets</li> </ul>



*(continued)*

Category	Permissions
Preferences	<ul style="list-style-type: none"> <li>Edit system preferences</li> <li>Export system preferences</li> <li>Import system preferences</li> <li>Edit user preferences</li> <li>Import user preferences</li> <li>Export user preferences (all)</li> </ul>
Calibrations	<ul style="list-style-type: none"> <li>Perform spatial calibration</li> <li>Perform spectral calibration</li> </ul>
Install check	Run install standard check
Archiving	<ul style="list-style-type: none"> <li>Archive</li> <li>Purge</li> <li>Restore</li> </ul>
SAE configuration	Log in to timed-out user sessions

### Edit a user role

1. In the **Roles** screen, select a user role, then click  **Edit**.
2. Edit settings as needed. You cannot edit the Administrator user role.
3. Click **Save**.

### View and print a user report

1. Select the **User** or **Roles** tab. Click  **View Report**.
2. In the **Report** screen, click toolbar options to manipulate the report as needed. Place the mouse pointer over an item for a description of the item.
3. To print the report, click  **Print**. Close the report.

### Save electronic copies (PDF) of the report

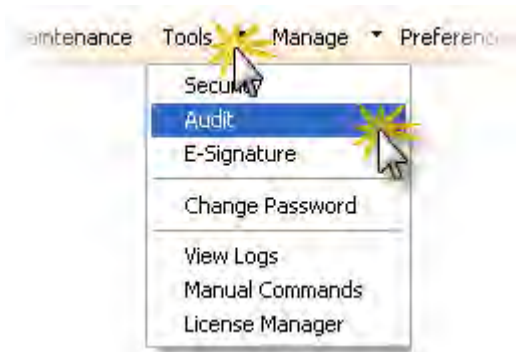
To save the report electronically (PDF), print the report and select a PDF printer.

## Manage auditing

### Access the Audit Settings screen

The **Audit Settings** screen controls the events that are audited, and the reasons available to users when audit mode is set to **Prompt** or **Required**.

Access the Audit Settings screen.



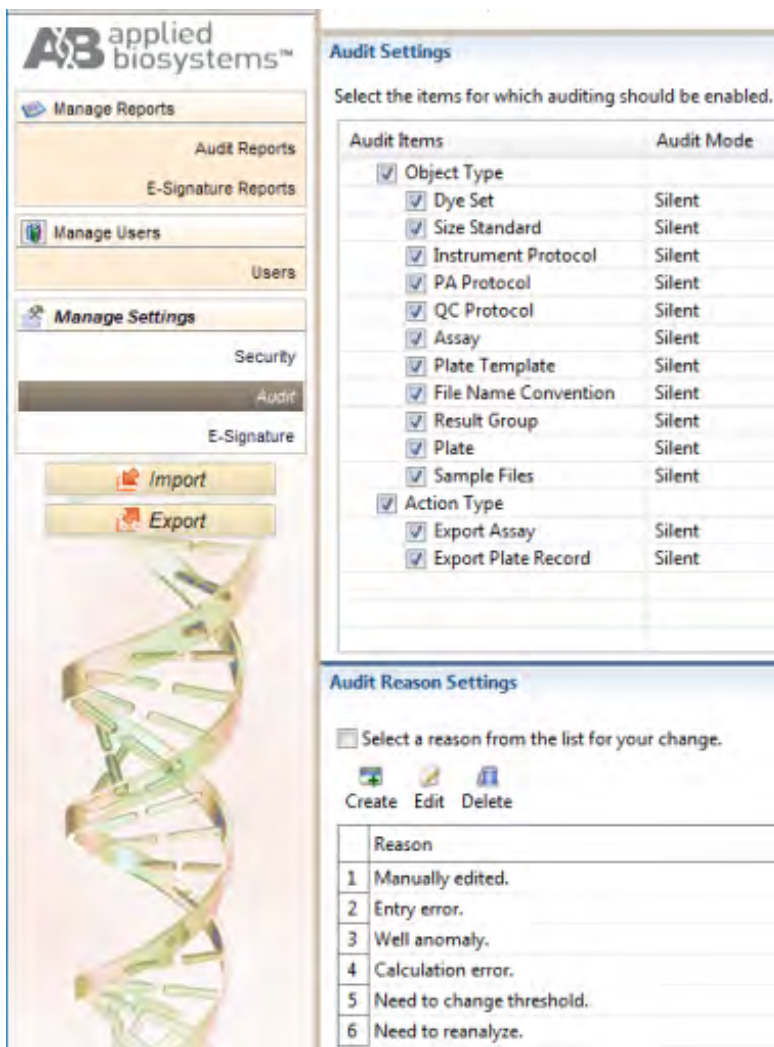


Figure 39 Audit Settings

## Select objects to audit

### 1. Select the objects and/or actions to audit.

Objects you can select for auditing (audit records displayed in Object Audit History):

- Dye set
- Size standard
- Instrument protocol
- PA protocol (primary analysis)
- Assay
- Plate template
- File name convention
- Results group
- Plate
- Sample files

Actions you can select for auditing (audit records displayed in Action Log):

- Export assay
- Export plate record

---

**Note:** For a list of items that the system audits silently in addition to the configurable items listed above, see “Generate audit reports” on page 231.

---

### 2. Set the Audit Mode for each item you enable for auditing:

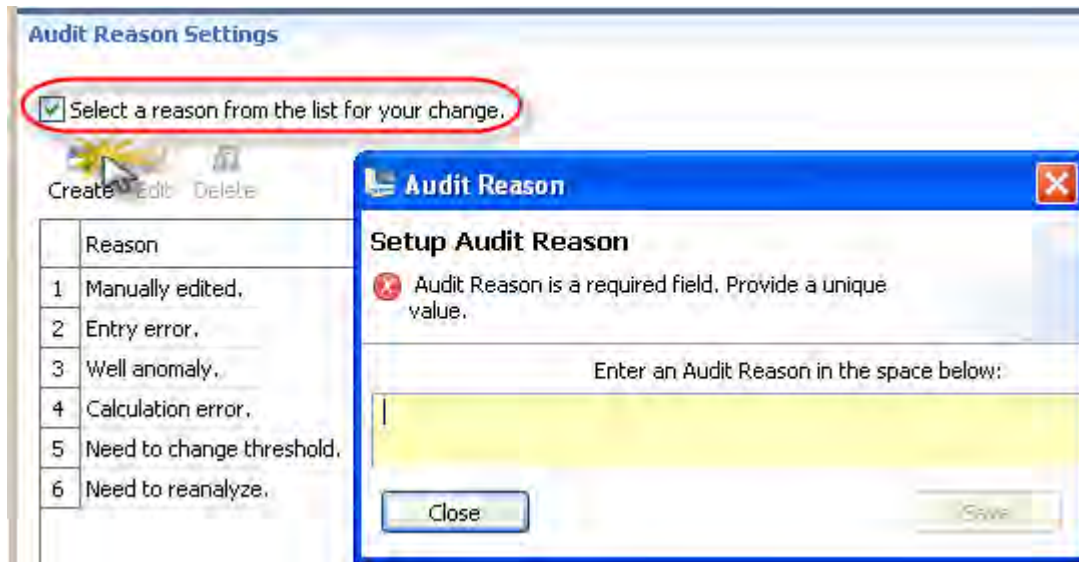
- **Prompt**—The event is audited, a reason prompt is displayed, but the user can cancel and continue without entering a reason.
- **Required**—The event is audited, a reason prompt is displayed, and the user must specify a reason.
- **Silent**—The event is audited, no reason prompt is displayed.

### 3. Click **Save Settings**.

## Create audit reason settings

You can create, modify and delete the reasons that are available for selection in the **Audit Reason** dialog box (displayed when a user performs an audited action).

1. To require users to select a pre-defined reason in the Audit Reason dialog box (displayed when a user performs an audited action), select the **Select a reason from the list for your change** checkbox. Users are not permitted to enter a reason.



2. As needed, click **Create**, or select a reason, then click **Edit** or **Delete**.

## Generate audit reports

### Display audit histories

1. Access the **Audit Reports** screen.



---

**Note:** To access the Audit Reports screen, the user role for an account must specify the Configure SAE permission. Users without the Configure SAE permission can view object audit histories for individual entries in the libraries by selecting entries, then clicking **View Audit History** (see “View audit and e-signature histories for library entries” on page 165).

---

2. Select a tab to display:

- **Object Audit History**—The most recent audit for all user objects (samples and objects in the Library) that have been audited.
- **System Configuration History**—SAE configuration records, including audit history for each user account.
- **Action log**—System-specified audit events.

3. (Optional) Modify the display:

- Sort the table. See “Sort by one or multiple columns” on page 94.
- Specify filters (date range, user name, action, object or record type, object or record name, reason), then click **Go**.

---

**Note:** The **Reason** field in System Configuration History is not used.

---

- Select a record, then click **Show Object History** or **Show Audit Details**.
- In the history dialog box, select a record, then click **Show Audit Details**.
- Click **Table Settings**, then specify the columns to show or hide.

## Review the object audit history

### Audit records

The **Object Audit History** lists the most recent audit for the user objects listed below (samples and objects in the libraries) that have been audited.

- Dye set
- Size standard
- Instrument protocol
- PA protocol (primary analysis)
- Assay
- Plate template
- File name convention
- Results group
- Plate
- Sample files



## Audit action

Possible actions for all objects are: update, create, and delete. Audit records are generated under the following conditions:

Action	Description
<b>Update</b>	<p>The auditing of updates depends on whether an object is modified or overwritten:</p> <ul style="list-style-type: none"> <li>• <b>Modified</b>—A record is created when an object is modified.</li> <li>• <b>Updated</b>—A record is not created when an object is overwritten in the library.</li> </ul> <p>Example: You create a plate, then create a results group from within the plate and save it to the library. You then open the plate, edit the results group from within the plate, then save it to the library. A message indicates that the results group already exists and asks if you want to overwrite it. You click Yes. This action is considered a creation of a new results group, not a modification of the existing results group. No Update record is created; a Create record is created.</p>
<b>Create</b>	<p>A record is created when you:</p> <ul style="list-style-type: none"> <li>• Create an item in the library.</li> <li>• Create an item from within another item.</li> <li>• Modify an item from within another item, then overwrite the item in the library when you save it (as described in the "Updated" bullet above).</li> </ul> <p><b>Note:</b> An audit record is not created when a sample file is generated. However, an audit record is generated when a sample is renamed.</p>
<b>Delete</b>	<p>The auditing of deletions depends on the item deleted:</p> <ul style="list-style-type: none"> <li>• <b>Items in the library</b>—A record is retained until it is deleted from the library. The deletion of the item from the library is not audited. For example, if you <i>delete</i> a size standard from the library, no audit record for the deletion is listed in the Object Audit Detail History.</li> <li>• <b>Items within other items</b>—The deletion of an item from within another item is audited.</li> </ul>

## Display the object history

The object history shows the audit history for the object and for all objects contained in the selected object. For example, when you create an assay, a copy of the instrument protocol and the primary analysis protocol (and therefore dye set, and size standard) are included in the assay object. The objects contained within an object have audit histories distinct from the audit history of the objects stored in the Library.

To display the history for an object:

Select the object, then click **Show Object History**.

## System configuration history

Table 1 Audit – System configuration history

Record Type	Action	Corresponds to
Security settings	Update	<ul style="list-style-type: none"> <li>• Enable security</li> <li>• Disable security</li> <li>• Modify security policies:               <ul style="list-style-type: none"> <li>– Session timeout settings</li> </ul> </li> </ul>
Account settings	Update	<ul style="list-style-type: none"> <li>• Modify user name settings</li> <li>• Modify password settings</li> <li>• Modify security policies:               <ul style="list-style-type: none"> <li>– Password expiration</li> <li>– Account suspension</li> </ul> </li> </ul>
Audit reason for change	Update	Modify reason for change
	Create	Create reason for change
	Delete	Delete reason for change
Audit settings	Update	<ul style="list-style-type: none"> <li>• Enable auditing</li> <li>• Disable auditing</li> </ul>
Audit type	Update	Modify audit settings
E-Signature function	Update	<ul style="list-style-type: none"> <li>• Modify the authorities for a “prompt before” function</li> <li>• Modify the Enable state of either a “check after” or “prompt before” function</li> </ul>
E-Signature settings	Update	<ul style="list-style-type: none"> <li>• Enable e-signature</li> <li>• Disable e-signature</li> </ul>
E-Signature type	Update	<ul style="list-style-type: none"> <li>• Modify e-signature settings</li> <li>• Modify the enable state of an E-Signature Type</li> </ul>
Role assignment	Create	<ul style="list-style-type: none"> <li>• Create a new user account</li> <li>• Assign a different user role to an existing user account</li> </ul>
	Delete	Assign a different user role to an existing user account
Role permissions	Update	Modify user role permissions
	Create	Create a user role - Creates one role assignment record for each permission in a role
	Delete	Delete a user role - Creates one role delete record for each permission in the deleted role

Table 1 Audit – System configuration history (continued)

Record Type	Action	Corresponds to
User account	Update	<ul style="list-style-type: none"> <li>Edit</li> <li>Suspend</li> </ul>
	Create	Create new user account
User role	Update	Modify user role
	Create	Create user role
	Delete	Delete user role

## Action log

The action log lists system-specified audit events.

All items in the action log are audited silently, except for the items noted as configurable. Configurable items may include comments in the action log.

Table 2 Audit – Action log

Category	Action
Assay	Assay exported successfully
Log In	<ul style="list-style-type: none"> <li>User logged in</li> <li>Login failed</li> <li>User logged out</li> </ul>
Maintenance Wizards	<ul style="list-style-type: none"> <li>Remove Bubbles Wizard started</li> <li>Change Polymer Type Wizard started</li> <li>Change Array Wizard started</li> <li>Replenish Polymer Wizard started</li> <li>Fill Polymer Wizard started</li> <li>Water Wash Wizard started</li> <li>Instrument Shutdown Wizard started</li> </ul>
Plate	Plate exported successfully
Run	<ul style="list-style-type: none"> <li>Start</li> <li>Pause</li> <li>Resume</li> <li>Stop (Abort injection)</li> <li>Terminate (injection list)</li> </ul>
SAE Configuration	<ul style="list-style-type: none"> <li>Export</li> </ul>

Table 2 Audit – Action log (continued)

Category	Action
System Audit Records	<ul style="list-style-type: none"> <li>• Archive</li> <li>• Purge</li> <li>• Restore</li> </ul>
System Action Records	<ul style="list-style-type: none"> <li>• Archive</li> <li>• Purge</li> <li>• Restore</li> </ul>
User Profile	<ul style="list-style-type: none"> <li>• Export</li> </ul>

### View and print audit reports

1. Display the records of interest.
2. Filter the list to decrease the time required to generate reports.

---

**IMPORTANT!** You cannot cancel a report after you click a view button.


---

3. Click  **View Audit Summary Report** or  **View Audit Detailed Report**.

System Configuration History Summary Report						
#	Date	User Name	User Full Name	Record Type	Record Name	Action
1	28-Jan-2009 05:01:08 PM	Administrator	Administrator	Security Settings		Update
2	28-Jan-2009 05:00:57 PM	Administrator	Administrator	Security Settings		Update

System Configuration History Detailed Report						
1	<b>Date:</b> 28-Jan-2009 05:01:08 PM	<b>Action:</b> Update				
	<b>User Name:</b> Administrator	<b>User Full Name:</b> Administrator				
	<b>Record Type:</b> Security Settings	<b>Record Name:</b>				
#	Record Type	Object Name	Old Value	Current Value	Action	
1	Security Settings	Security On / Security Off	DISABLED	ENABLED	Update	
2	<b>Date:</b> 28-Jan-2009 05:00:57 PM	<b>Action:</b> Update				
	<b>User Name:</b> Administrator	<b>User Full Name:</b> Administrator				
	<b>Record Type:</b> Security Settings	<b>Record Name:</b>				
#	Record Type	Object Name	Old Value	Current Value	Action	
1	Security Settings	Security On / Security Off	ENABLED	DISABLED	Update	

4. (Optional) In the Report screen, click toolbar options to manipulate the report. Place the mouse pointer over an item for a description of the item.
5. To print the report, click  **Print**.

---

**IMPORTANT!** Font setting changes are activated after you close, then reopen the report.

---

**IMPORTANT!** If you change font settings before you generate a report, the report may not be generated. Generate the report again.

---



6. To save the report electronically (PDF), print the report and select a PDF printer.

## Archive, purge, and restore audit records


The audit archive function makes a copy of audit records. Purge makes a copy of audit records, and then deletes them. You can use the Restore function to restore purged audit records.

### Archive and purge

To selectively archive or purge (delete) system configuration or action audit records:


1. Select records in the appropriate screen.
2. Click  **Archive Audit Records** or  **Purge Audit Records**.
3. If you select Archive:
  - Specify a location and name for the .asz audit archive file.
  - (Optional) Click **Yes** to Purge (delete) the records after archive.

### Restore

To restore system configuration or action audit records, click  **Restore**, then select the .asz file to restore.

### Export audit records

As needed, you can export audit records to a TXT file for additional manipulation and reporting outside the software.

1. Display the records of interest.
2. Select the records to export.
3. Click  **Export Audit Records**.
4. Specify a name and location for the export TXT file.
5. Click **Save**.

---

**Note:** If you export audit records for samples that are not in their original location (samples have been deleted or moved), an error message is displayed. Return sample data files to their original location, then export again.

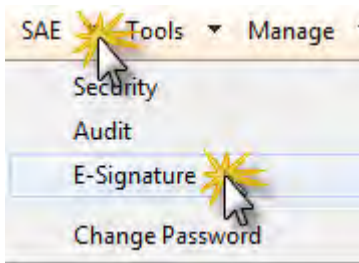
---

## Manage electronic signature (E-sig)

**IMPORTANT!** Changes to e-signature settings are not activated until you log out of the software, then log back in.

### Access the E-Signature Settings screen

Access the **E-Signature Settings** screen.



**E-Signature Settings**

Select the electronic signature types that should be allowed.

E-Signature Type
<input type="checkbox"/> Approve Dye Set
<input type="checkbox"/> Approve Size Standard
<input type="checkbox"/> Approve Spatial Calibration
<input type="checkbox"/> Approve Spectral Calibration
<input type="checkbox"/> Approve Instrument Protocol
<input type="checkbox"/> Approve Sizecalling Protocol
<input type="checkbox"/> Approve Basecalling Protocol
<input type="checkbox"/> Approve QC Protocol
<input type="checkbox"/> Approve Assay
<input type="checkbox"/> Approve Plate Template
<input type="checkbox"/> Approve Plate
<input type="checkbox"/> Approve Sample
<input type="checkbox"/> Approve Sequencing Install Standard Results
<input type="checkbox"/> Approve MicroSeqID Install Standard Results
<input type="checkbox"/> Approve BDTv1.1POP6 Install Standard Results
<input type="checkbox"/> Approve Fragment Install Standard Results
<input type="checkbox"/> Approve HID Install Standard Results

Select the functions after which the system will prompt for an electronic signature of the selected type.

Function

Select the functions before which the system will check for required electronic signatures.

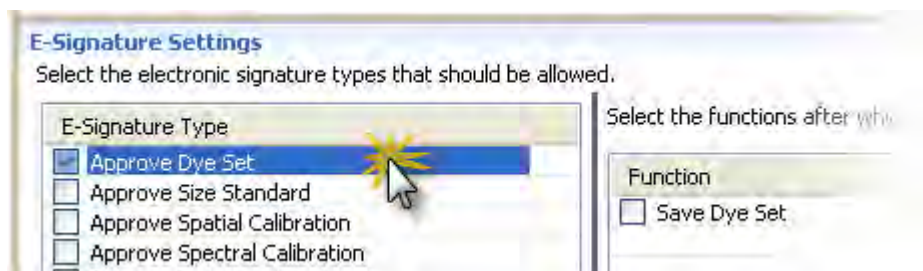
Function	# Signatures Required	Authorities Required

## Select the actions that allow signature

**IMPORTANT!** Do not change e-sig settings during a spectral calibration.

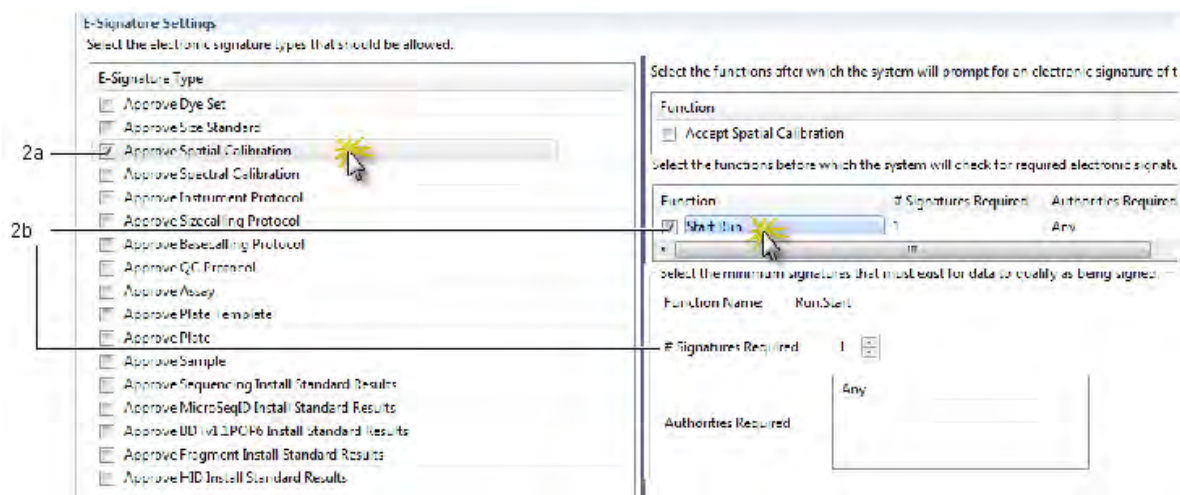
By default, no events require electronic signature. To use e-sig, enable events that require an e-signature.

1. Select the checkbox next to an item in the **E-Signature Type** list to identify events for which to allow electronic signature. This selection activates the **E-Sig** button for the selected items; it does require an electronic signature for these selections.



2. (Optional) For each item that you select:
  - a. From the top-right of the screen, select a function *after which* the system will prompt for electronic signature. This selection presents an e-sig prompt to users when they perform a function. Users can sign or can continue without signing.

- b. From the bottom-right of the screen, select a function (for example, start run) before which the system will check for required e-sigs. This selection presents an e-sig prompt to users when they start a run if the required signatures have not previously been made. Users must sign before they can continue. For “check before” functions, you can also:
- Change the number of signatures required.
  - Set a special authority for a signature: click the **Authorities Required** field, then select the user account or the user role to require for e-sig of this function. By default, each required signature needs no special authority; any user can sign.
  - Click **Apply**.



3. Click **Save Settings**.
4. Log out of the software, then log back in, to activate the settings.

## E-signature settings

Table 3 E-signature settings: functions to prompt after

E-Signature type	Function to prompt after
Approve Dye Set	Save
Approve Size Standard	Save
Approve Spatial Calibration	Accept
Approve Spectral Calibration	Accept
Approve Instrument Protocol	Save
Approve Sizecalling Protocol	Save
Approve Basecalling Protocol	Save
Approve QC Protocol	Save
Approve Assay	Save



**Table 3 E-signature settings: functions to prompt after** *(continued)*

E-Signature type	Function to prompt after
Approve Plate Template	Save
Approve Plate	Save
Approve Sample	Save
Approve Sequencing Install Standard Results	Accept
Approve MicroSeqID Install Standard Results	Accept
Approve BDTv1.1 POP6 Install Standard Results	Accept
Approve Fragment Install Standard Results	Accept
Approve HID Install Standard Results	Accept

**Table 4 E-signature settings: functions to check before**

E-Signature type	Function to check before	Signatures and authorities required (defaults if enabled)
Approve Spatial Calibration	Start Run	1 signature, any authorities (any user, any user role)
Approve Spectral Calibration		
Approve Plate		
Approve Sequencing Install Standard Results		
Approve MicroSeq ID Install Standard Results		
Approve BDTv1.1 POP6 Install Standard Results		
Approve Fragment Install Standard Results		
Approve HID Install Standard Results		

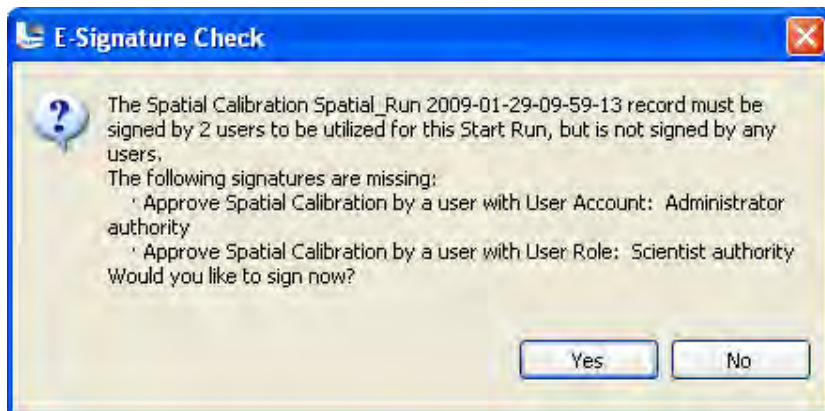
### How the software prompts electronic signature before a run

If the system is configured to check that data is signed before starting a run and the data for the run is not signed, a message is displayed when the user clicks Start Run.

#### Example

The e-sig system is configured to require signatures from two users (one from the user account named Administrator, and the other from any user account with a scientist user role) for a spatial calibration before it can be used in a run. The spatial calibration has not been signed.

A user starts a run. The following message is displayed:



Before the run can start, the following users must sign:

- The Administrator user
- Any other user with the Scientist role specified and electronic signature enabled in their user account

If a user that does not meet the specified criteria signs, a message is displayed to indicate which users have e-signed.

## Generate e-sig reports

### Display e-sig records

1. Access the E-Signature Reports screen.



2. (Optional) Edit display settings:
  - Specify filters (date range, user name, object type, object name), then click **Go**.
  - Select a record, then click **Show Object History**.
  - In the history dialog box, select a record, then click **Show E-Signature Details**.
  - Double-click column headers to sort. Multi-column sorting is supported (see “Sort by one or multiple columns” on page 94).
  - Customize the table (see “Customize a table” on page 94).
3. The records that are displayed (if they are specified in E-Signature settings) are:
  - Approve Dye Set
  - Approve Size Standard
  - Approve Spatial Calibration
  - Approve Spectral Calibration
  - Approve Instrument Protocol
  - Approve Sizecall Protocol
  - Approve Basecall Protocol
  - Approve QC Protocol
  - Approve Assay
  - Approve Plate Template
  - Approve Plate
  - Approve Sample
  - Approve BDTv1.1POP6 Install Standard Results
  - Approve Sequencing Install Standard Results
  - Approve Microseq ID Install Standard Results
  - Approve Fragment Install Standard Results
  - Approve HID Install Standard Results




## View and print e-signature reports

1. Display the records of interest as described in “Display e-sig records” on page 242.

---


**Note:** Filter the list to decrease the time required to generate reports.

---

2. Click  **View E-Sig Summary Report** or  **View E-Sig Detailed Report**.
3. (Optional) In the Report screen, click toolbar options to manipulate the report. Place the mouse pointer over an item for a description of the item.
4. To print the report, click  **Print**.
5. To save the report electronically (PDF), print the report and select a PDF printer.
6. Close the report.


## Export e-sig records

As needed, you can export e-sig records to a TXT file for additional manipulation and reporting outside the software.

1. Display the records of interest as described in “Display e-sig records” on page 242.
2. Select the records to export.
3. Click  **Export E-Sig Records**.
4. Specify a name and location for the export TXT file.
5. Click **Save**.

## Export and import user accounts security audit and electronic signature settings

### Export user accounts, security, audit, and electronic signature settings

1. In any screen in the SAE module, click  **Export** in the navigation pane.




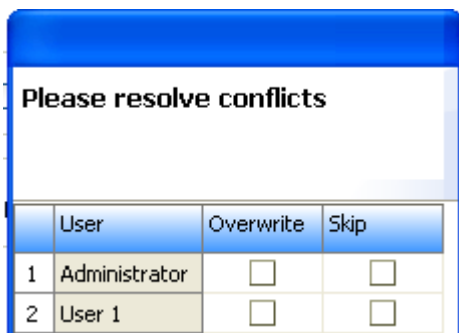
2. Select the items to export:



- **User Profiles**—Contains all settings in the following screens:
    - **Edit User**—All user accounts with Active status
    - **User Role**—All user roles and associated permissions (in case a user account specifies a user role that does not exist on the system into which you import the profiles)
  - **System Configuration**—Contains all settings in the following screens:
    - **Security**—Account setup and security policies
    - **Audit**—Objects selected for auditing, audit modes, and reasons
    - **E-Signature Settings**—Objects selected for E-Signature, functions, number of signatures, and authorities
    - **User Roles**—All user roles and associated permissions
3. Click **Export**.
  4. Specify the name and location for the exported .dat file, then click **Save**. A message is displayed when the export completes.

### Import user accounts, security, audit, and electronic signature settings

1. In any screen in the SAE module, click  **Import** in the navigation pane.
2. Select the .dat file to import, then click **Open**. A message is displayed asking if you want to overwrite the current system configuration. Click **Yes**.  
If any imported user accounts already exist on the system, you are prompted to overwrite or skip each account.



	User	Overwrite	Skip
1	Administrator	<input type="checkbox"/>	<input type="checkbox"/>
2	User 1	<input type="checkbox"/>	<input type="checkbox"/>

## Users

### Users overview of System Security Audit Trail and E-Signature

The Security, Audit, E-Signature (SAE) module provides the following functionality:

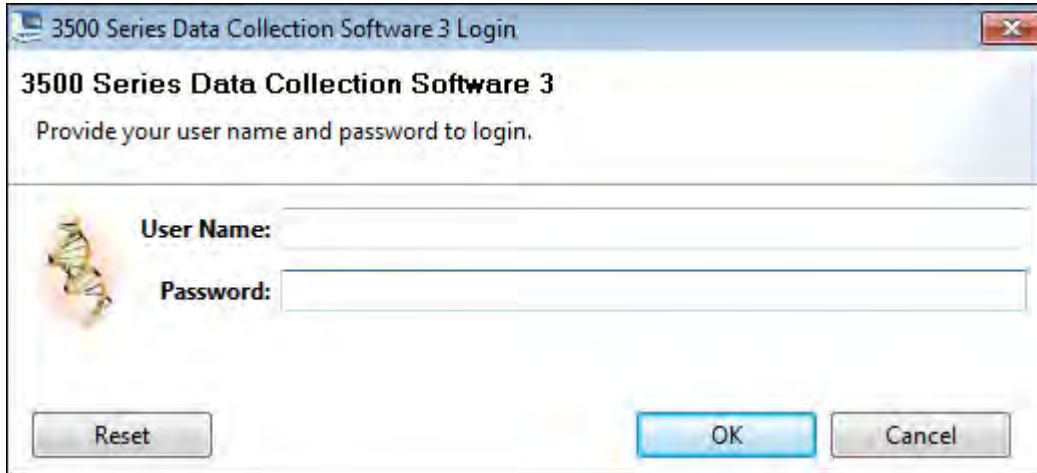
- **System security**—Controls user access to the software.
- **Auditing**—Tracks changes made to library items, actions performed by users, and changes to the SAE settings.
- **Electronic signature (e-sig)**—Requires users to provide a user name and password when performing certain functions.

Depending on the way that your administrator configures these features, you may see the following dialog boxes and prompts when you use the software.

## Security

### Log in

Enter your user name and password to access the software.



Your access to functions in the software is based on the permissions associated with your user account. Functions for which you do not have permissions are dimmed.

If your system is configured for password expiration, you will periodically be prompted to change your password. If your system is configured to monitor failed log in attempts, you will be locked out of the software if you incorrectly enter your user name or password more than a specified number of times.

### Permissions

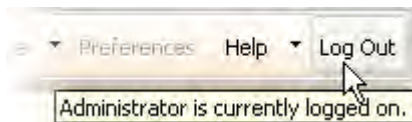
If your user account does not have permission to perform a function in the software, the associated menu commands are dimmed.

### Determine the name of the logged-in user

To display the full name of the logged-in user:

Place the mouse pointer on the **Logout** menu.

The full name of the logged-in user is also displayed in the **Load Plates for Run** screen and the **Monitor Run** screen.



### Change your password when it expires

When your password is about to expire, a message is displayed when you log in.

To change your password, select **Tools** ▶ **Change Password**. Enter your current password, enter the new password two times, then click **OK**.

## Activate a suspended account

If your system is configured to suspend a user account for failed logins, and you enter an incorrect user name and password more than the allowed number of times, your user account is suspended, and the **Log In** dialog box indicates that your account is inactive.

To activate a suspended account, you can either:

- Wait until the suspension period ends  
*or*
- An administrator can change the account status from **Suspended** to **Active**

---

**Note:** While a user is suspended, a different user can click **Reset**, then log in.

---

## Session timeout

If your system is configured to timeout and there is no user activity for the specified time, the Log In dialog box indicates that your user session has timed out. You must enter your user name and password to access the software.

---

**Note:** The administrator or another user with permission to log in to timed-out sessions can click **Reset**, then log in.

---



The screenshot shows a dialog box with a red border. At the top, a message box with a red border contains the text: "The user session has timed out. Please provide your user name and password to unlock your session." Below this message, there are two input fields: "User Name:" with the text "Administrator" and "Password:" which is empty. At the bottom of the dialog box, there are three buttons: "Reset", "OK", and "Cancel".



## Audit

If your system is configured for auditing, you may be prompted to specify a reason when you make certain changes in the software. Based on your system configuration, you can either select a reason or enter a reason for change.




## Electronic signature

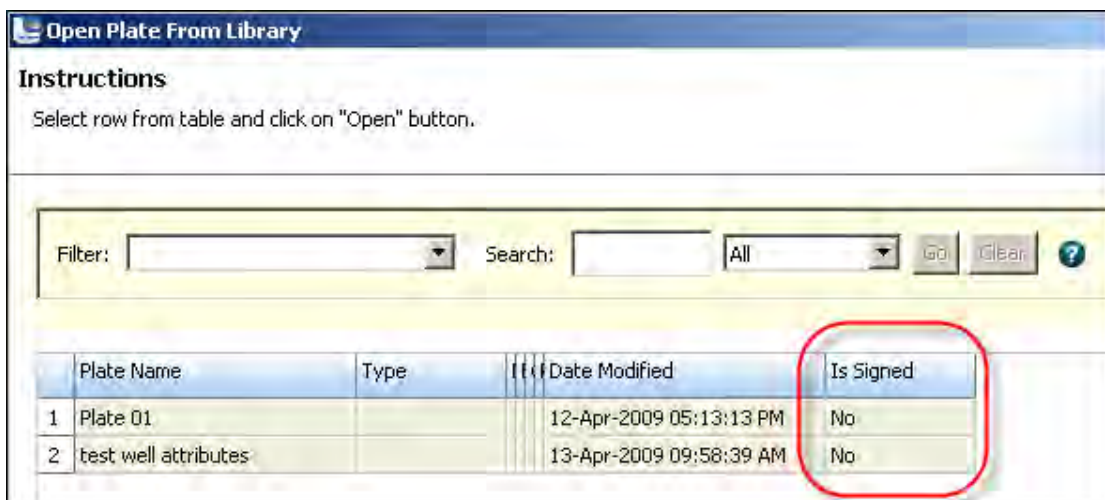
If your system is configured for electronic signature, you may be prompted to provide your user name and password when you perform certain actions in the software.



If an item is set to require two signatures, the signers are not required to sign at the same time. When the first signer signs, the E-Sig status is set to **Partially Signed**. When the second signer signs, the E-Sig status is set to **Signed**.

You may also be permitted to sign objects such as plates, calibrations, or other library items. If e-sig is enabled for items, any of the following may apply:

- The  **E-Signature** button is enabled in the library or the calibration.
- You are prompted to sign as described in “How the software prompts electronic signature before a run” on page 241.
- The **Open Plates** dialog box or the library displays an “**Is signed**” column that reflects the e-sig status of an item.



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## Maintenance schedule





**WARNING!** This section lists the common tasks required to maintain the instrument in good working condition. Wear appropriate protection, including gloves, laboratory goggles, and coat whenever you work with the fluids used on this instrument, or parts that may come into contact with these fluids.

**IMPORTANT!** Use only the cleaning agents listed in this guide. Use of cleaning agents other than those listed in this guide may damage the instrument.

## Review calendar reminders

1. Review the calendar reminders list in the **Dashboard** daily, then perform the scheduled tasks.

▼ Calendar Reminders					
Name	Priority	Notification Date	Description	Action	
Run Install Check	HIGH	13-Sep-2013 12:00:00 AM	Run Install Check	✓	✗
Perform Planned Maintenance	HIGH	13-Sep-2013 12:00:00 AM	Perform Planned Maintenance	✓	✗
Clean the anode buffer cup pin-...	HIGH	03-Oct-2013 12:00:00 AM	Clean the anode buffer cup pin-valve assembly on the polymer del...	✓	✗
Replace cathode buffer containe...	HIGH	13-Sep-2013 12:00:00 AM	Replace cathode buffer container septa	✓	✗
Restart computer, Instrument	MEDI...	03-Oct-2013 12:00:00 AM	Restart computer, Instrument	✓	✗

2. When you complete a task, click  to mark it as complete, click  to mark it as dismissed.

Completed and dismissed tasks are:

- Recorded in the **Notification Log**. See “Review the Notifications Log” on page 256.
- Removed from the **Calendar Reminder** section, and they do not appear again unless they are repeating tasks. Dismissed tasks can be logged in the Notifications Log.

---

**Note:** It is the end users’ responsibility to comply with maintenance prompts displayed in the software by completing the maintenance tasks at the recommended frequencies as shown in “Maintenance schedule” on page 251.

---

## Daily instrument maintenance tasks

Clean the assemblies, anode buffer container, and cathode buffer container, and ensure that the outside of the assemblies is dry.

---

**IMPORTANT!** Use only the cleaning agents listed in this guide. Use of cleaning agents not listed in this manual can impair instrument function.

---

Task	Frequency	For information, see ...
Click <b>Refresh</b> , then check consumables on the <b>Dashboard</b> —View the gauges on the Dashboard to see the status for anode buffer container, cathode buffer container, and polymer.	Before each run	“Check system status in the Dashboard” on page 36
Visually inspect the level of fluid inside the anode buffer container and the cathode buffer container. The fluid must line up with the fill line.		“Prepare the Anode Buffer Container (ABC)” on page 258 “Prepare the Cathode Buffer Container (CBC)” on page 259
Ensure that the CBC septa are properly seated on the container.		“Ensure proper installation of CBC septa” on page 40
Ensure that the plate assemblies are properly assembled. Align the holes in the plate retainer with the holes in the septa to avoid damaging capillary tips.		“Prepare the plate assembly” on page 70
Ensure that the plate assemblies and the cathode buffer container are positioned on the plate deck properly. They should sit securely on the deck.		“Load the plate in the instrument” on page 72
Ensure the array locking lever on the capillary array is secured.		Figure 42
Check for bubbles in the pump block and channels. Use the <b>Remove Bubble wizard</b> to remove bubbles.	Daily or before each run	“Remove bubbles from the polymer pump” on page 268
Check the loading-end header to ensure that the capillary tips are not crushed or damaged.		“Install or change the capillary array” on page 266

(continued)

Task	Frequency	For information, see ...
Ensure that the pump block is in pushed back position.	Daily	Figure 42
Clean the instrument surfaces of dried residue, spilled buffer, or dirt.		“Clean the instrument” on page 257
Check for leaks and dried residue around the buffer-pin valve, check valve, and array locking lever. If leaks persist, contact Thermo Fisher Scientific.		“Check calendar reminders” on page 36

## Weekly instrument maintenance tasks

Task	Frequency	For information, see ...
Check the storage conditions of the used arrays to ensure the array tip is covered in the reservoir.	Weekly	“Store a capillary array” on page 267
Run the <b>Wash Pump and Channels wizard</b> .		“Wash the pump chamber and channels” on page 268
Use a lab wipe to clean the anode buffer container valve pin assembly on the polymer delivery pump.		Figure 42
Restart the computer and instrument.		“Restart the instrument and the computer” on page 279

## Monthly instrument maintenance tasks

Task	Frequency	For information, see ...
Run install check.	Monthly or as needed	“Run an install check” on page 144
Flush the pump trap.		“Flush the water trap (pump trap)” on page 269
Empty the oven condensation reservoir.		Figure 42
Replace cathode buffer container septa.		“Prepare the Cathode Buffer Container (CBC)” on page 259
Clean the autosampler.		“Clean the instrument” on page 257
Clean the drip tray.		
Check disk space.		“Monitor disk space” on page 276

(continued)

Task	Frequency	For information, see ...
If Security, Audit, and E-sig is enabled, archive and purge audit records.	Monthly or as needed	“Archive and purge” on page 237
Defragment the hard drive.	Monthly, or before fragmentation reaches 10%	“Defragment the computer hard drive” on page 277

## Quarterly maintenance tasks

Task	Frequency	For information, see ...
Archive and purge audit records	Every three months	“Archive and purge” on page 237

## Annual planned maintenance tasks

Call your Thermo Fisher Scientific representative to schedule annual planned maintenance.

## As-Needed instrument maintenance tasks

Task	Frequency	For information, see ...
Change the tray.	As needed	“Clean the instrument” on page 257
Remove dried polymer from the capillary tips with a lint-free tissue moistened with deionized water.		
Archive and purge library objects. Dashboard ▶ Manage ▶ Archive or Dashboard ▶ Manage ▶ Purge.		Chapter 8, “Manage library resources”

## Use the maintenance calendar

The Maintenance calendar is a monthly or daily view of the routine maintenance tasks scheduled for your instrument. When a task is due to be performed, it is listed in the Calendar Reminders list in the **Dashboard** (see “Review the Notifications Log” on page 256).

To access the maintenance calendar, click the **Maintenance** tab, then click **Schedule**.

A set of recommended tasks are scheduled in the calendar, flagged with FR (Factory Repeating) in the monthly view and F (Factory) in the daily view. User-specified repeating tasks are flagged with R (Repeating) in the monthly view.

Weekly factory repeating tasks in calendar	Monthly factory repeating tasks in calendar
<ul style="list-style-type: none"> <li>• Clean the anode buffer cup pin-valve assembly on the polymer delivery pump</li> <li>• Restart instrument and computer</li> </ul>	<ul style="list-style-type: none"> <li>• Replace cathode buffer container septa</li> <li>• Clean drip tray</li> <li>• Clean autosampler</li> <li>• Check disk space</li> <li>• Defragment hard drive</li> <li>• Run install check</li> <li>• Flush pump trap</li> </ul>

You can change the priority of factory tasks, but you cannot remove them from the calendar or alter the frequency at which the notifications for the tasks are displayed.

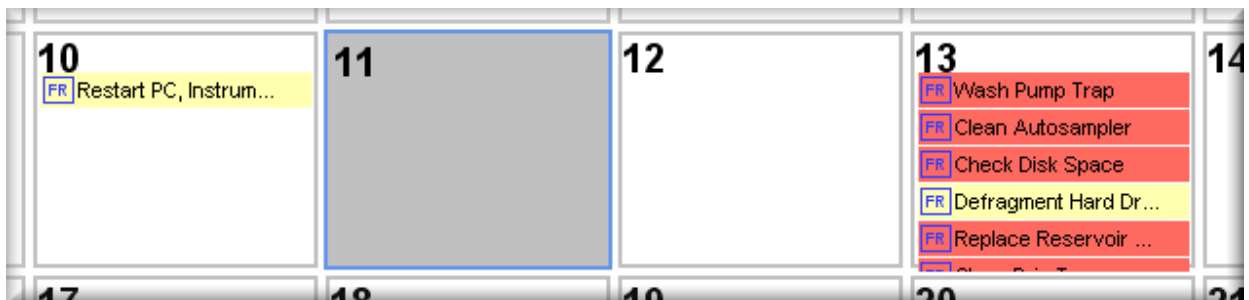
Additionally, we suggest that you add to the maintenance calendar:

- The regular maintenance tasks.
- A maintenance task to replace a consumable based on its installation date (for example, create a task to replace the polymer for two days before the polymer will expire).

## Create calendar entries

To create a new scheduled task, click **Create** and follow the prompts.

The following figure is an example of scheduled events in the calendar.



The Month and Day tabs allow you to view your schedule in different formats. Click **Detach** to move the calendar window.

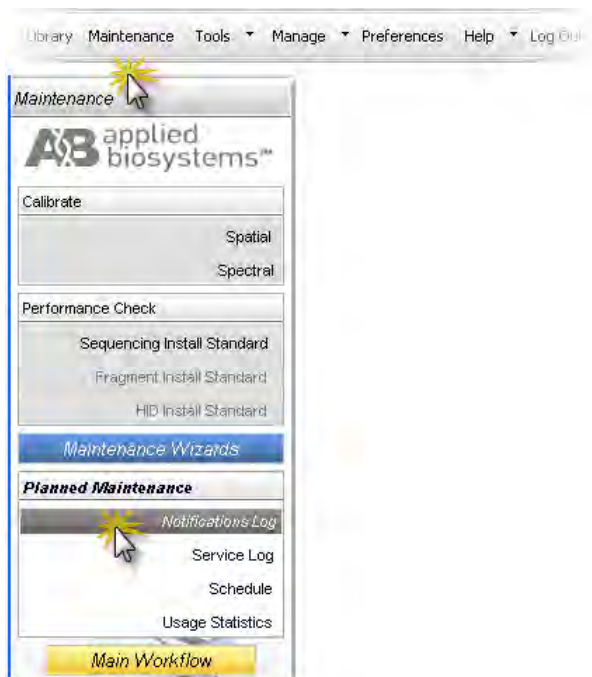
## View the Planned Maintenance Report

1. Click the **Maintenance** tab, then click **Schedule**.
2. Click **Planned Maintenance Report**.
3. Specify the date range, then click **OK**.
4. Select **Print** as needed.
5. To save the report electronically (PDF), print the report and select a PDF printer.

## Review the Notifications Log

The Notifications Log is a history of the action taken on calendar reminders messages in the **Dashboard** (see “Review calendar reminders” on page 251).

1. Access the **Notifications Log**.



2. View the **Notification Log Report** and print as needed.

---

**Note:** Multi-column sorting is supported (see “Sort by one or multiple columns” on page 94).

---



## Export the consumables log

1. In any screen, select **Tools ▶ Export Consumables Log**.
2. Select a location and enter a name for the export file.

---

**IMPORTANT!** In the exported file, the conditioning reagent part description incorrectly lists "Polymer Pouch". However, the lot number that is listed is correct for the conditioning reagent.

---

## Clean the instrument

---

**IMPORTANT!** Wear appropriate protection, including gloves, laboratory goggles, and coat whenever you work with the fluids used on this instrument, or parts that may come into contact with these fluids.

---

---

**IMPORTANT!** Use only the cleaning agents listed in this guide. Use of cleaning agents other than those listed in this guide may damage the instrument.

---

1. Ensure the oven is closed.
2. Press the Tray button on the front of the instrument to move the autosampler to the forward position.
3. Wipe off any liquid on or around the autosampler using a lint-free tissue.
4. Clean off any polymer build-up crystals on the instrument, including the capillary tips, with deionized water and lint-free tissue.
5. Clean the array plug with deionized water and lint-free tissue.
6. Clean out the drip trays with deionized water, or ethanol, and lint-free tissue.

---

**Note:** The drip tray can be removed.

---

## Install buffers

---

**IMPORTANT!** Wear appropriate protection, including gloves, laboratory goggles, and coat whenever you work with the fluids used on this instrument, or parts that may come into contact with these fluids.

---

---

**IMPORTANT!** Use only the parts listed in Appendix D, "Catalog numbers".

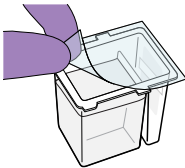
---

## Prepare the Anode Buffer Container (ABC)

1. Check the expiration date on the label to ensure that the ABC is not expired and will not expire during use.
2. Allow the refrigerated ABC to equilibrate to room temperature before first use. Do not remove the seal until you have completed step 5.
3. Verify that the seal is intact. Do not use if the buffer level is too low or the seal has been compromised. A fill tolerance of  $\pm 1$  mm is acceptable.
4. Invert the ABC, then tilt it slightly to move most of the buffer to the larger side of the container. The smaller side of the container should contain  $<1$  mL of the buffer.



5. Verify that the buffer is at the fill line.
6. Peel off the seal at the top of the ABC.



7. With the RFID label toward instrument, place the ABC into the anode-end of the instrument, below the pump. Position the anode in the large chamber of the ABC, then push the ABC up and back to install.

---

**IMPORTANT!** The RFID label must be facing the instrument (away from you) to ensure that the RFID information is read accurately by the instrument.

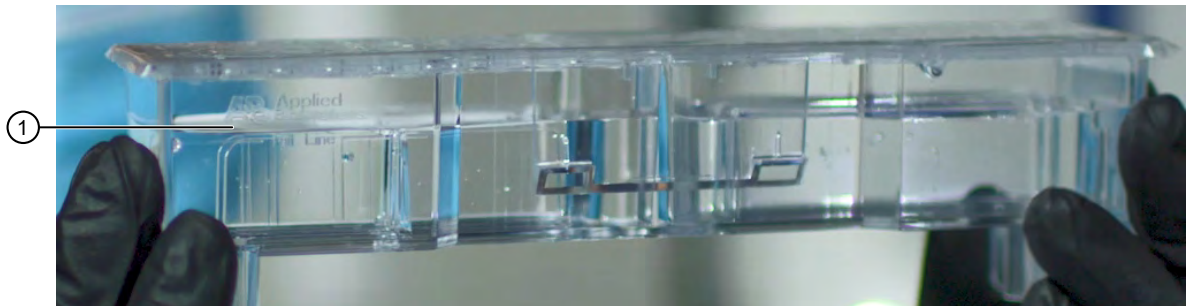
---



8. Close the instrument door to re-initialize.
9. In the **Dashboard**, click **Refresh**, then check the **Quick View** section for updated status.

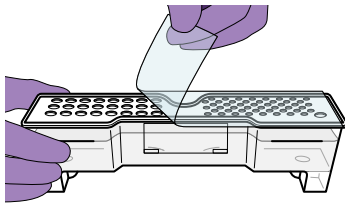
## Prepare the Cathode Buffer Container (CBC)

1. Check the expiration date on the label to ensure that the CBC is not expired and will not expire during use.
2. Allow refrigerated CBC to equilibrate to ambient temperature.
3. Wipe away condensation on the CBC exterior with a lint-free tissue. Condensation can cause arcing and termination of the run.
4. Check that the seal is intact. Do not use if the buffer level is too low or the seal has been compromised. A fill tolerance of  $\pm 0.5$  mm is acceptable.

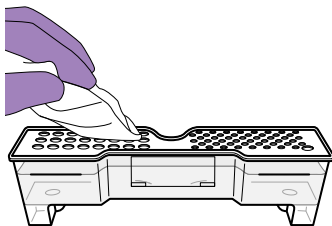


① Fill line

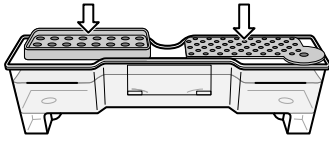
5. Tilt the CBC back and forth gently and carefully to ensure that the buffer is evenly distributed across the top of the baffles. If you do not tilt the CBC back and forth, the buffer sticks to the baffles because of surface tension.
6. Verify that the buffer is at or above the fill line.
7. When ready to install the CBC, place the container on a flat surface (such as a lab bench) and peel off the seal.



8. Wipe off any buffer on top of the CBC with a lint-free tissue. Ensure that the top of the container is dry. Moisture can cause arcing, termination of a run, or damage to the instrument.



9. Place the septa (Cat. No. [4410715](#)) on the CBC.



- a. Align the buffer septum (the part that is symmetrical) over the 24 holes of the CBC.
- b. Push the septum lightly into the holes to start, then push firmly to seat it.

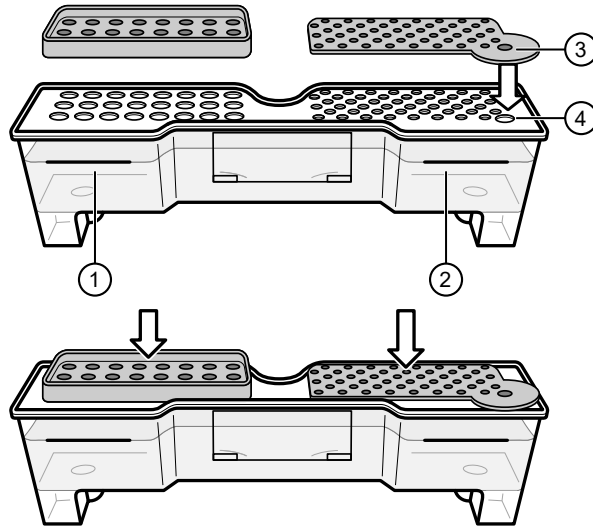
---

**IMPORTANT!** Look at the CBC from the side and ensure that there is no gap between the container and the lip of the septum.

---

- c. Align the capillary washing septum over the other chamber of the CBC.  
The capillary washing septum has 48 slitted holes and one rounded starter tab for alignment. Position the rounded starter tab of the septum over the larger alignment hole on the washing chamber, then press down.

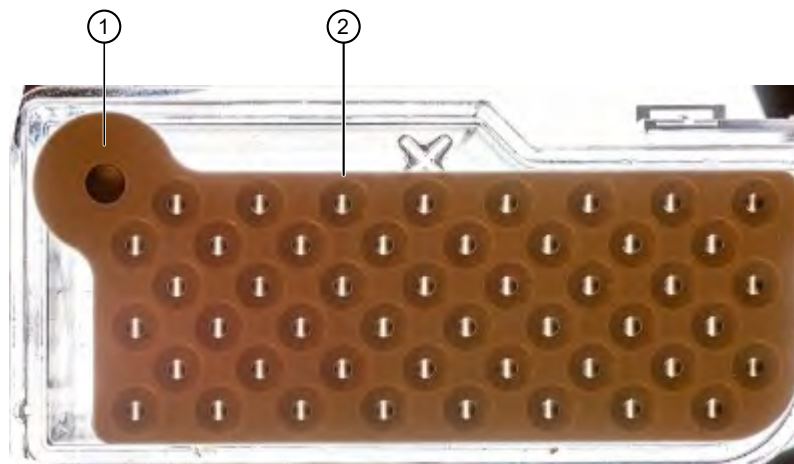
d. Push the septum lightly into the holes to start, then push firmly to seat it.



- ① Buffer chamber and septum
- ② Washing chamber and septum
- ③ Starter tab
- ④ Alignment hole

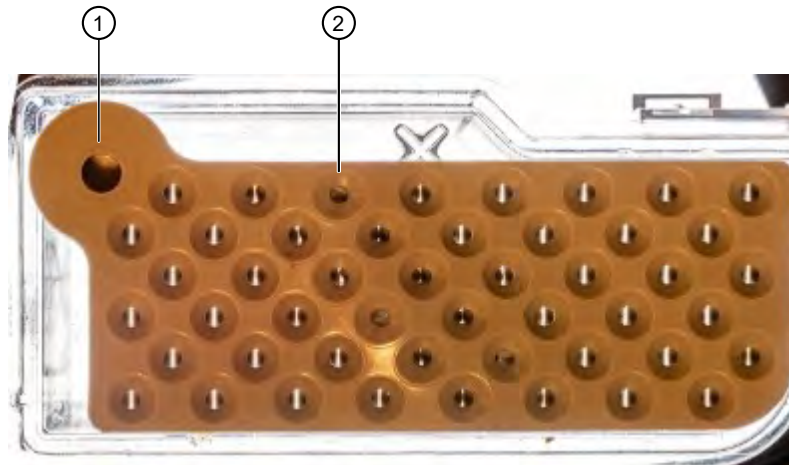
**IMPORTANT!** Ensure the septa are securely seated to prevent displacement of the septa during operation. Inspect the underside of the CBC lid to ensure that all capillary washing septum blades are fully engaged and unobstructed.

**IMPORTANT!** A correctly inserted capillary washing septum shows a clear, linear slit in all wells. To easily view the slits, illuminate the CBC from the bottom, such as with an LED screen, and observe the CBC from above. If any holes do not show a clear, linear slit, firmly press down on those specific holes to ensure that the septum blades are visually engaged and the slit of light is unobstructed.



**Figure 40** Illuminated CBC with the capillary washing septum correctly in place

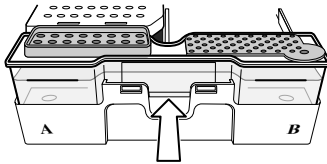
- ① Starter tab positioned in alignment hole
- ② Linear slit visible



**Figure 41** Illuminated CBC with the capillary washing septum not in place

- ① Starter tab positioned in alignment hole
- ② Linear slit not visible

10. Click the **Tray** button on the front panel to move the autosampler to the front position.
11. With the tab facing you and the RFID tag to the right, install the CBC on the autosampler. When properly installed, the CBC tabs will click as you snap them into place on the autosampler.



12. Click the **Tray** button to retract the autosampler, then close the instrument door to initialize.
13. In the **Dashboard**, click **Refresh**, then check the **Quick View** section for updated status.

## Replenish, change, flush, and store polymer

**IMPORTANT!** Note the following:

- Wear appropriate protection, including gloves, laboratory goggles, and coat whenever you work with the fluids used on this instrument, or parts that may come into contact with these fluids.
- Use only the parts listed in Appendix D, “Catalog numbers”.
- To minimize background fluorescence, use clean, powder-free, silicone-free latex gloves whenever you handle the pump assembly or any item in the polymer path.

## Precautions for use

- Do not reuse a polymer pouch that has been installed on another type of instrument. For example, if you remove a partially used polymer pouch from an 8-capillary instrument, do not reuse that polymer on a 24-capillary instrument.
- If you remove a polymer pouch for storage (2–8°C), place a pouch cap (Cat. No. 4412619) onto the pouch, then place an empty pouch (or conditioning reagent) on the connector to prevent desiccation of any residual polymer on the connector. Follow the instructions in the wizard to ensure proper operation of the pouch and the instrument.

## Replenish polymer or change polymer type

1. Check the expiration date on the label to ensure that the polymer is not expired and will not expire during intended use.

---

**IMPORTANT!** Do not use if the product is expired, if the pouch or label is damaged, or if the top seal is missing or damaged.

---

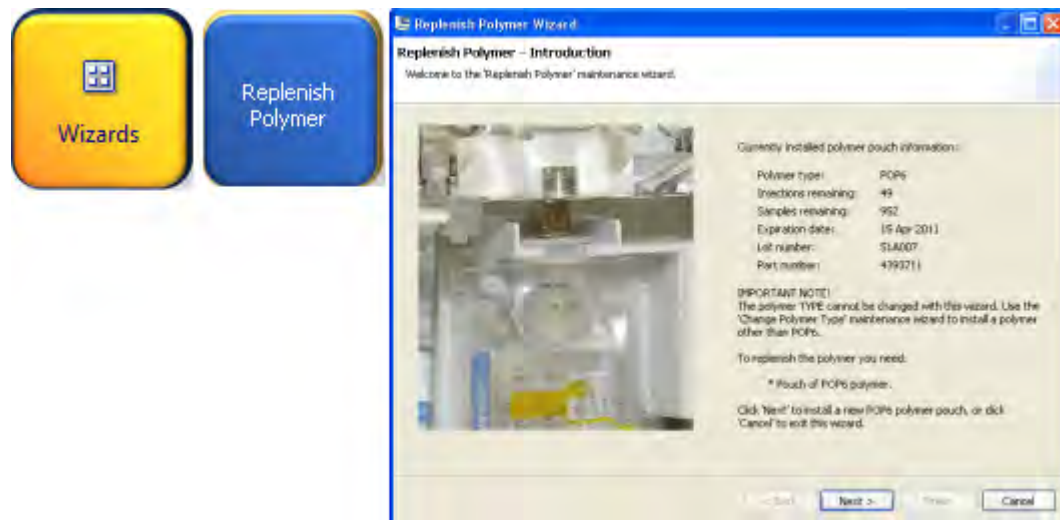
2. Allow the refrigerated polymer to equilibrate to room temperature (15–30°C) before use.
3. In the Dashboard, click **Wizards**, then click **Replenish Polymer** (requires 10–20 minutes) or **Change Polymer Type** (requires 60–70 minutes).

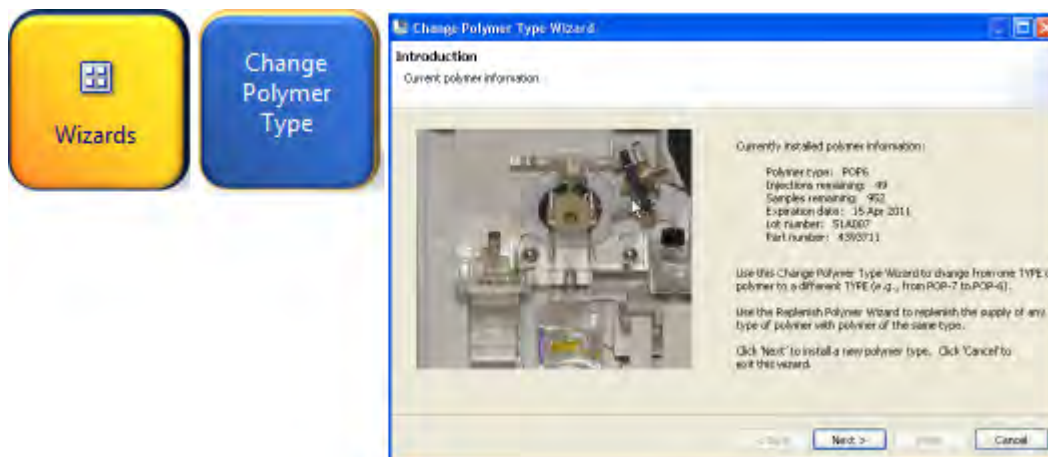
---

**Note:** If you are changing the polymer type, you also need Conditioning Reagent.

---

4. Follow the prompts in the Wizard window.





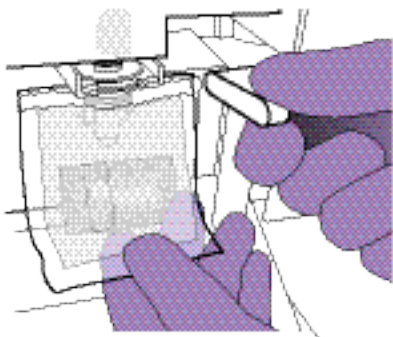
- When instructed to install the polymer, peel off the seal at the top of the pouch fitting.

---

**Note:** You may notice a tiny droplet of polymer inside the fitting (residual from the pouch filling process). This is *not* expected to cause any performance issues.

---

- With the RFID label *facing* the instrument, slide the pouch fitting onto the slot of the lever assembly. Push the lever up to snap the pouch into the connector end of the instrument pump.




---

**Note:** The RFID label must face the instrument (away from you) to ensure that the RFID information is read accurately by the instrument.

---

- In the Dashboard, click **Refresh**, then check the Quick View section for the updated polymer status.

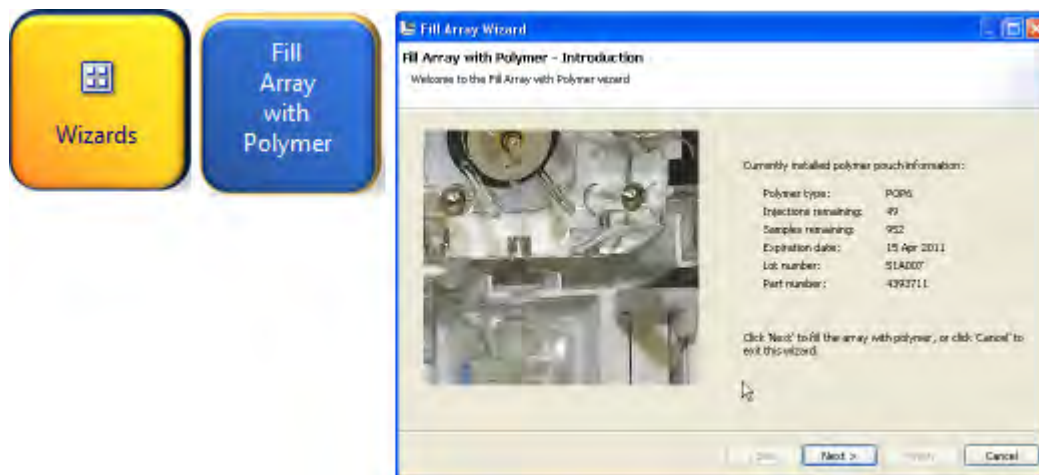
## Store partially used polymer

If you remove a polymer pouch for storage (2–8°C), place a pouch cap (Cat. No. [4412619](#)) onto the pouch. Install an empty pouch or conditioning reagent pouch on the instrument to prevent desiccation of any residual polymer on the connector. Follow the instructions in the maintenance wizards to ensure proper installation of the polymer pouch.



## Fill capillary array with fresh polymer

1. In the **Dashboard**, click **Wizards**.
2. In the **Maintenance wizards** screen, click **Fill Array with Polymer**.
3. Follow the prompts in the **Fill Array wizard** window.



4. Click **Refresh** in the Dashboard to update the screen.
5. Check the **Quick View** section of the Dashboard for updated status after filling of the capillary array with fresh polymer.

## Change and store a capillary array



**WARNING! SHARP.** The electrodes on the load-end of the capillary array have small, blunt ends that can lead to piercing injury.

---

**IMPORTANT!** Wear appropriate protection, including gloves, laboratory goggles, and coat whenever you work with the fluids used on this instrument, or parts that may come into contact with these fluids.

---

## Install or change the capillary array

**IMPORTANT!** Before installing a capillary array, examine the loading-end header to ensure that the capillary tips are not crushed or damaged.

**Note:** The **Install Capillary Array wizard** takes 15–45 minutes to complete.

1. In the **Dashboard**, click **Wizards**.
2. In the **Maintenance wizards** screen, click **Install Capillary Array**.
3. Follow the prompts in the Install Capillary Array wizard window.
4. Check the **Quick View** section of the Dashboard for updated status of the capillary array.



## Store a capillary array



**WARNING! SHARP.** The electrodes on the load-end of the capillary array have small, blunt ends that can lead to piercing injury.

If you remove a capillary array for storage, insert the loading-end of the capillary array in distilled water to prevent the polymer from drying in the capillaries. Check periodically and add distilled water as needed.



## Maintain the pump

---

**IMPORTANT!** Wear appropriate protection, including gloves, laboratory goggles, and coat whenever you work with the fluids used on this instrument, or parts that may come into contact with these fluids.

---

---

**IMPORTANT!** To minimize background fluorescence, use clean, powder-free, silicone-free latex gloves whenever you handle the pump assembly or any item in the polymer path.

---

## Avoiding damage to the pump assembly

The polymer delivery pump can be irreversibly damaged in the following situations:

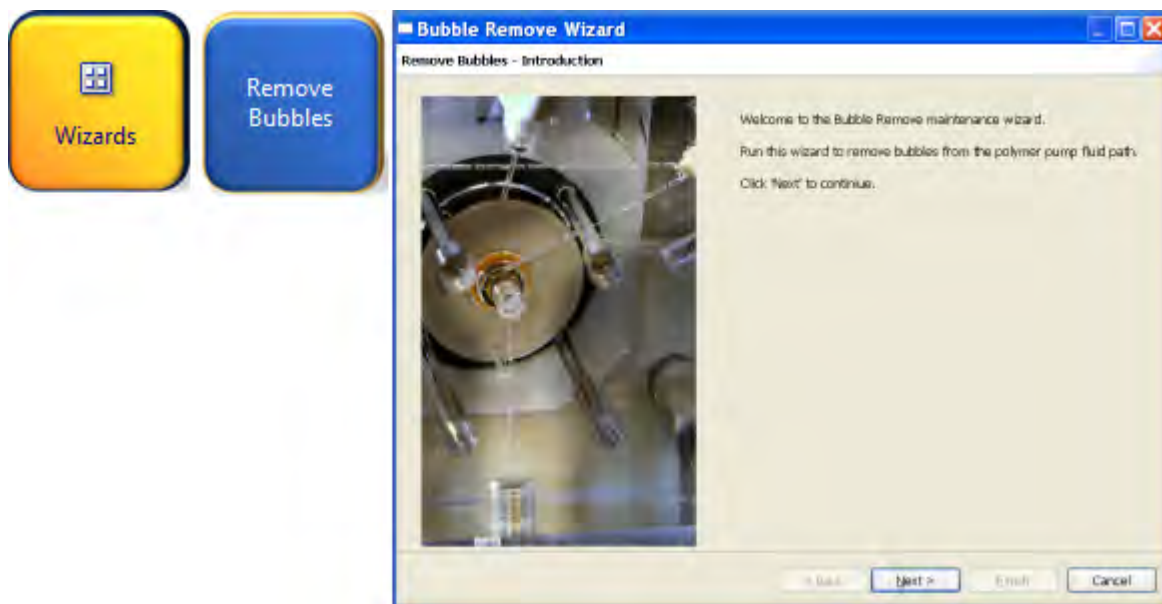
- Polymer dries in the polymer channels of the pump assembly, which can scratch the channels in the pump, and can cause blockage.
- The pump assembly is exposed to organic solvent, which can cause cracking and clouding of the acrylic pump material.
- The pump assembly is exposed to temperatures greater than 40°C, which can damage the pump components.
- Arcing occurs in the pump assembly, which can damage the acrylic pump material.

## Remove bubbles from the polymer pump

Remove bubbles from the polymer pump fluid path before each run. See “Daily instrument maintenance tasks” on page 252 for more information.

**Note:** The **Bubble Remove wizard** takes 5–15 minutes to complete.

1. In the **Dashboard**, click **Wizards**.
2. In the **Maintenance wizards** screen, click **Remove Bubbles**.
3. Follow the prompts in the Bubble Remove wizard window.
4. Check the **Quick View** section of the Dashboard for updated status of the polymer pouch after removing bubbles from the polymer pump fluid path.



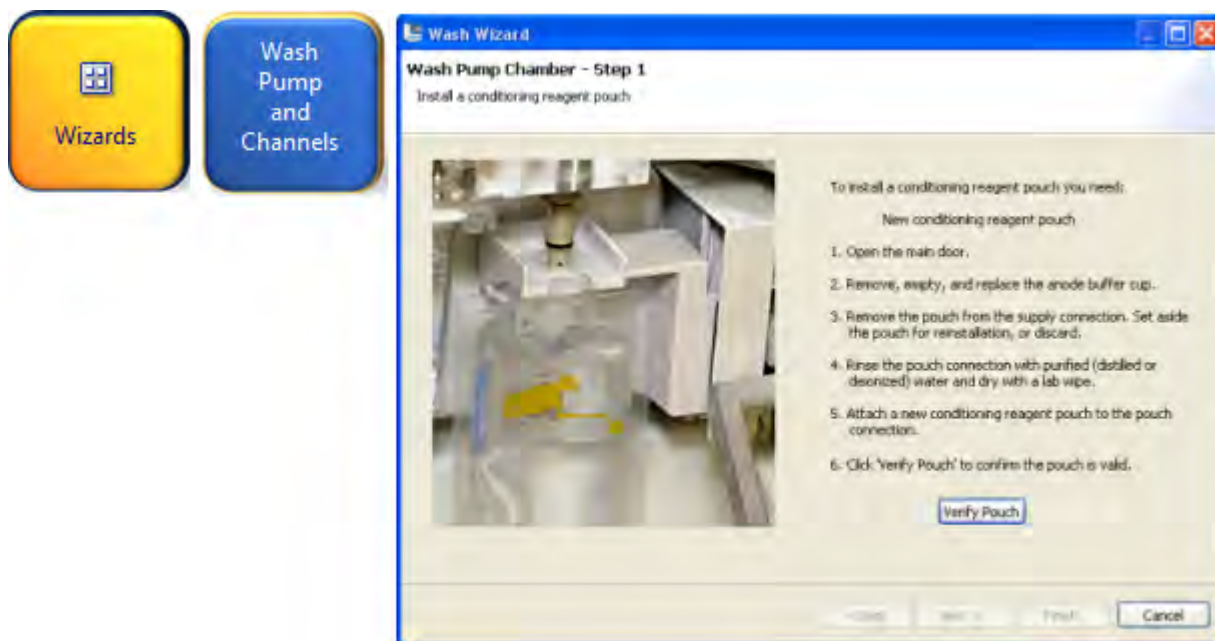
## Wash the pump chamber and channels

In the following situations, use the Polymer Delivery Pump Cleaning Kit (Cat. No. 4414007 ) in addition to the **Wash Pump Chamber and Channels** wizard to thoroughly clean the polymer delivery pump:

- Polymer has dried in the channels of the lower polymer block.  
Mechanical malfunctions may cause dried polymer to appear in the polymer delivery pump. Washing with either the **Wash Pump Chamber and Channels** wizard or this kit may not remove dried polymer – the lower polymer block may need to be replaced by Thermo Fisher Scientific.
- A contaminant in the polymer delivery pump is suspected of causing problems. The check valve fitting might be clogged or contaminated.

The Wash Pump and Channels wizard takes >40 minutes to complete.

1. In the **Dashboard**, click **Wizards**.
2. In the **Maintenance wizards** screen, click **Wash Pump and Channels**.
3. Follow the prompts in the wizard window.



## Flush the water trap (pump trap)

Flush the water trap monthly to prolong the life of the pump and to remove diluted polymer from the pump.

Flush with distilled or deionized water and ensure that the water flows into the overflow container. Dispose of the excess water (inside the overflow container). See “Chemical safety” on page 341.

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**Note:** Leave the trap filled with either distilled or deionized water.

---

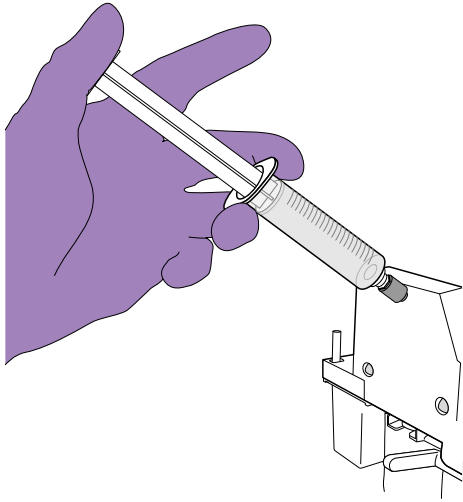
1. Fill the supplied 20 mL, all-plastic Luer lock syringe (in the Polymer Delivery Pump Cleaning Kit, Cat. No. 4414007) with distilled or deionized water. Expel any bubbles from the syringe.

---

**IMPORTANT!** Do not use a syringe smaller than 20 mL. Doing so may generate excessive pressure within the trap.

---

2. Attach the syringe to the forward-facing Luer fitting at the top of the pump block. Hold the fitting with one hand while threading the syringe onto the fitting with the other hand.



3. Open the Luer fitting by grasping the body of the fitting and turning it to loosen.
4. Grasp the attached syringe and turn counterclockwise approximately one-half turn.
5. Slowly depress the plunger.

---

**IMPORTANT!** DO NOT USE EXCESSIVE FORCE when you push the syringe plunger as this may damage the trap seals. Take approximately 30 seconds to flush 5 mL of either distilled or deionized water through the trap.

---

**Note:** Because the water trap volume is approximately 325  $\mu\text{L}$ , a relatively small volume of water is adequate for complete flushing. However, a larger volume improves flushing as long as force and flow rate are kept within the limits given above.

---

6. Remove the syringe from the Luer fitting. Hold the fitting with one hand while turning the syringe counterclockwise with the other hand.
7. Close the Luer fitting by lightly turning clockwise until the fitting seals against the block.

# Shutdown move and reactivate the instrument

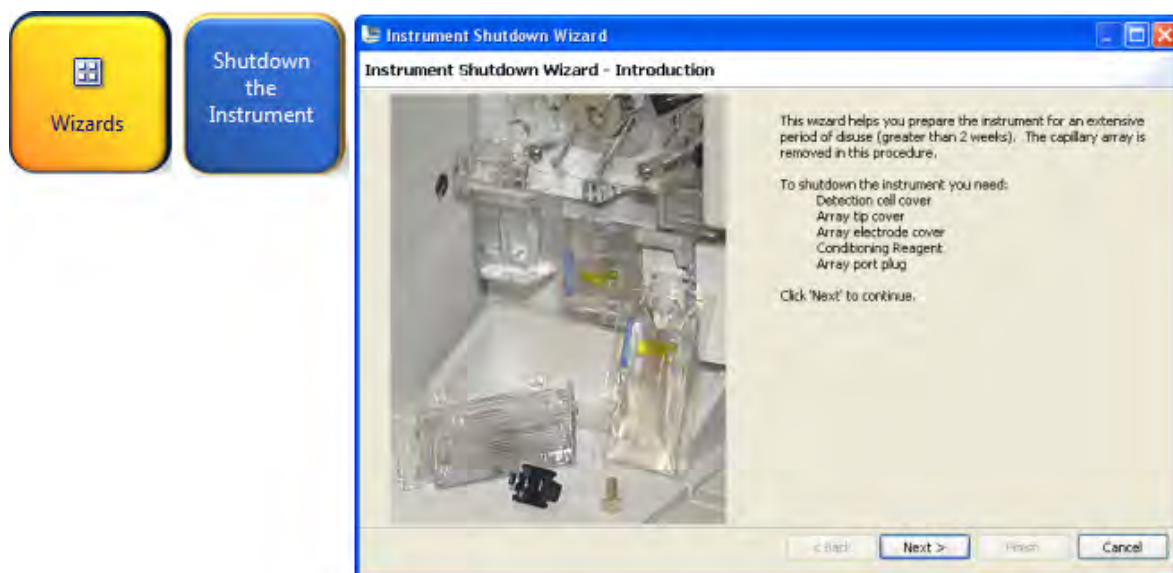
## Shutdown the instrument

A conditioning reagent pouch is required for this procedure.

Use the **Instrument Shutdown wizard** for short- and long-term shutdown.

**Note:** The Instrument Shutdown wizard takes 60 minutes to complete.

1. In the **Dashboard**, click **Wizards**.
2. In the **Maintenance wizards** screen, click **Shutdown the Instrument**.
3. Follow the prompts in the Instrument Shutdown wizard window. Perform the appropriate shutdown procedure based on the information in the following table:



**IMPORTANT!** Place a conditioning reagent pouch onto the instrument before performing instrument shutdown.

If the instrument will be unattended for ...	Perform this shutdown procedure ...
< 1 week	No action is required.
1 to 2 weeks	Keep the load-end of the capillary array in 1X buffer to prevent the polymer from drying in the capillaries. If fluid level is low, add DI water to buffer solution. Install the new CBC when ready to resume runs.
> 2 weeks	<ol style="list-style-type: none"> <li>1. Run the Install Capillary wizard and store the capillary array.</li> <li>2. Clean any spills or residual polymer.</li> <li>3. Run the Shutdown the Instrument wizard.</li> <li>4. Unplug the instrument.</li> </ol>



## Move and level the instrument

---

**IMPORTANT!** If you relocate the instrument, we recommend that you have an IQ OQ performed. Contact Thermo Fisher Scientific to schedule the IQ OQ service.

---



**WARNING!** PHYSICAL INJURY HAZARD. Do not attempt to lift the instrument or any other heavy objects unless you have received related training. Incorrect lifting can cause painful and sometimes permanent back injury. Use proper lifting techniques when lifting or moving the instrument. Two or three people are required to lift the instrument, depending upon instrument weight.

1. Remove the following components from the instrument:
  - Any plate assemblies from the autosampler.
  - CBC from the autosampler.
  - Capillary array: Click **Shutdown the Instrument** in the Maintenance Wizards. See “Shutdown the instrument” on page 271.
  - Anode buffer reservoir.
2. Switch off the circuit breaker on the back of the instrument.
3. Disconnect the power cord and the Ethernet cable.

---

**IMPORTANT!** While moving the instrument, avoid any shock or vibration.

---

4. Move the instrument.
5. Turn the instrument legs to level the instrument.

To move the instrument corner ...	Turn the leg ...
up	right (clockwise)
down	left (counterclockwise)

6. Have an IQ OQ performed before using the instrument.

---

**IMPORTANT!** After performing a conditioning wash, ensure that the buffer level inside the ABC is at or above fill line before proceeding to the next step.

---



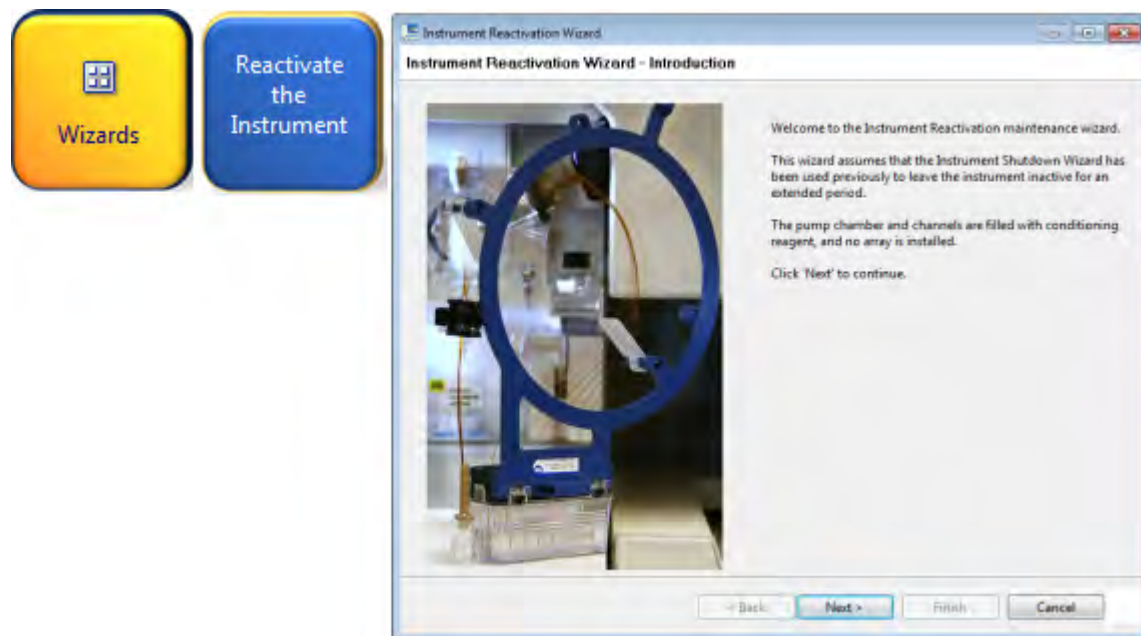
## Reactivate the instrument

---

**Note:** The **Instrument Reactivate wizard** takes ~45 minutes to complete.

---

1. In the **Dashboard**, click **Wizards**.
2. In the **Maintenance wizards** screen, click **Reactivate the Instrument**.
3. Follow the prompts in the Instrument Reactivation wizard window.



## Maintain the computer

This section lists the common tasks required to maintain the computer for your 3500 instrument in good working condition.

---

**Note:** In the event of a power disruption, restart the computer (Appendix A, “Troubleshooting”).

---

## Back up the datastore during software uninstall

---

**IMPORTANT!** Do not uninstall the software unless instructed to do so by Thermo Fisher Scientific.

---

When you uninstall the software, you are prompted to back up the datastore (the directory that contains all library items you created, such as plates and protocols).

Select a location other than the install directory for the datastore backup.

---

**IMPORTANT!** Do not back up the datastore to the installation directory. The installation directory is deleted during the uninstall.

---

## Archive, purge, and restore data

---

**IMPORTANT!** The customer is responsible for validation of archive, restore, and purge functions.

---

- **Archive**—Makes a copy of the data in an external file that you can save in another location.
- **Purge**—Allows you to delete (purge) user-created items stored in the library. Factory-provided items are not purged. You have an option to archive the items, also.
- **Restore**—Restores archived data back to the system.

---

**IMPORTANT!** These functions affect items stored in the library (datastore). These functions do not affect sample data files.

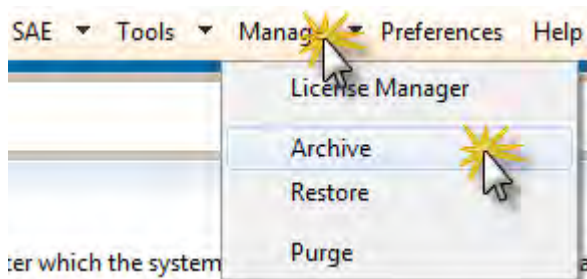
---

### Frequency

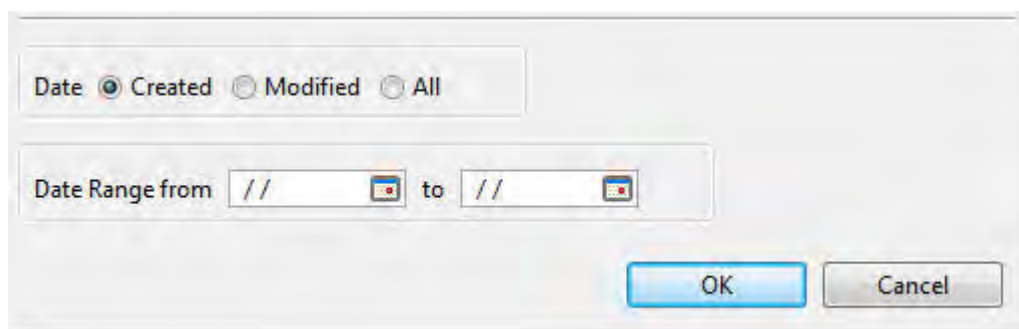
We recommend that you purge the library objects once every three months.

### Archive library items

1. Access the **Archive** screen.



2. Specify the date category, specify a date range that is earlier than the date on which you made the duplicates of the library items you want to retain, then click **OK**.



3. Specify a location and file name for the archive (.dsz) file, then click **Save**.

---

**IMPORTANT!** Do not specify <<install directory>>:\Applied Biosystems\3500\datastore as the archive location. If you do so, your archive can be deleted if you uninstall the software.

---

If you specify a location to which you do not have permission to save, a warning message is displayed and gives you the option to save in another location.

A message is displayed when the archive is complete.

## Archive data files

1. Use the Windows™ backup function (**Start ▶ Control Panel ▶ Backup and Restore**) to archive the data files.

---

**Note:** If you export audit records for samples that are not in their original location (samples have been deleted or moved), an error message is displayed. Return sample data files to their original location, then export again.

---

2. Copy the archive to a network or external drive.

## Restore

This function restores items archived from the library. To restore audit records, see “Archive, purge, and restore audit records” on page 237.

1. Access the **Restore** function.



2. Select the archive (.dsz) file to restore, then click **Open**.

If the archive file contains items that exist in the system, a message is displayed.



3. Select an option to continue.

A message is displayed when the restore is complete.

## Purge library entries

This function purges (deletes) items stored in the library. To purge audit records, see “Archive, purge, and restore audit records” on page 237.

1. Access the **Purge** function.



2. Click **Yes** in the Purge warning message stating that you are about to permanently delete all files in the library.
3. Specify the date category and range, then click **OK**.
4. Click **Yes** in the Purge warning message.  
A message is displayed when all records are deleted.

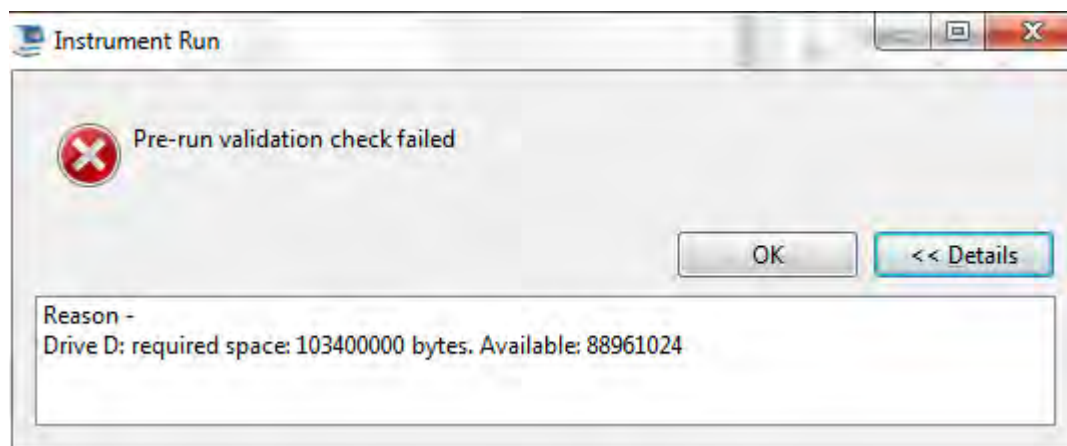
## Monitor disk space

Ensure that you have sufficient drive space by regularly:

- Archiving data
- Deleting unneeded files
- Emptying the trash
- Defragmenting the drives

## Automatic disk space check before a run

Before a run, the software checks free disk space and displays a message when the hard disk is 70–75% full. At 78% full, the software will not start a run.



## Manually check hard disk space

1. Go to **My Computer**, right-click the drive, then select **Properties** ▶ **General**.
2. If there is insufficient space on the hard disk:
  - Archive the sample files.
  - Delete the sample file data from the drive D and empty the contents of the Recycle Bin.

## Defragment the computer hard drive

This option can be set as a reminder in the scheduler. The fragmentation of files decreases the performance of both the Data Collection software and the computer operating system. Programs take a longer time to access files by performing multiple search operations of the fragments.

Go to **Start** ▶ **Programs** ▶ **Accessories** ▶ **System Tools** ▶ **Disk Defragmenter** and follow the prompts.

---

**Note:** You can click **Analyze** to see if you should defragment or not.

---

# Service Log and Usage Statistics

The Service Log and Usage Statistics functions are for use by Thermo Fisher Scientific service engineers at the time of service.



# Troubleshooting

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If you encounter any unforeseen and potentially hazardous event while operating the instrument, turn off the power, unplug the instrument, and call your Thermo Fisher Scientific service representative.


---

**IMPORTANT!** See “Safety and electromagnetic compatibility (EMC) standards” on page 338 for instrumentation and chemical safety information and guidelines.

---

## Restart the instrument and the computer

When to use this procedure:

- If communication errors are displayed
- If the front panel indicator is blinking red or amber
- At the end of spatial calibration, if **Accept/Reject** buttons are dimmed
- If maintenance wizards are taking longer than expected
- If software operations are taking longer than expected
- If a "Camera frame number mismatch detected" message is displayed
- If the Server Monitor icon displays 

When you are instructed to restart the instrument and the computer:

1. Exit the software.
2. Power off the computer.
3. Make sure the instrument door is closed, then power off the instrument.
4. When the computer is completely powered off, wait 60 seconds, then power on the computer. Wait until the Windows™ login screen is displayed. Do not log in.
5. Power on the instrument and wait until the green status light on the front panel is on and not flashing before proceeding.
6. Log in to Windows™ operating system.

---

**IMPORTANT!** Use the same administrator Windows™ user account to log in to the instrument computer. Use of a non-administrator Windows™ user account, or use of different administrator Windows™ user accounts can interfere with software operation.

---

7. Look in the Windows™ taskbar at the bottom right of the desktop and make sure the Server Monitor icon is displayed. If it is not, go to "Step one: Start the Server Monitor" on page 34.



8. Start the software.

## Instrument components

Figure 42, Figure 43, and Figure 44 are provided below for reference in this section.

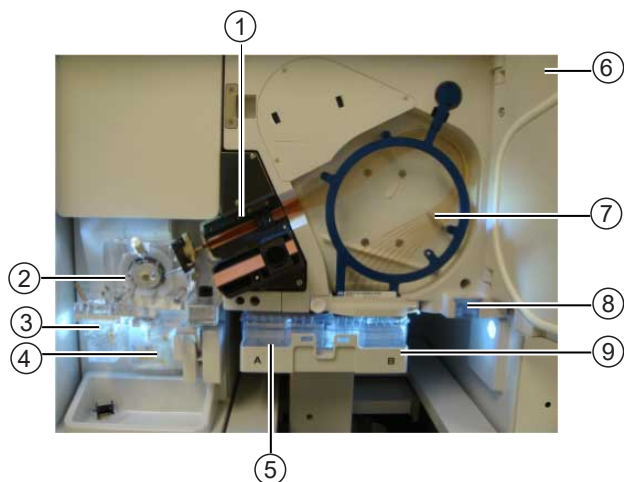


Figure 42 Instrument interior

- ① Detection cell heater block
- ② Polymer delivery pump (PDP)
- ③ Anode buffer container (ABC)
- ④ Polymer or conditioning pouch
- ⑤ Cathode buffer container (CBC)
- ⑥ Oven door
- ⑦ Capillary array
- ⑧ Oven condensation reservoir
- ⑨ Autosampler

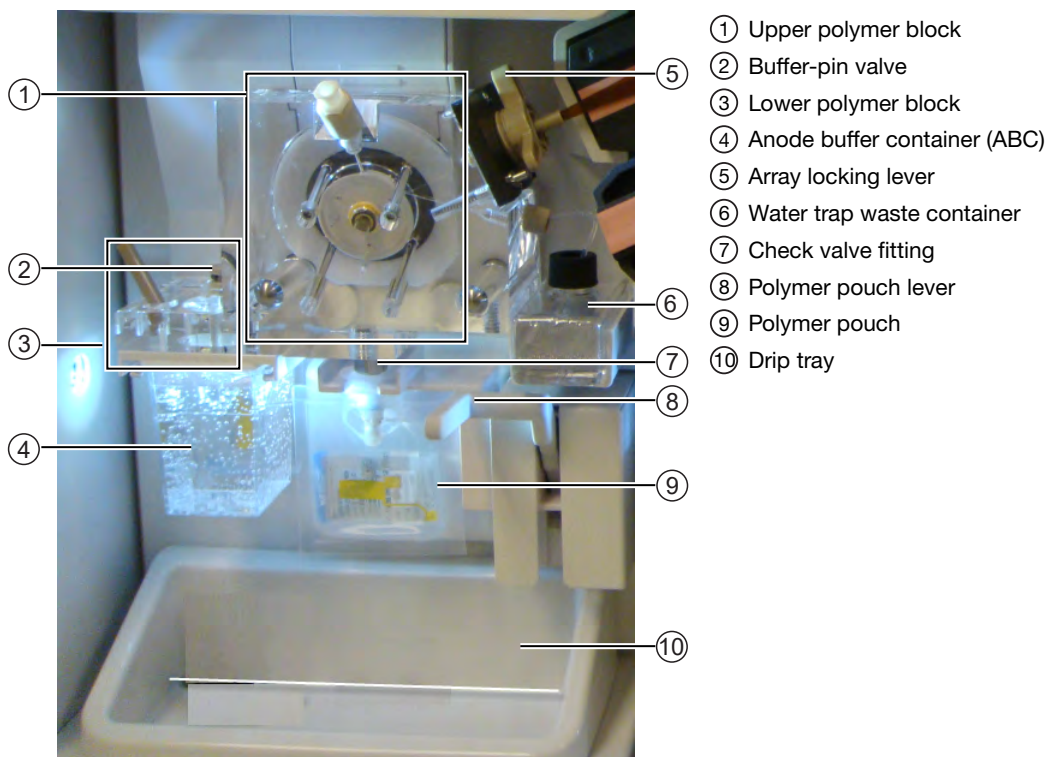


Figure 43 Polymer delivery pump (PDP)



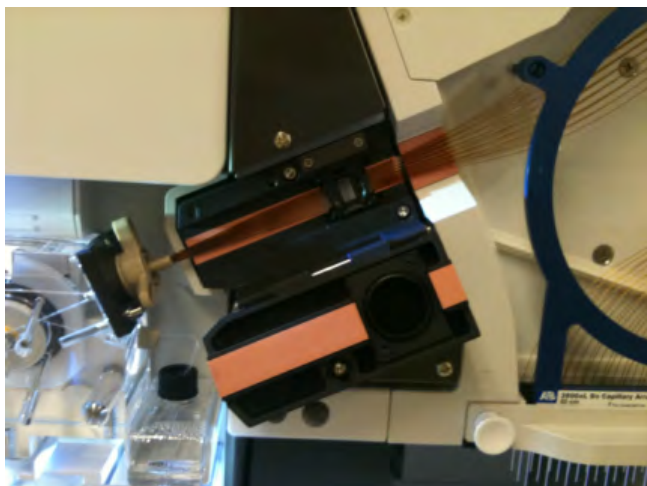



Figure 44 Detection cell

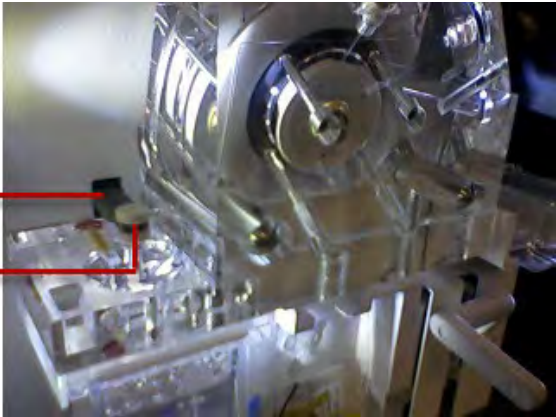
## Instrument troubleshooting

Symptom	Possible cause	Action
Power failure to instrument and computer	Power failure.	Restart the instrument and the computer (see “Restart the instrument and the computer” on page 279).
Front panel indicator: Amber light (blinking)	Run paused	Resume run.
	Door open	Close the instrument door.
	Communication issue between instrument and software.	Restart the instrument and the computer (see “Restart the instrument and the computer” on page 279).
CBC septum is lifted off the container 	Septum was not seated properly when installed.	See “Ensure proper installation of CBC septa” on page 40.

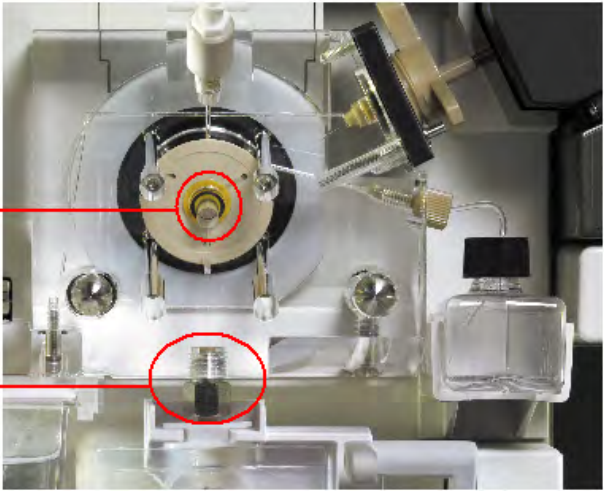
(continued)

Symptom	Possible cause	Action
Autosampler does not move the plate to a higher position	Array electrodes are bent. The plate is not aligned correctly resulting in the array tips missing center of septa. The plate retainer may not be snapped onto the plate base.	Ensure that the plate retainer, plate (or tube strip), and plate base are assembled correctly. Listen for a snap when the plate retainer and the plate base are clipped together. See “Prepare the plate assembly” on page 70.  <b>IMPORTANT!</b> If array tips are bent, replace the array.
	The plate base is not sitting properly on the autosampler.	The plate base should sit flat on the autosampler. When placing the plate on the autosampler, ensure that the pins in the autosampler are properly aligned with the holes at the bottom of the plate base, and that the left and right sides are latched.
	The plate retainer is lifted off the plate base by array.	Securely clip the plate retainer and plate base together.
	The septum is lifted off the CBC.	Ensure that the septum is completely inserted into position. Listen for the light clicking sound that occurs when the septum is pressed down firmly into position.
Polymer delivery pump (PDP) is extremely noisy and vibrating while running any wizard	The array locking lever is not in the correct position.  <b>IMPORTANT!</b> If the lever is not in the correct position, you will receive “Leak error” message.	Lock the lever in the correct position. If this is not possible contact Thermo Fisher Scientific.

(continued)

Symptom	Possible cause	Action
<p>Polymer delivery pump (PDP) is extremely noisy and vibrating while running any wizard</p>	<p>Polymer delivery pump block is not pushed back into position after capillary array change</p>	<p>Gently push the buffer-pin valve lever (yoke). If the lever does not move up and down freely, Restart the instrument and the computer. (see “Restart the instrument and the computer” on page 279).</p> <p>After the instrument has restarted, check the lever movement. If the lever does not move up and down freely, contact Thermo Fisher Scientific.</p> <p>If the lever moves up and down freely, push the upper polymer block all the way back against the wall.</p>
 <p><b>Figure 45 Buffer-pin valve lever (yoke)</b></p> <p>① Yoke ② Buffer-pin valve</p>		
<p>Polymer is not pumping properly - wizard fails - filling array</p>	<p>Check Valve is clogged Crystals present in polymer delivery pump path</p>	<p>Run the <b>Wash Pump and Channels wizard</b>.</p> <p>See “Flush the water trap (pump trap)” on page 269 and “Wash the pump chamber and channels” on page 268.</p> <p>If the problem persists, contact Thermo Fisher Scientific.</p>


(continued)

Symptom	Possible cause	Action
<p>Polymer is not pumping properly - wizard fails - filling array</p>	 <p>Figure 46 Pump chamber and valve fitting</p> <ul style="list-style-type: none"> <li>① Debris in chamber</li> <li>② Check valve fitting</li> </ul>	
<p>Buffer-pin valve does not move</p>	<p>Polymer crystallizations have formed around the buffer-pin valve</p> <p>The vent hole behind the buffer-pin valve is clogged</p> <p>The PDP block is not in the correct position</p>	<p>If you see any crystals, leaks, and dried residue around the buffer-pin valve, clean the valve and the array locking lever immediately.</p> <p>Add DI water to the buffer solution to dissolve crystals.</p> <p><b>Note:</b> Use the lint-free swabs, included in the PDP Cleaning kit (Cat. No. 4414007 ).</p> <p>If leaks persist, contact Thermo Fisher Scientific.</p> <p>Perform maintenance tasks routinely as described in “Maintenance schedule” on page 251. If leaks persist, contact Thermo Fisher Scientific.</p> <p>Clean the vent hole behind the buffer-pin valve with DI water.</p> <p>See "Polymer delivery pump (PDP) is extremely noisy and vibrating while running any wizard" . If the problem persists, contact Thermo Fisher Scientific.</p>

(continued)

Symptom	Possible cause	Action
Polymer crystals on the buffer-pin valve	Buffer valve leakage	Clean the buffer-pin valve. Perform maintenance tasks routinely as described in “Maintenance schedule” on page 251.
Fluid does not move through the polymer delivery pump and into the ABC from polymer or conditioning pouch	Blockage in fluid path or problem with polymer delivery pump	Contact Thermo Fisher Scientific.
Poor signal and resolution after replenishing polymer	The Check Valve is clogged (see Figure 46.	Wash the channels using the Polymer Delivery Pump Cleaning Kit (Cat. No. 4414007 ). If the problem persists, contact Thermo Fisher Scientific.
Any of the following visual or audible conditions: <ul style="list-style-type: none"> <li>• Unstable current</li> <li>• Arc-detect errors</li> <li>• A crackling noise at the beginning of electrophoresis</li> <li>• A blue lightning symbol below the oven</li> <li>• An error message regarding electrical current</li> <li>• Electric discharge</li> </ul>	The buffer level is below the fill line.	Verify that buffer level is at or above the fill line.
	The buffer spilled on top of the CBC.	<b>IMPORTANT!</b> Ensure that the environment (humidity) is non-condensing.  Wipe away spills, moisture, and condensation with a lint-free lab cloth. If the problem persists, contact Thermo Fisher Scientific.
	The buffer spilled on top of the Autosampler.	
	Condensation on the CBC.	
	Condensation around the septa.	
	Condensation on the lower part of the oven door, near the array header.	
	Condensation inside the oven.	
	There is not enough fluid in larger chamber of ABC, or the anode buffer has spilled into smaller overflow chamber.	

(continued)

Symptom	Possible cause	Action
<p>When you remove the heat seal from a new pouch, some residual seal remains on top of the pouch.</p> 	<p>The top seal of the pouch has become delaminated and left the polyethylene behind on the pouch cap.</p>	<p>Use a pipette tip to remove the entire seal from the pouch cap before installing on the instrument.</p>

## RFID troubleshooting

Symptom	Possible cause	Action
<p>Unable to read RFID information.</p> <p><b>“Failure to Read from RFID tag”</b></p>	<p>Consumable package is improperly installed or label is defective.</p> <p>Polymer/Conditioning reagent pouch is not positioned properly.</p>	<p>Ensure that the RFID label is not visibly damaged and consumable package is properly installed.</p> <p>Ensure that label is close, and parallel, to the instrument.</p> <p>Reposition or re-install pouch, then click <b>Refresh</b> on the Dashboard.</p>
	<p>Malfunctioning RFID label or reader.</p>	<p>Restart the instrument and the computer (see “Restart the instrument and the computer” on page 279).</p> <p>Install a new consumable (if available).</p> <p>If problem persists, contact Thermo Fisher Scientific.</p>
		<p>Place a used CBC, ABC, pouch, or array on the instrument:</p> <ul style="list-style-type: none"> <li>• If the instrument can read the RFID label, install a new CBC, ABC, pouch, or array.</li> <li>• If the instrument cannot read the RFID label, contact Thermo Fisher Scientific.</li> </ul>

## Error messages

Symptom	Possible cause	Action
“An error has been detected from the instrument.”	Instrument monitor circuit failure	Restart the instrument and the computer. (see “Restart the instrument and the computer” on page 279).
“Unable to transmit measurement data. Internal data buffer overflow.”	Communications error.	Restart the instrument and the computer. (see “Restart the instrument and the computer” on page 279).
Electric discharge message during runs.	The ABC buffer may be low.	Replace the ABC. Ensure that the ABC is being replaced per calendar notifications.
“Leak error” message.	The array locking lever is not in the correct position.	Secure the array locking lever (see Figure 43).
“Leak error” occurs when capillary arrays are filled with fresh polymer or when replenishing polymer, causing the wizard to fail to complete.	Debris is clogging the check valve (CV) fitting (see Figure 46).	While wearing gloves, use a lint-free cloth and water to wipe the CV Fitting. <b>Note:</b> To prevent crystals from forming around the check valve, always install the Conditioning Reagent Pouch after removing a used or a partially used polymer pouch. Completely remove the top seal of the Polymer pouch or Conditioning Reagent Pouch before use. If the problem persists, contact Thermo Fisher Scientific.
	The Yoke is not seated properly on the buffer-pin valve.	Make sure the buffer-pin valve lever (yoke) is seated properly on the buffer-pin valve (see Figure 45). If the lever does not move up and down freely, close the door. Restart the instrument and the computer. (see “Restart the instrument and the computer” on page 279). After the instrument has restarted, check the lever movement. If the lever does not move up and down freely, contact Thermo Fisher Scientific. If the lever moves up and down freely, push the upper polymer block all the way back against the wall.
<ul style="list-style-type: none"> <li>“Leak detected during polymer delivery”</li> <li>“Leak detected during bubble compression”</li> </ul>	Bubbles in the polymer system.	Run the <b>Remove Bubbles wizard</b> to clear bubbles.

(continued)

Symptom	Possible cause	Action
The run aborts.	Leak in the polymer system.	Check for evidence of leaks. If polymer leak occurred, conduct a water wash and wash the pump trap using the Polymer Delivery Pump Cleaning Kit (Cat. No. 4414007 ) supplied with the instrument.
	Buffer valve leakage.	Check the buffer-pin valve and see if it closes correctly. Clean the buffer-pin valve. Ensure that the maintenance schedule is followed per the software notifications.
	Filling the array during install array.	Run <b>Fill the Array with fresh Polymer</b> wizard, or run <b>Change Polymer Type</b> wizard.
“Bubble” error	Bubbles present	Run the <b>Remove Bubbles</b> wizard.
“Java update scheduler” error message	The Java updater is unable to complete the update.	Close the Java update scheduler. <b>Note:</b> The Java update scheduler does not affect the performance of the software or the quality and accuracy of the data collected.
“Invalid Contents” message In <b>Assign Plate Contents</b> screen when you use Ctrl+D	The first row you have selected to fill from is empty.	<ul style="list-style-type: none"> <li>Enter sample name or select an assay in the first row in you have selected to fill from.</li> <li>Use the table view to add the assay to the samples.</li> </ul>
“Injection failed” message after some of the injections complete.	Capillary RFID cannot be read.	Check the connection between the instrument and computer. Restart the instrument and the computer (see “Restart the instrument and the computer” on page 279).
“Instrument is not connected” message after you start the software.	Bad connection between the computer and instrument.	Check the connection between the instrument and computer and restart both the instrument and computer (see “Restart the instrument and the computer” on page 279).
“Internal buffer data overflow” message.		
“Camera frame number mismatch detected”	The communication between the instrument and the computer has been interrupted and cannot be re-established automatically.	Restart the instrument and the computer. See “Restart the instrument and the computer” on page 279.







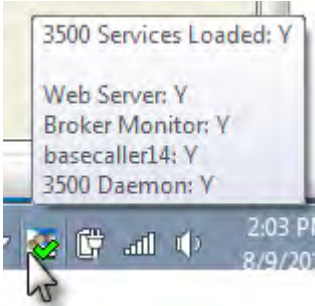
## Dashboard troubleshooting

Symptom	Possible Cause	Action
When you click <b>Refresh</b> on the <b>Dashboard</b> , and consumables information is listed as “ <b>Unknown</b> .”	Bad connection between the computer and instrument.	Check the connection between the instrument and computer.
Consumables status in the Dashboard is not updated.	Dashboard does not update automatically.	Click <b>Refresh</b> .
After installing new CBC or ABC, the consumables status in the Dashboard is not updated automatically.	Dashboard does not update automatically.	Click <b>Refresh</b> after changing or installing consumables.
Expiration dates are displayed in red.	The consumable is within the following days of expiration: Pouch 7 days, Buffers 7 days, Capillary array 1 day	No action.
Dashboard indicates a consumable is expired, but expiry date on consumable indicates it is not expired.	RFID issue.	Restart the instrument and the computer (see “Restart the instrument and the computer” on page 279).  Contact Thermo Fisher Scientific

## Software troubleshooting – general

Symptom	Possible cause	Action
When you start the 3500 Series Data Collection Software v3.3, “ <b>Windows cannot find 3500.exe</b> ” message is displayed.	The Norton Antivirus Sonar Protection feature is enabled on the instrument computer.	<ul style="list-style-type: none"> <li>Disable the optional Sonar feature in Norton Antivirus software (contact your IT department for assistance).</li> <li>Contact Thermo Fisher Scientific.</li> </ul>

(continued)

Symptom	Possible cause	Action
<p>Status icon is  instead of .</p> 	One or more of the services are stopped.	<p>Hover the mouse pointer over the status icon. If any item does not display a checkmark, select  ▶ <b>Programs</b> ▶ <b>Applied Biosystems</b> ▶ <b>3500</b> ▶ <b>Server Monitor</b>.</p> <p>Right-click the status icon, then select <b>Services</b>. If any item does not display a checkmark, click the item to start the service.</p> 
<b>Print</b> dialog box is not displayed when you select or click <b>Print</b> .	Dialog boxes are sometimes displayed behind the main screen	Minimize the main screen.
The Load plate for run message does not display correctly.	The window is not refreshing properly.	Click <b>OK</b> to dismiss the message and continue.
Save option is not available (only Save As) when you edit a plate template from the library.	You must select a plate template from the main workflow to edit it.	Go to <b>Define Plate Properties</b> screen ▶ <b>Open Plate</b> ▶ <b>Edit Existing Template</b> .
<b>Specimen</b> name and <b>Amplicon</b> name are specified in File Name Convention but not included in sample name.	The Specimen Name attribute is not functional. Even when selected, specimen name is not included in the file name.	<p>Enter the Specimen name and Amplicon name in the <b>Sample Name</b> field in the <b>Assign Plate Contents</b> screen, <b>Customize Sample</b> information section.</p> <p>To view Specimen Name and Amplicon Name in the Customize Sample Information section, a Sequencing assay must be assigned to a well.</p> <p><b>Note:</b> The Specimen Name and Amplicon Name fields are available in the Plate View only, not the Table View of the Assign Plate Contents screen.</p>
Software is not behaving as expected.	You open the instrument door after you start a run	Do not open the instrument door during a run.
	You restarted the instrument only, not the computer.	<p>Restart the instrument and the computer (see “Restart the instrument and the computer” on page 279).</p> <p><b>Note:</b> Restart the instrument and the computer as part of weekly maintenance.</p>

(continued)

Symptom	Possible cause	Action
Software operations are taking longer than expected.	Communication problem between the computer and instrument.	Restart the instrument and the computer (see “Restart the instrument and the computer” on page 279).
	Audit records need archiving and purging	See “Archive, purge, and restore data” on page 274.

## Run, re-run, or re-inject troubleshooting

Symptom	Possible cause	Action
Run stops unexpectedly or will not start	Plate or sample information contains invisible, non-ASCII characters.	<b>IMPORTANT!</b> If you copy/paste sample or plate information into the Assign Plate Contents screen or into a plate import file, copy from a plain text editor such as Notepad. Do not copy from a word processing program such as Microsoft™ Word™, which may include invisible, non-ASCII characters. Non-ASCII characters in plate or sample information may cause a run to stop or may prevent a run from starting.
"Camera frame number mismatch detected"	The communication between the instrument and the computer has been interrupted and cannot be re-established automatically.	Restart the instrument and the computer. See “Restart the instrument and the computer” on page 279.
If you re-run a plate that specifies a re-injection, and the re-injection specifies a protocol other than the protocol used for the original injection, the new protocol for the re-injection is not used	New protocols are not retained for re-injections.	Before re-running a plate, examine the protocols specified for re-injections and change as needed.

## Data/electropherogram troubleshooting

Symptom	Possible cause	Action
Signal too high.	Sample concentration is too high.	Dilute the sample. Decrease the injection time.
	Too much DNA added to the reaction, resulting in uneven signal distribution.	Optimize reaction conditions.
No signal.	Blocked capillary.	Run the <b>Fill Array with Polymer wizard</b> . Install a new capillary array.
	Bent capillary array tips or cracked or broken capillary array.	Visually inspect the capillary array, including the detector window area for signs of breakage. Replace the capillary array.
	Failed reaction	Repeat reaction.
Low signal.	Degraded formamide.	Use a fresh aliquot of Hi-Di™ Formamide (see “Hi-Di™ Formamide” on page 25 for storage conditions).
	Not enough sample: Pipetting error.	Prepare new sample.
	Sample has high salt concentration.	Dilute or desalt samples.
	Insufficient mixing.	Vortex the sample thoroughly, and then centrifuge the tube to condense the sample to the bottom of the tube.
	Weak amplification of DNA.	Reamplify the DNA.
		Check DNA quality.
	Sample volume is <10 µL.	Check that sample volume is at least 10 µL.
Autosampler out of calibration.	Contact Thermo Fisher Scientific.	
Elevated baseline.	Possible contaminant in the polymer path.	Run the <b>Wash Pump and Channels wizard</b> .
	Poor spectral calibration.	Perform new spectral calibration.
Loss of resolution.	Too much sample injected.	Dilute the sample and re-inject.
	Poor quality water.	Use distilled or deionized water.
	Degraded polymer.	Replace polymer.
	Capillary array used for more than 160 injections.	Replace the capillary array. Run the <b>Install Capillary Array wizard</b> .

(continued)

Symptom	Possible cause	Action
Loss of resolution.	Degraded formamide.	Prepare fresh Hi-Di™ Formamide (see “Hi-Di™ Formamide” on page 25 for storage conditions) for sample preparation.
	Sample has high salt concentration.	Dilute or desalt samples.
Poor resolution in some capillaries.	Insufficient filling of capillary array.	Tighten the connectors and array locking lever. Run the <b>Fill Array with Polymer wizard</b> and look for polymer leakage. Check for broken capillaries, run the <b>Install Capillary Array wizard</b> if needed.
		Re-inject the same samples.
	Poor quality samples.	Check the sample preparation.
	Leak in system.	Tighten the connectors and array locking lever.
No current.	Not enough buffer in ABC.	Ensure that the buffer is filled up to the fill line. See “Check buffer fill levels” on page 39.
	Bubble(s) present in the lower polymer block and/or the array and/or channels.	Pause the run and inspect for bubbles in the tubing connectors. Run the <b>Remove Bubbles wizard</b> .
Elevated current.	Degraded polymer.	Run the <b>Replenish Polymer wizard</b> .
	Arcing in the lower polymer block.	Inspect the lower polymer block for discoloration or damage. Contact Thermo Fisher Scientific.
Fluctuating current.	Bubble in polymer block.	Pause run and inspect for bubbles hidden in the tubing connectors. Run the <b>Remove Bubbles wizard</b> .
	Slow leak	Check polymer blocks for leaks. Tighten the connectors and array locking lever.
	Not enough buffer in ABC.	Ensure that the buffer is filled up to the fill line. See “Check buffer fill levels” on page 39.
	Arcing	Check for moisture in and around the septa, the CBC, the oven, and the autosampler. Wipe condensation.
Poor performance of capillary array used for fewer than 100 runs.	Poor quality samples, possible cleanup problems.	Desalt samples.
	Improperly stored formamide.	Prepare fresh Hi-Di™ Formamide (see “Hi-Di™ Formamide” on page 25 for storage conditions) for sample preparation.
	Leak in system.	Tighten the connectors and array locking lever.

(continued)

Symptom	Possible cause	Action
Migration time becomes progressively slower.	Leak in system.	Tighten the connectors and array locking lever.
	Improper filling of the system with polymer.	Polymer delivery pump may need to be serviced. If the issue persists, contact Thermo Fisher Scientific.
Migration time becomes progressively faster.	Buffer valve leakage.	Ensure the buffer-pin valve is closed correctly.
Extra peaks in the electropherogram.	Data off scale.	Dilute the sample and re-inject the sample.
	Possible contaminant in sample.	Re-amplify the DNA.
	Sample re-naturation.	Heat-denature the sample in properly stored formamide (see “Hi-Di™ Formamide” on page 25 for storage conditions) and immediately place on ice.
Electrophoresis current is unstable.	Bubbles in the polymer system.	Run the <b>Remove Bubbles wizard</b> .
Electrophoresis failure.	Buffer below fill line.	Ensure that the buffer is filled up to the fill line. “Check buffer fill levels” on page 39 .
	There is not enough fluid in larger chamber of ABC, or the anode buffer has spilled into smaller overflow chamber.	Pipette the buffer from the smaller overflow chamber to the larger chamber. Ensure that the buffer is filled to within $\pm 1$ mm of the fill line.  When installing new ABC, tilt the container to move buffer to the larger side of the container as described “Prepare the Anode Buffer Container (ABC)” on page 258.
Extra peaks in the electropherogram.	Data off scale.	Dilute the sample and re-inject the sample.
	Possible contaminant in sample.	Re-amplify the DNA.
	Sample re-naturation.	Heat-denature the sample in good quality formamide and immediately place on ice.

## Review Results troubleshooting

Symptom	Possible Cause	Action
<p>Zoom errors in electropherogram graphical displays (<b>Monitor Run, Review Results, Spectral Calibration, and Install Check</b>):</p> <ul style="list-style-type: none"> <li>The zoom feature does not re-baseline the sample data view,</li> <li>or</li> <li>The X axis of the sample plot does not stay at the bottom of the screen. It moves up toward the region the user has zoomed in on, making data difficult to review</li> </ul>	<p>The zoom feature does not re-baseline the sample data view.</p>	<p>No action.</p>
<p>Samples are not imported when you select multiple folders for import</p>	<p>At least one file is not in the correct format for import, therefore no files are imported.</p>	<p>Select individual folders or files for import instead of multiple folders.</p>
<p><b>Plate Owner</b> truncated in <b>Annotation ▶ Run Configuration</b></p>	<p>Special characters were included when entering plate information.</p>	<p>Use only alpha-numeric characters for plate information. Special characters in plate information fields may not be correctly displayed in some software screens.</p>
<p>Sample files are not displayed when imported</p>	<p>You imported (HID) files and you did not click HID Samples.</p>	<p>Click <b>HID Samples</b>.</p>
<p>Peaks are not labeled when you access the screen</p>	<p>Labels are not automatically applied.</p>	<p>See “Label peaks” on page 119.</p>
<p>x and y scaling plot settings are not applied when you click <b>Apply</b></p>	<p>Scaling settings are applied only when you click <b>Zoom</b>.</p>	<p>Click <b>Zoom</b>.</p>
<p>The sizing quality result reported in the software differs from the sizing quality result for reported in the GeneMapper™ <i>ID-X</i> Software</p>	<p>You imported (FSA) files instead of (HID) files.</p> <p>The software does not consider the presence of broad peaks when determining sizing quality for fragment analysis data, therefore the sizing quality result reported in the software will differ from the sizing quality result reported in the GeneMapper™ <i>ID-X</i> Software, which considers broad peaks in sizing quality.</p>	<p>No action.</p>

(continued)

Symptom	Possible Cause	Action
Sizing Overlay report displays data for all capillaries including those that fail sizing	Plots displayed in <b>Sizing Overlay Plot</b> are based on the samples selected.	Select only the capillaries that pass sizing to include in the report.
Dye/Sample Peak column values in an exported sizing table are split in to two separate columns, the column name containing the Sample Peak values is incorrectly named, and the column headers after Dye/Sample are shifted one column to the right.	You changed the order of columns before exporting. <b>Note:</b> The exported data are accurate, the column headers are shifted to the right.	Edit the exported file: Cut/paste column headers one column to the right, enter correct headers for the Dye and Sample Peak columns.

Dye/ Sample Peak	Run Name	Sample Peak values listed in separate column
B	1	
B	2	
B	3	

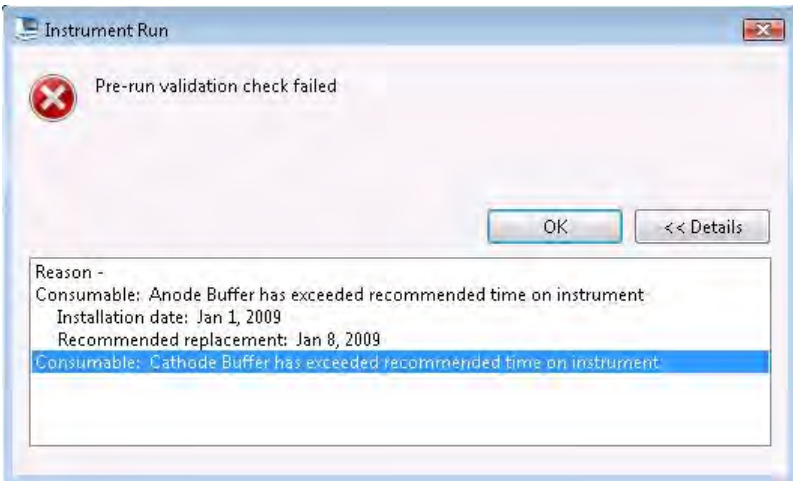

Dye	Sample Peak	Run Name	Data Point
B	1	Run 2013-04-17-1	17
B	2	Run 2013-04-17-1	91
B	3	Run 2013-04-17-1	191
B	4	Run 2013-04-17-1	216
B	5	Run 2013-04-17-1	337

## Link/load plate troubleshooting

Symptom	Possible cause	Action
Plate was linked, but now it is unlinked.	If you access the <b>Load Plates for Run</b> screen from the navigation pane, a plate may not be linked (indicated by the active <b>Link Plate</b> button).	Access the <b>Load Plates for Run</b> screen from the navigation pane and click <b>Link Plate</b> .
“No plate in position A” message.	You physically loaded plate in position B (plate B position) and try to link plate.	Click <b>Link Plates</b> and link the plate directly to position B (plate B position).
“No plate detected” message	The plate is in position B.	Place the plate in position A. See “Load the plate in the instrument” on page 72.
		Manually link the plate to position B. See “Link the plate” on page 72.
	You selected Quick Start. <b>Note:</b> Quick Start expects the plate to be in position A.	Do not use Quick Start, instead open plate and link via the main workflow.
	The Autosampler has not completed initialization.	Wait for the green light to light on the front panel before linking the plate. It takes approximately 10 seconds for the instrument to initialize after the instrument door is closed.
	Malfunctioning plate sensor(s).	Contact Thermo Fisher Scientific.



(continued)

Symptom	Possible cause	Action
Pre-run validation check does not display a date for a consumable.	The software does not display a date if it is identical to the preceding date. In the example below, the installation and recommended replacement dates for cathode buffer are identical to the dates for anode buffer.	No action.
	 <p>The screenshot shows a dialog box titled 'Instrument Run' with a red 'X' icon and the message 'Pre-run validation check failed'. Below the message are 'OK' and '&lt;&lt; Details' buttons. A text area contains the following information: 'Reason - Consumable: Anode Buffer has exceeded recommended time on instrument. Installation date: Jan 1, 2009. Recommended replacement: Jan 8, 2009. Consumable: Cathode Buffer has exceeded recommended time on instrument.' The 'Consumable' line is highlighted in blue.</p>	
Link/Unlink Plate error message.	Listed in Details.	Click <b>Details</b> to determine the cause of the error.  When the plate is successfully loaded, the <b>Load Plates for Run</b> screen is displayed.
	 <p>The screenshot shows a dialog box titled 'Link/Unlink Plate' with a red 'X' icon and the message 'Plate Setup Error'. Below the message are 'OK' and '&lt;&lt; Details' buttons. A text area contains the following information: 'Reason - Incompatible capillary array configuration between Instrument and Run Module. Run Module RapidSeq50_POP6xl_E is configured for 24 capillaries. Instrument is configured for 8 capillaries. No Sequencing Install Standard has been performed. To proceed, Please perform a Sequencing Install Standard calibration.' A mouse cursor is pointing at the '&lt;&lt; Details' button.</p>	
“No plate detected” message	The plate is in position B.	Place the plate in position A.
Create Injection List and Start Run buttons dimmed	The <b>Pause After Last Injection</b> preference is set, and the instrument is paused	Go to <b>Monitor Run</b> and resume the run. When the run is complete, Create Injection List and Start Run buttons are active.



## Assign Plate Contents troubleshooting

Symptom	Possible Cause	Action
Error message is displayed when you export a newly created plate from the <b>Assign Plate Contents</b> screen.	Plate is not saved.	Save the plate, close the plate, open the plate, then export.

## Spatial calibration troubleshooting

Symptom	Possible cause	Action
“ <b>Start</b> ” Spatial Calibration button is disabled.	Communication failure between the Data Collection Software and instrument	Check the connection between the instrument and computer.  Restart instrument and computer (see “Restart the instrument and the computer” on page 279).
Unusual peaks or a flat line for the spatial calibration.	Improper installation of the array window in the detection cell (see Figure 44).	Run the <b>Install a Capillary Array wizard</b> to uninstall, then re-install the array. If the calibration fails again: <ul style="list-style-type: none"> <li>• Fill the capillaries with polymer.</li> <li>• Repeat the spatial calibration.</li> </ul>
	Broken capillary resulting in a bad array fill.	Check for a broken capillary, particularly in the detection cell area. If necessary, replace the capillary array using the <b>Install Capillary Array wizard</b> .
Persistently bad spatial calibration results.	Bad capillary array.	Replace the capillary array using the <b>Install Capillary Array wizard</b> , then repeat the calibration.  If the problem persists, contact Thermo Fisher Scientific.
“ <b>Spatial Calibration Error</b> ” message.	Conditioning reagent is installed.  The instrument cannot perform Spatial Calibration with Array fill.	Replace the conditioning reagent with polymer.
Spatial calibration takes >5 minutes to complete, and green light goes from blinking to solid	Communication problem between the computer and instrument.	Restart the instrument and the computer (see “Restart the instrument and the computer” on page 279).

(continued)

Symptom	Possible cause	Action
Spatial calibration takes >5 minutes to complete, and green light goes from blinking to solid	Oven is on.	Do not preheat the oven before running the spatial calibration.
Accept/Reject buttons are dimmed.	Communication problem between the computer and instrument.	Restart the instrument and the computer (see “Restart the instrument and the computer” on page 279).

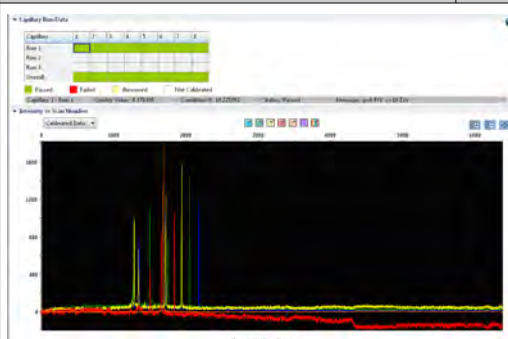
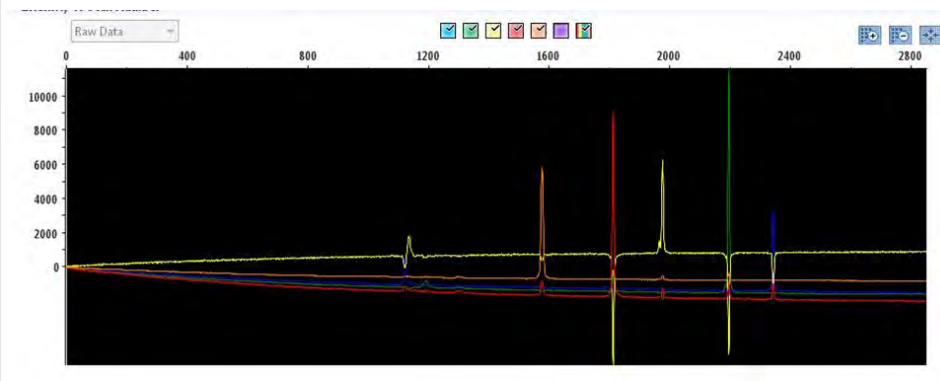
## Spectral calibration troubleshooting

Symptom	Possible cause	Action
No signal	Incorrect preparation of sample	Replace samples with fresh samples prepared with fresh Hi-Di™ Formamide (see “Hi-Di™ Formamide” on page 25 for storage conditions).
	Bubbles in sample wells	Centrifuge samples to remove bubbles.
	Capillaries are not aspirating sample	Check that sample volume is at least 10 µL. If sample volume is adequate, contact Thermo Fisher Scientific.
	The capillary tips may be hitting the bottom of the wells. Autosampler not correctly aligned.	Contact Thermo Fisher Scientific.
Peak heights in the Spectral report are different from the values seen when viewing the spectral data in the electropherogram display.	The raw data electropherogram display in the software does not have the Run Scale Divisor applied to the data. The final peak height values displayed in the Spectral report have the Run Scale Divisor applied.	No action.

(continued)

Symptom	Possible cause	Action
The Spectral peaks in the raw data view appear to be in the wrong order or there are extraneous peaks	Septa contamination.	Replace the CBC septa.  <b>IMPORTANT!</b> Make sure to replace the CBC septa as part of monthly maintenance.
No history is stored for a failed run.	No history is stored for a failed run.	To retain a history for a failed run, generate a report <i>before</i> you click <b>Reject Results</b> .  To generate a report, click <b>View Summary Report</b> or <b>View Detail Report</b> .  To save the report electronically, select a PDF printer.
Extra peaks or spikes in the raw data or “Bad dye order detected” error message.	Bubbles in the polymer system.	Run the <b>Remove Bubbles wizard</b> .
	Septa contamination.	Replace the CBC septa.
	Possible contaminant, crystal deposits, or precipitate.	Allow the polymer to come to room temperature. Do not heat to bring to room temperature.

(continued)

Symptom	Possible cause	Action
		
Spectral calibration fails, or “No spectral files found” message is displayed.	Blocked capillary	Run the <b>Fill Array with Polymer wizard</b> to clear blockage.
	Insufficient filling of array.	Check for broken capillaries. Run the <b>Fill Array with Polymer wizard</b> .
	Expired calibration standards or old reagents.	Check the expiration date and storage conditions of the calibration standards and/or reagents. If necessary, replace with a fresh lot.
Data Error - One or more peaks fall below the minimum required amplitude of 750.	One or more peaks fall below the minimum required amplitude of 750.	Rerun the spectral standards.
Elevated baseline.	Poor spectral calibration.	Perform new spectral calibration.
Pull-down (mirror image) peaks (see the following figure)	The first time you perform a spectral calibration (for each dye set) after installing a new capillary array, you may notice pull-down peaks (or mirror image peaks). These pull-down peaks will eventually correct themselves once the run completes.	No action.
		



(continued)

Symptom	Possible cause	Action
AnyDye Set Spectral Calibration fails.	Problem with spectral calibration	See “Perform a spectral calibration” on page 133.
	AnyDye dye set is not set up correctly.	See “Create a new dye set using the AnyDye template” on page 195.

## Sequencing install standard troubleshooting

Symptom	Possible cause	Action
No signal	Incorrect preparation of standard	Replace samples with fresh samples prepared with fresh Hi-Di™ Formamide (see “Hi-Di™ Formamide” on page 25 for storage conditions).
	Bubbles in sample wells	Centrifuge samples to remove bubbles.
	Capillaries are not aspirating sample	Check that sample volume is at least 10 µL. If sample volume is adequate, contact Thermo Fisher Scientific.
	The capillary tips may be hitting the bottom of the wells. Autosampler not correctly aligned.	Contact Thermo Fisher Scientific.
The Sequencing install check fails: Failed capillaries <ul style="list-style-type: none"> <li>One or more (for 8-capillary).</li> <li>Three or more (for 24-capillary).</li> </ul> Accept button is not active, Reject button is active.	Blocked capillary	Run the <b>Fill Array with Polymer wizard</b> . Install a new capillary array.
	Insufficient filling of array.	Check for broken capillaries. Run the <b>Fill Array with Polymer wizard</b> .
	Expired sequencing standard or old reagents.	Check the expiration date and storage conditions of the sequencing standard and/or reagents. If necessary, replace with a fresh lot.
	Bubbles in the polymer system.	Run the <b>Remove Bubbles wizard</b> .

(continued)

Symptom	Possible cause	Action
The Sequencing install check fails: Failed capillaries <ul style="list-style-type: none"> <li>One or more (for 8-capillary).</li> <li>Three or more (for 24-capillary).</li> </ul> Accept button is not active, Reject button is active.	Possible contaminant or crystal deposits in the polymer.	Properly bring the polymer to room temperature; do not heat.
The starting well value you set reset to A01 after you start the install check.	If you navigate away from the Install Check screen after you start the install check, the starting well may be reset to A01. This is a display issue only; the starting well you specify is used for the install check.	No action.

## Fragment/HID install standard troubleshooting

Symptom	Possible cause	Action
Fragment/HID report contains blank pages or incomplete information.	All dyes are not selected before you generate the report.	Select all dyes, then generate the report.
No signal	Incorrect preparation of sample	Replace samples with fresh samples prepared with fresh Hi-Di™ Formamide.
	Bubbles in sample wells	Centrifuge samples to remove bubbles.
	The capillary tips may not be touching the samples.	Check the volume of your samples. If no results, call your Thermo Fisher Scientific representative.
	The capillary tips may be hitting the bottom of the wells. Autosampler not correctly aligned.	Call your Thermo Fisher Scientific representative.
Fragment/HID install check fails.	Blocked capillary	Refill capillary array. You may have to install a fresh array or consider that capillary non-usable for purposes of planning your runs.
	Insufficient filling of array.	Check for broken capillaries and refill the capillary array.



(continued)



Symptom	Possible cause	Action
Fragment/HID install check fails.	Expired matrix standards or old reagents.	Check the expiration date and storage conditions of the matrix standards and/or reagents. If necessary, replace with a fresh lot.
	Bubbles in the polymer system.	Select the <b>Bubble Remove wizard</b> to clear the bubbles.
	Possible contaminant or crystal deposits in the polymer.	Properly bring the polymer to room temperature; do not heat.
The starting well value you set reset to A01 after you start the install check.	If you navigate away from the Install Check screen after you start the install check, the starting well may be reset to A01. This is a display issue only; the starting well you specify is used for the install check.	No action.

## Monitor Run troubleshooting

Symptom	Possible Cause	Action
The instrument run unexpectedly pauses.	RFID read/write error.	Click <b>Refresh</b> in the Dashboard. If consumables status does not refresh, restart the instrument and the computer (see “Restart the instrument and the computer” on page 279).
Only some injections from a series of injections are completed.  The autosampler does not move on to the next injection	Bad connection between the instrument and computer	Check the connection between the instrument and the computer. Restart the instrument and the computer (see “Restart the instrument and the computer” on page 279).
Estimated Time Remaining in <b>Monitor Run</b> is longer than expected.	Estimated Time Remaining is the time remaining in the instrument run. This estimate is adjusted after the completion of every step in an injection.	To view time remaining per injection, scroll to the Time Remaining column in the Injection List Details.
Contents of tooltip in Flag list is truncated	Special characters were included when entering sample information	Use only alpha-numeric characters for sample information. Special characters in sample information fields may not be correctly displayed in other software screens.



(continued)

Symptom	Possible Cause	Action
Re-inject button is dimmed when you select an injection	Injection contains samples with assays that specify more than one instrument protocol.	Select in the injection list the injection with the instrument protocol of interest, select in the array view the capillary that corresponds to the well of interest, then click Re-inject.
 QV flag for sequencing data, but data quality is good	Contiguous Read Length of the amplicon is less than the Contiguous Read Length Pass value specified in Basecalling Protocol QV settings or Trace Quality preference settings.	<ul style="list-style-type: none"> <li>If the expected read length of the amplicon is &lt;300, adjust the Contiguous Read Length Pass value.</li> <li>If the expected read length of the amplicon <math>\geq 300</math>, review the sample quality throughout the entire trace.</li> </ul>
 QV flag for sequencing data	Run Time in Instrument Protocol is too short for the amplicon.	Adjust Run Time.
	Incorrect Mobility file for dye/polymer is selected in Basecalling Protocol.	Select the correct Mobility file for dye/polymer in Basecalling Protocol, then re-inject.  Apply correct Basecalling Protocol in secondary sequence analysis software.

## Audit troubleshooting

Symptom	Possible Cause	Action
“Export did not complete successfully”	You exported records for samples that are not in their original location (samples have been deleted or moved).	Return sample data files to their original location, then export again.
Audit report does not print after you change font settings.	Font settings are not activated until you close the report.	Close the report, reopen it, then print.

## Electronic signature troubleshooting

Symptom	Possible Cause	Action
The dye set calibrated is not listed in a spectral calibration e-signature record.	The e-signature function creates a record when a spectral calibration is performed, but does not record the dye set calibrated.	To include the dye set calibrated in the e-signature record, enter the dye set in the Comments field.
Electronic signature prompt is displayed when you edit sample comments.	Electronic signature prompt is displayed for sample comments, regardless of the electronic signature setting.	No action.

## Manual commands troubleshooting

Symptom	Possible Cause	Action
When you select <b>Tools ▶ Manual Commands</b> , Set defined command for Consumables, then select a Read Command, the information displayed is not readable.	The feedback from Consumables Read Tag commands does not display valid information.	See the Dashboard for consumables RFID tag information.

## Troubleshooting procedures

### Run Troubleshooting Utility.bat

If instructed to do so by a Thermo Fisher Scientific representative:

1. Navigate to x:\AppliedBiosystems\3500\Troubleshoot.
2. Double-click **TroubleshootingUtility.bat**.
3. Navigate to s:\TroubleshootData, then email the data-<yyyy-mm-dd-hh-mm-ss-mmm>.tslog file to your Thermo Fisher Scientific representative.

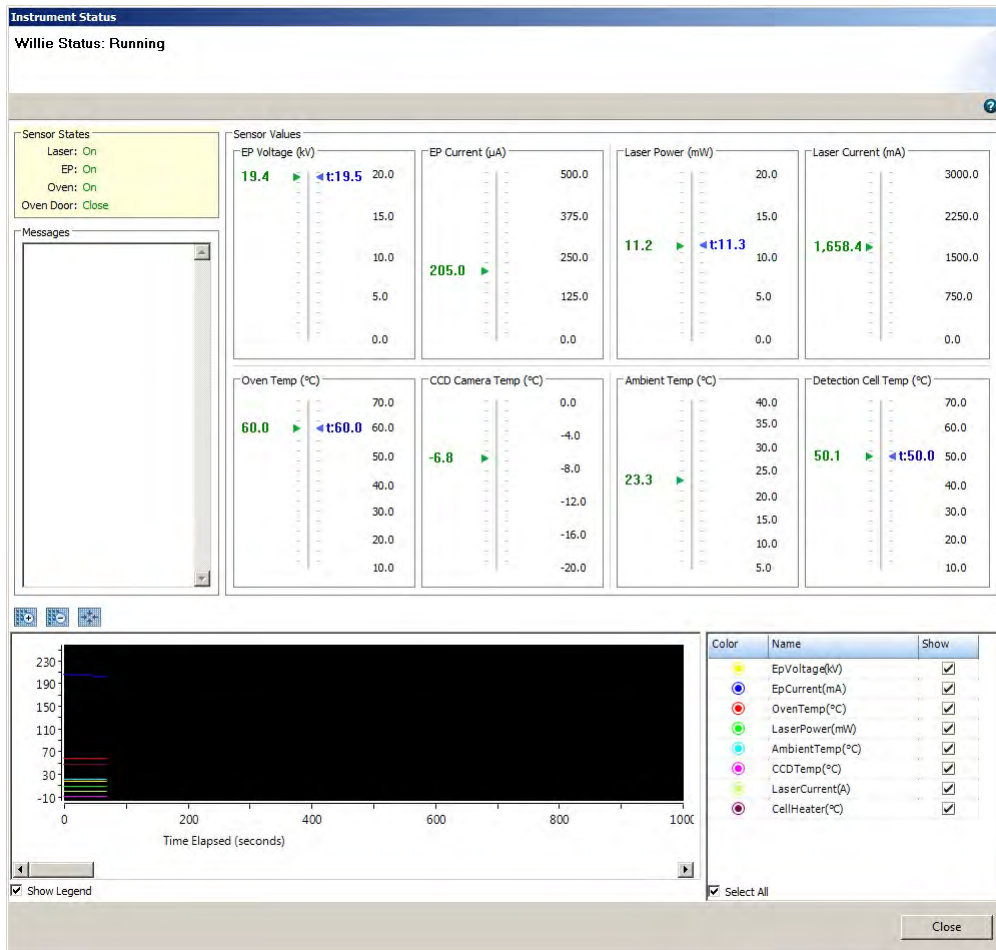
### View the log files

Use a text editor (such as Wordpad) to view the software-generated log files:

Log file	Description	Location
3500UsageStatistics.txt	Provides a summary of the number of plates run and number of run types	<<install drive>>\Applied Biosystems\3500\LogFiles You can also view this log from the Maintenance workflow under <b>Planned Maintenance ▶ Usage Statistics</b> .
3500ConsumableUpdates.txt	Provides a summary of consumables installation information and dates	<<install drive>>\Applied Biosystems\3500\LogFiles

## View instrument sensor details

Click **View Instrument Sensor Details** in the Dashboard to display instrument information.



**Figure 47 Instrument sensor details**

Run status of the instrument is displayed while a run is in progress.

## Review error message details

Error messages in the software include a Details button.

Click **Details** to display more information about an error message.



## Reset the instrument

Resetting powers off, then powers on, the instrument. Reset the instrument when:

- There is a fatal error as indicated by the red status light
- The instrument does not respond to the Data Collection software

1. Shut down the computer.
2. Close the instrument doors.
3. Reset the instrument with the Reset button, as shown.

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**Note:** The Reset button is accessible through a small hole to the left of the Tray button.

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Reset button



# Run modules and dye sets

## Run modules

Table 5 Sequencing analysis run modules

Run module type	Run module name	Configuration		23 hours Throughput <sup>[1]</sup>			Performance
		Cap. length (cm)	Polymer type	Run time (min)	3500 (8-cap.)	3500xL (24-cap.)	Contig. Read Length (CRL) <sup>[2]</sup>
Short read sequencing	ShortReadSeq50_POP7	50	POP-7™	≤30	≥368	≥1104	≥300
	ShortReadSeq50_POP7xl						
Short read sequencing BigDye XTerminator™	BDxShortReadSeq50_POP7	50	POP-7™	≤30	≥368	≥1104	≥300
	BDxShortReadSeq50_POP7xl						
Rapid sequencing	RapidSeq50_POP6	50	POP-6™	≤65	≥168	≥504	≥450
	RapidSeq50_POP6xl						
	RapidSeq50_POP7	50	POP-7™	≤40	≥280	≥840	≥500
	RapidSeq50_POP7xl						
Rapid sequencing	RapidSeq36_POP4	36	POP-4™	≤45	≥240	≥720	≥400
	RapidSeq36_POP4xl						
	RapidSeq36_POP6	36	POP-6™	≤65	≥168	≥504	≥600
	RapidSeq36_POP6xl						
	RapidSeq36_POP7	36	POP-7™	≤30	≥368	≥1104	≥600
	RapidSeq36_POP7xl						
Rapid sequencing BigDye XTerminator™	BDxRapidSeq50_POP6	50	POP-6™	≤65	≥168	≥504	≥450
	BDxRapidSeq50_POP6xl						
	BDxRapidSeq50_POP7	50	POP-7™	≤40	≥280	≥840	≥500
	BDxRapidSeq50_POP7xl						

Table 5 Sequencing analysis run modules (continued)

Run module type	Run module name	Configuration		23 hours Throughput <sup>[1]</sup>			Performance
		Cap. length (cm)	Polymer type	Run time (min)	3500 (8-cap.)	3500xL (24-cap.)	Contig. Read Length (CRL) <sup>[2]</sup>
Rapid sequencing BigDye XTerminator™	BDxRapidSeq36_POP4 BDxRapidSeq36_POP4xl	36	POP-4™	≤45	≥240	≥720	≥400
	BDxRapidSeq36_POP6 BDxRapidSeq36_POP6xl	36	POP-6™	≤66	≥164	≥494	≥600
	BDxRapidSeq36_POP7 BDxRapidSeq36_POP7xl	36	POP-7™	≤30	≥368	≥1104	≥600
Fast sequencing	FastSeq50_POP6 FastSeq50_POP6xl	50	POP-6™	≤90	≥122	≥368	≥600
	FastSeq50_POP7 FastSeq50_POP7xl	50	POP-7™	≤65	≥168	≥504	≥700
Fast sequencing	FastSeq36_POP7 FastSeq36_POP7xl	36	POP-7™	≤60	≥184	≥552	≥750
Fast sequencing BigDye XTerminator™	BDxFastSeq50_POP6 BDxFastSeq50_POP6xl	50	POP-6™	≤90	≥122	≥368	≥600
	BDxFastSeq50_POP7 BDxFastSeq50_POP7xl	50	POP-7™	≤65	≥168	≥504	≥700
Fast sequencing BigDye XTerminator™	BDxFastSeq36_POP7 BDxFastSeq36_POP7xl	36	POP-7™	≤60	≥240	≥552	≥750
Standard sequencing	StdSeq50_POP6 StdSeq50_POP6xl	50	POP-6™	≤135	≥80	≥240	≥600
	StdSeq50_POP7 StdSeq50_POP7xl	50	POP-7™	≤125	≥88	≥264	≥850
Standard sequencing BigDye XTerminator™	BDxStdSeq50_POP6 BDxStdSeq50_POP6xl	50	POP-6™	≤140	≥80	≥240	≥600
	BDxStdSeq50_POP7 BDxStdSeq50_POP7xl	50	POP-7™	≤125	≥88	≥264	≥850

**Table 5 Sequencing analysis run modules (continued)**

Run module type	Run module name	Configuration		23 hours Throughput <sup>[1]</sup>			Performance
		Cap. length (cm)	Polymer type	Run time (min)	3500 (8-cap.)	3500xL (24-cap.)	Contig. Read Length (CRL) <sup>[2]</sup>
Microbial sequencing	MicroSeq50_POP6	50	POP-6™	≤135	≥80	≥240	≥600
	MicroSeq50_POP6xl						
Microbial sequencing	MicroSeq50_POP7	50	POP-7™	≤125	≥88	≥264	≥850
	MicroSeq50_POP7xl						

<sup>[1]</sup> Throughput (Samples / Day): The total number of samples run in 23 hours (0.5 hour for user interaction and 0.5 hour for warm-up time).

<sup>[2]</sup> The maximum number of contiguous bases in the analyzed sequence with an average QV ≥20, calculated over a sliding window 20 base pairs wide from an AB Long Read Standard sequencing sample. This calculation starts with base number 1. The read length is counted from the middle base of the 1st good window to the middle base of the last good window, where a “good” window is one in which the average QV ≥20.

Table 6 Fragment and HID analysis run modules

Run module type	Run module name	Configuration		23 hours throughput <sup>[1]</sup>			Performance			
		Cap. length (cm)	Pol. type	Run time (min)	3500 (8-cap.)	3500xL (24-cap.)	Range <sup>[2]</sup>	Sizing Precision <sup>[3]</sup>		
								50bp-400bp	401bp-600bp	601bp-1200bp
Frag. analysis	FragmentAnalysis50_POP7 FragmentAnalysis50_POP7xl	50	POP-7™	≤45	≥280	≥840 <sup>[4]</sup>	≤40 to ≥520	<0.15	<0.30	NA <sup>[5]</sup>
	FragmentAnalysis50_POP6 FragmentAnalysis50_POP6xl	50	POP-6™	≤100	≥112	≥336	≤20 to ≥550	<0.15	<0.30	NA <sup>[5]</sup>
	FragmentAnalysis36_POP4 FragmentAnalysis36_POP4xl	36	POP-4™	≤35	≥312	≥936	≤60 to ≥400	<0.15	NA <sup>[5]</sup>	NA <sup>[5]</sup>
	FragmentAnalysis36_POP7 FragmentAnalysis36_POP7xl	36	POP-7™	≤30	≥368	≥1104	≤60 to ≥400	<0.15	NA <sup>[5]</sup>	NA <sup>[5]</sup>
Frag. analysis	FragAnalysis36_POP6 FragAnalysis36_POP6xl	36	POP-6™	≤60	≥184	≥552	≤60 to ≥400	<0.15	<0.30	NA <sup>[5]</sup>
Long frag. analysis	LongFragAnalysis50_POP7 LongFragAnalysis50_POP7xl	50	POP-7™	≤130	≥84	≥254	≤40 to ≥700	<0.15	<0.30	<0.45
HID	HID36_POP4 HID36_POP4xl	36	POP-4™	≤35	≥312	≥936	≤60 to ≥400	<0.15	NA <sup>[5]</sup>	NA <sup>[5]</sup>
SNaPshot™	SNaPshot50_POP7 SNaPshot50_POP7xl	50	POP-7™	≤30	≥376	≥1104	≤40 to ≥120	<0.50	NA <sup>[5]</sup>	NA <sup>[5]</sup>

<sup>[1]</sup> Throughput (Samples / Day): The total number of samples run in 23 hours (0.5 hour for user interaction and 0.5 hour for warm-up time).

<sup>[2]</sup> Resolution Range: The range of bases over which the resolution (peak spacing interval divided by the peak width at half-max in a GS600 or GS1200 LIZ size standard sample sized with a third order fit) is ≥1. The table shows the resolution range in ≥90% of samples.

<sup>[3]</sup> Sizing Precision: Standard deviation of sizes for one allele in the DS-33 install standard sized with the GS600 LIZ size standard across multiple capillaries in the same run. For one injection to pass, 100% of the alleles in that injection must meet the intra-run sizing precision specifications. The table shows the sizing precision of 100% of alleles in ≥90% of samples.

<sup>[4]</sup> Throughput is an estimate extrapolated from average run time.

<sup>[5]</sup> Not applicable because of the size of the fragments collected in the run.



## Dye sets

### Sequencing analysis dye sets

Table 7 Sequence analysis dye sets

Dye Set	Application Name
E (v1.1 BigDye™ Terminator)	Rapid DNA sequencing
Z (v3.1 BigDye™ Terminator)	DNA sequencing

### Fragment analysis dye sets for all applications

Table 8 Fragment analysis dye sets

	Application
E5	SNaPshot™ kit
G5	DNA sizing for 5-dye chemistry
J6 or J6-T	DNA sizing for 6-dye chemistry
F	DNA sizing for 4-dye chemistry
D	DNA sizing for 4-dye chemistry
AnyDye	DNA sizing

### HID analysis dye sets

Table 9 AmpFℓSTR™ Kit Table

AmpFℓSTR™ Kits	Dye set (use with HID Fragment Analysis 36_POP4 run module)
4-dye: <ul style="list-style-type: none"> <li>• COfiler™</li> <li>• Profiler Plus™</li> <li>• Profiler Plus™/ID</li> <li>• SGM Plus™</li> <li>• Other 4-dye kits</li> </ul>	F

Table 9 AmpF $\ell$ STR Kit Table (continued)

AmpF $\ell$ STR™ Kits	Dye set (use with HID Fragment Analysis 36_POP4 run module)
5-dye: <ul style="list-style-type: none"> <li>• Identifiler™</li> <li>• Identifiler™ Direct</li> <li>• Identifiler™ Plus</li> <li>• MiniFiler™</li> <li>• NGM™</li> <li>• NGM SElect™</li> <li>• NGM SElect™ Express</li> <li>• SEfiler Plus™</li> <li>• Sinofiler™</li> <li>• Yfiler™</li> <li>• Yfiler™ Direct</li> <li>• Other 5-dye kits</li> </ul>	G5
6-dye: <ul style="list-style-type: none"> <li>• GlobalFiler™</li> <li>• GlobalFiler™ Express</li> <li>• NGM Detect™</li> </ul>	J6



# Instrument specifications

## Instrument specifications

**Table 10** Applied Biosystems™ 3500/3500xL Genetic Analyzer physical dimensions, weight, and power consumption

Parameter	Instrument footprint	Recommended clearance
Depth	61 cm (24 in.)	25.4 cm (10 in.) <sup>[1]</sup>
Width	61 cm (24 in.) (closed door) 122 cm (48 in.) (open door)	158 cm (62 in.) <sup>[2]</sup>
Height	72 cm (28.3 in.)	31 cm (12 in.)
Weight	≈82 kg (180 lbs)	

<sup>[1]</sup> At the rear of the instrument to ensure adequate airflow and cooling

<sup>[2]</sup> For the instrument, computer, and computer monitor.

**Table 11** Computer dimensions and weight

Parameter	Computer	Monitor	Keyboard
Depth	41.7 cm (16.42 in.)	19.3 cm (7.6 in.)	44.7 cm (17.5 in.)
Width	17.5 cm (6.89 in.)	44.7 cm (17.5 in.)	15.25 cm (6 in.)
Height	37.4 cm (14.7 in.)	36.6 cm (14.4 in.)	5 cm (2 in.)
Weight	9.6. kg (21 lbs)	6.9 kg (15.2 lbs)	0.09 kg (0.2 lbs)

**Table 12** Applied Biosystems™ 3500/3500xL Genetic Analyzer operating specifications

Component	Specification
Laser	<ul style="list-style-type: none"> <li>Long-life, single-line 505 nm, solid-state laser excitation source</li> <li>Laser Output power 20mW</li> <li>Beam divergence 1.4 mrad</li> </ul>
LED	<ul style="list-style-type: none"> <li>Emitting color Natural White</li> <li>Luminous Intensity 250 Cd</li> </ul>
Electrophoresis Voltage	Up to 20 kV
Oven Temperature	Active temperature control from 18°C to 70°C



**Table 12 Applied Biosystems 3500/3500xL Genetic AnalyzerRUO operating specifications (continued)**

Component	Specification
Minimum Computer Requirements	<ul style="list-style-type: none"> <li>• Hardware:               <ul style="list-style-type: none"> <li>– OptiPlex™ XE, E8400, 3 GHZ Processor</li> <li>or</li> <li>– OptiPlex™ XE2, with Intel™ Core I7-47705, 3.1 GHz Processor</li> </ul> </li> <li>• Operating system: Windows™ 10 64-bit (IOT Enterprise)</li> <li>• Installed RAM: 16 GB</li> <li>• Hard drive: 500 GB SATA 3.0 Gb/s and 8 MB Data Burst Cache</li> </ul>

## Environmental requirements

**Table 13 Environmental requirements**

Condition	Requirement
Installation site	Indoor use only, Professional Healthcare Environment
Electromagnetic interference	<p>Do not use this device in close proximity to sources of strong electromagnetic radiation (for example, unshielded intentional RF sources). Strong electromagnetic radiation may interfere with the proper operation of the device.</p> <p>This equipment has been designed and tested to CISPR 11 Class A. The emissions characteristics of this equipment make it suitable for use in industrial areas and hospitals (CISPR 11 Class A). If it is used in a residential environment (for which CISPR 11 Class B is normally required), this equipment might not offer adequate protection to radio-frequency communication services. The user might need to take mitigation measures, such as relocating or re-orienting the equipment.</p>
Altitude	Safety tested up to 2,000 m (6,562 ft)
Electrical ratings	<p>Power cord with ground pin required</p> <ul style="list-style-type: none"> <li>• Instrument—AC 100–240 V ±10%, 50/60 Hz, power rated 320 VA</li> <li>• Computer—AC 100–240 V ±10%, 50/60 Hz, power rated 125 VA</li> <li>• Monitor—AC 100–240 V ±10%, 50/60 Hz, power rated 65 VA</li> </ul>
Mains AC line voltage tolerances	Up to ±10 percent of nominal voltage
Transient category	Installation categories II
Pollution degree	2



**Table 13 Environmental requirements** *(continued)*

Condition	Requirement
Liquid waste collection	Dispose of the polymer, buffer, reagents and any liquid waste as hazardous waste in compliance with local and national regulations.
Operating conditions	15–30°C (59–86°F) (Room temperature should not fluctuate $\pm 2^\circ\text{C}$ during an instrument run) 20–80% relative humidity, noncondensing
Transport and storage conditions	–30 to +60°C (–22 to +140°F) Minimum 20% relative humidity, maximum 85% (non-condensing)



**WARNING!** Portable RF communications equipment (including peripherals such as antenna cables and external antennas) should be used no closer than 30 cm (12 inches) to any part of the 3500/3500xL Genetic Analyzer, including cables specified by the manufacturer. Otherwise, degradation of the performance of this equipment could result.



**WARNING!** Use of this equipment adjacent or stacked with other equipment should be avoided because it could result in improper operation.



**WARNING!** Use of accessories, transducers, and cables other than those specified or provided by the manufacturer of this equipment could result in increased electromagnetic emissions or decreased electromagnetic immunity of this equipment and result in improper operation.

## Power and communication connections



- ① Ethernet port for computer instrument connection
- ② Circuit breaker
- ③ Connector for instrument power cable



# Catalog numbers

## Plates bases retainers and septa

**Table 14** Plates and caps

Part Description	General purpose supply, obtain from any laboratory supplier
96-well	General purpose supply, obtain from any laboratory supplier: 96-well PCR microtiter plate, standard or optical-grade polypropylene, 0.1 mL or 0.2 mL, half- or semi-skirted design, with or without barcode.
8-tube strips	General purpose supply, obtain from any laboratory supplier: <ul style="list-style-type: none"> <li>• 8-strip PCR tubes, standard- or optical-grade polypropylene, 0.1 mL</li> <li>• 8-strip full-height PCR tubes, standard- or optical-grade polypropylene, 0.2 mL</li> </ul>
Tube caps	8-tube PCR strip caps, domed, standard- or optical-grade polypropylene, for 0.1 mL or 0.2 mL 8-strip PCR tubes
Plate, 384-well	General purpose supply, obtain from any laboratory supplier: 384-well PCR microtiter plate, standard or optical-grade polypropylene, 0.02 mL, fully-skirted design, with or without barcode

**Table 15** Bases, retainers, and septa

Part Description	Cat. No.
Retainer and base, 8-tube RUO	4410231
Retainer and base (Fast), 8-tube RUO	4410233
Retainer and base (Standard), 96-well	4410227
Retainer and base (Standard), 96-well RUO	4410228
Retainer and base (Fast), 96-well RUO	4409530
Retainer and base (Standard), 384-well, RUO	4410235
Septa, 8-strip RUO	4410701
Septa, 96-well	4410700
Septa, 384-well RUO	4412520



## Instrument consumables

Name	Cat. No.
Anode Buffer Container	4393927
Capillary array, 8-Capillary, 36-cm	4404683
Capillary array, 24-Capillary, 36-cm	4404687
Capillary array, 8-Capillary, 50-cm	4404685
Capillary array, 24-Capillary, 50-cm	4404689
Cathode Buffer Container	4408256
Conditioning reagent	4393718
Polymer, POP-6™ (960)	4393712
Polymer, POP-6™ (384)	4393717
Polymer, POP-6™ (96)	A26071
Polymer, POP-7™ (960)	4393714
Polymer, POP-7™ (384)	4393708
Polymer, POP-7™ (96)	A26073
Polymer, POP-4™ (960) <sup>[1]</sup>	4393710
Polymer, POP-4™ (384) <sup>[1]</sup>	4393715
Polymer, POP-4™ (96)	A26070
Polymer pouch cap	4412619
Hi-Di™ Formamide Four 5-mL bottles	4440753

<sup>[1]</sup> Validated for HID applications.

## Sequencing analysis reagents and consumables

Name	Cat. No.
<b>BigDye™ Terminator v1.1</b>	
3500/3500xL Sequencing Standards, BigDye™ Terminator v1.1	4404314
BigDye™ Terminator v1.1 Matrix Standards Kit	4336824
BigDye™ Terminator v1.1 Cycle Sequencing Kit	4337449



(continued)

Name	Cat. No.
<b>BigDye™ Terminator v3.1</b>	
3500/3500xL Sequencing Standards, BigDye™ Terminator v3.1	4404312
BigDye™ Terminator v3.1 Matrix Standards Kit	4336974
BigDye™ Terminator v3.1 Cycle Sequencing Kit	4337454
<b>BigDye™ Direct</b>	
BigDye™ Direct Cycle Sequencing Kit	4458689

## Fragment and HID analysis reagents

Name	Cat. No.
DS-02 Matrix Standard Kit (Dye Set E5)	4323014
DS-32 Matrix Standard Kit (Dye Set F)	4345831
DS-33 Matrix Standard Kit (Dye Set G5)	4345833
DS-36 Matrix Standard Kit (Dye set J6, 6-dye)	4425042
DS-37 Matrix Standard Kit (Dye set J6-T, 6-dye)	A31234
DS-33 GeneScan™ Installation Standards with GeneScan™ 600 LIZ™ Size Standard v2.0 (G5 dye set)	4376911
GeneScan™ 120 LIZ™ Size Standard	4324287
GeneScan™ 500 ROX™ Size Standard	401734
GeneScan™ 600 LIZ™ Size Standard v2.0	4408399
GeneScan™ 1200 LIZ™ Size Standard	4379950
AmpF $\ell$ STR™ Identifiler™ Allelic Ladder (For HID install check)	Contact Thermo Fisher Scientific



# Limitations

The 3500 instrument contains the limitations noted below. Please ensure that any use of the instrument takes into consideration these limitations.

## General

- **IMPORTANT!** Enter only alpha-numeric characters in the software. Special characters may not be correctly displayed in some software screens, may cause problems with plate, file, folder, user account, and/or library item names, and may interfere with starting a run and/or importing and exporting library items.
- **IMPORTANT!** If you copy/paste sample or plate information into the Assign Plate Contents screen or into a plate import file, copy from a plain text editor such as Notepad. Do not copy from a word processing program such as Microsoft™ Word™, which may include invisible, non-ASCII characters. Non-ASCII characters in plate or sample information may cause a run to stop or may prevent a run from starting.
- When importing a sample plate, use the format shown in “Create a plate import template” on page 95.
- If you re-run a plate that specifies a re-injection, and the re-injection specifies a protocol other than the protocol used for the original injection, the new protocol for the re-injection is not used. Before re-running a plate, examine the protocols specified for re-injections and change as needed.

## Computer

- The computer provided with the instrument contains validated software and settings. Do not update the Windows™ operating system or firewall settings.
- The computer provided with the instrument does not include antivirus software because customer preferences and network requirements vary. See “Antivirus software requirements” on page 20 for antivirus software that has been tested and approved for use with the software.

## Instrument and consumables

- Instrument firmware is to be updated only by a Thermo Fisher Scientific representative.
- Use only the parts listed in Appendix D, “Catalog numbers”.
- Replace the capillary array after 160 injections or expiration date listed on packaging and RFID label.
- Before each run, check buffer fill levels.
- In the event of a power disruption, restart the computer (“Restart the instrument and the computer” on page 279).
- If you observe “Unable to transmit measurement data. Internal data buffer overflow.” error, restart the computer (“Restart the instrument and the computer” on page 279).
- If you observe a “Failure to Read from RFID tag” error, see “Troubleshooting” on page 328.

## Calibration and install checks

- If an install check for the run application type (Sequencing, Fragment, or HID) has not been performed, a message is displayed and the run does not start.
- When running a spatial calibration, select Perform QC Checks as described in page 125. Refer to examples of passing spatial calibration as shown in “Example spatial profiles” on page 128.
- When performing a spectral calibration, select the dye set appropriate for your application as described in “Perform a spectral calibration” on page 133.
- If you navigate away from the Install Check screen after you start the install check, the starting well may be reset to A01. This is a display issue only; the starting well you specify is used for the install check.
- If you change font settings before you generate a report, the report may not be generated. Generate the report again.

## Security Audit and E-sig

- Before using the instrument, configure system security as described in “Configure the security system” on page 219.
- Changes to e-signature settings are not activated until you log out of the software, then log back in.
- If you change font settings before you generate an Object Audit report, the report may not be generated. Generate the report again.



## Review results

- For sequencing data, review sample quality as described in “Review traces” on page 106.
- For fragment analysis or HID data, review sample quality as described in Review sample quality (page 115).
- If you change the order of columns before exporting a sizing table, Dye/Sample Peak column values are split in to two separate columns, the column name containing the Sample Peak values is incorrectly named, and the column headers after Dye/Sample are shifted one column to the right. You can edit the exported file: Cut/paste column headers one column to the right, enter correct headers for the Dye and Sample Peak columns.



# Radio Frequency Identification (RFID) technology

The instrument uses four identical wireless radio frequency identification (RFID) read/write units to monitor instrument consumables (for more information, see “Instrument parts and functions” on page 18).

## Precautions for use



**WARNING!** Radio frequency identification (RFID) could possibly disrupt the operation of patient-worn and/or implanted active medical devices. To minimize such effects, do not come within 10 cm of this instrument if you have a patient-worn and/or implanted active medical device.



**WARNING!** Radio frequency identification (RFID) signals from external devices could possibly disrupt the operation of the 3500 RFID read/write units. RFID signals from the 3500 RFID read/write units could possibly disrupt the operation of external RFID devices. To minimize such effects, do not bring external RFID devices within 10 cm of this instrument during instrument operation.

## Locations of RFID read/write units

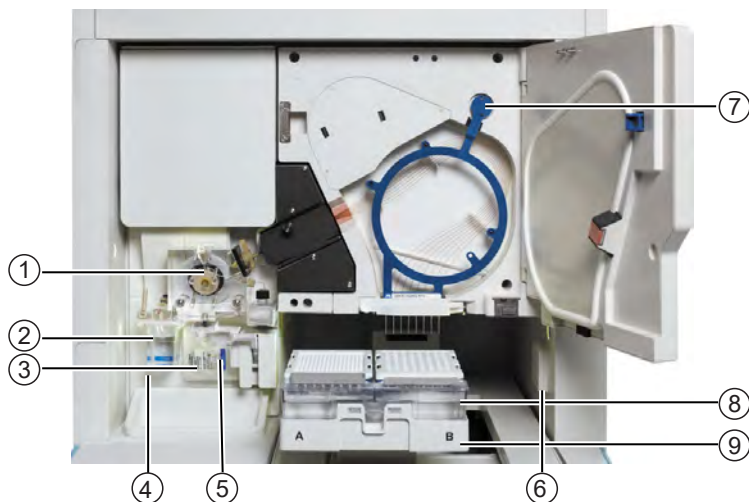


Figure 48 RFID read/write unit locations within instrument interior (shown with door open)

- ① Polymer delivery pump (PDP)
- ② Anode buffer container (ABC)
- ③ Polymer or conditioning pouch
- ④ ABC RFID read/write unit (behind reservoir)
- ⑤ Pouch read/write unit (behind pouch)
- ⑥ CBC RFID read/write unit
- ⑦ Capillary array read/write unit
- ⑧ Cathode buffer container (CBC)
- ⑨ Autosampler

## Function

The RFID read/write units:

1. Read up to 256 bytes from the RFID consumables tags.
2. Write up to 256 bytes to the RFID consumables tags.
3. Re-read the written data on the tags to confirm that it is accurate, using a checksum to verify data integrity.

The RFID read/write units perform the functions listed above at the start of each run.

## Specifications

**Table 16** RFID read/write unit specifications

Component	Specification
RFID read/write unit	<ul style="list-style-type: none"> <li>• Ultra-Compact Proximal-Type RFID Reader / Writer</li> <li>• Model ASI4000R2X</li> <li>• Manufactured by ART Finex Co., Ltd.</li> </ul>
RF frequency	13.56 MHz
RF output power	60 mW
RFID tags	Texas Instruments RI-I03-112A-03 tags, tested by the manufacturer to reliably read and write 100,000 times with zero data loss and retain written data for more than 10 years
Effective range between RFID tag and internal RFID read/write units	<ul style="list-style-type: none"> <li>• ABC tag: 3 cm</li> <li>• CBC tag: 4 cm</li> <li>• Capillary tag: 3 cm</li> <li>• Polymer tag: 3 cm</li> </ul>
Typical use range between RFID tag and internal RFID read/write units	0.5 cm
Minimum separation distance of the instrument from external RFID read/write units	10 cm
Minimum separation distance of the instrument from other wireless technologies such as WiFi, Bluetooth, or Cellular	10 cm
Minimum separation distance of the instrument from other laboratory equipment such as centrifuge or thermal cycler	1 m
Wireless security	<ul style="list-style-type: none"> <li>• RFID tag read/write/re-read with checksum</li> <li>• Password access for use of software</li> <li>• Base-64 encoding of data between the instrument and the computer</li> </ul>

## Troubleshooting

Table 17 RFID troubleshooting

Symptom	Possible cause	Action
Unable to read RFID information. "Failure to Read from RFID tag"	Consumable package is improperly installed or label is defective. Polymer/Conditioning reagent pouch is not positioned properly.	<p>Ensure that the RFID label is not visibly damaged and consumable package is properly installed.</p> <p>Ensure that label is close, and parallel, to the instrument.</p> <p>Reposition or re-install pouch, then click <b>Refresh</b> on the Dashboard.</p>
	Malfunctioning RFID label or reader.	<p>Restart the instrument and the computer (see "Restart the instrument and the computer" on page 279).</p> <p>Install a new consumable (if available).</p> <p>If problem persists, contact Thermo Fisher Scientific.</p>
		<p>Place a used CBC, ABC, pouch, or array on the instrument:</p> <ul style="list-style-type: none"> <li>• If the instrument can read the RFID label, install a new CBC, ABC, pouch, or array.</li> <li>• If the instrument cannot read the RFID label, contact Thermo Fisher Scientific.</li> </ul>





# Signal optimization and size standard normalization

## Signal optimization feature

The signal optimization feature reduces peak height variation across capillaries in an injection. This variation is introduced by the optics of the instrument and the injection conditions used. The signal optimization feature has two components:

- Spatial calibration-dependent signal optimization (24-capillary instruments only, always enabled)
- Capillary-position-dependent signal optimization (8-capillary and 24-capillary instruments, requires autosampler adjustment by field service engineer.)

For maximum signal optimization on 24-capillary instruments, we suggest that you use both components of the signal optimization feature.

## Spatial calibration-dependent signal optimization

**To enable this feature:** 24-capillary instruments only, always enabled. Not available on 8-capillary instruments.

**To disable this feature:** Cannot be disabled

During spatial calibration, a **Signal Optimization Factor** is calculated for each capillary using a fitted curve method. The fitted curve method minimizes background signal and reduces noise.

The adjusted signal intensity, not the signal intensity displayed for a capillary, is used to calculate the **Signal Optimization Factor** for the capillary. The **Signal Optimization Factor** for each capillary is displayed in the **Spatial Calibration** screen (the adjusted signal intensity is not displayed).



① Signal Optimization Factor



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**Note:** The signal intensity, average peak height, and uniformity displayed for the capillaries are used for the **Perform QC Checks** function in spatial calibration.

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The **Signal Optimization Factor** range is 0.5–2. Higher or lower values are rounded down or up to bring them within range. Therefore, you may observe two peaks with different intensities but with the same **Signal Optimization Factor**.

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**Note:** On 8-capillary instruments, the **Signal Optimization Factor** field displays 1.0 for all capillaries after a spatial calibration.

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The **Signal Optimization Factor** is applied to signal data for each capillary during data collection to minimize optical variation effects and increase signal uniformity between capillaries.

The **Signal Optimization Factor** is exported or printed and included in the spatial calibration report with the other spatial calibration results.

## Run module-dependent signal optimization

### To enable this feature:

- Create an "SO" instrument protocol with the HID36\_POP4(xl)\_SO run module *and*
- Create an "SO" assay with the "SO" instrument protocol *and*
- Use the "SO" assay 8-capillary and 24-capillary instruments, optional.

**To disable this feature:** Use an assay without \_SO suffix

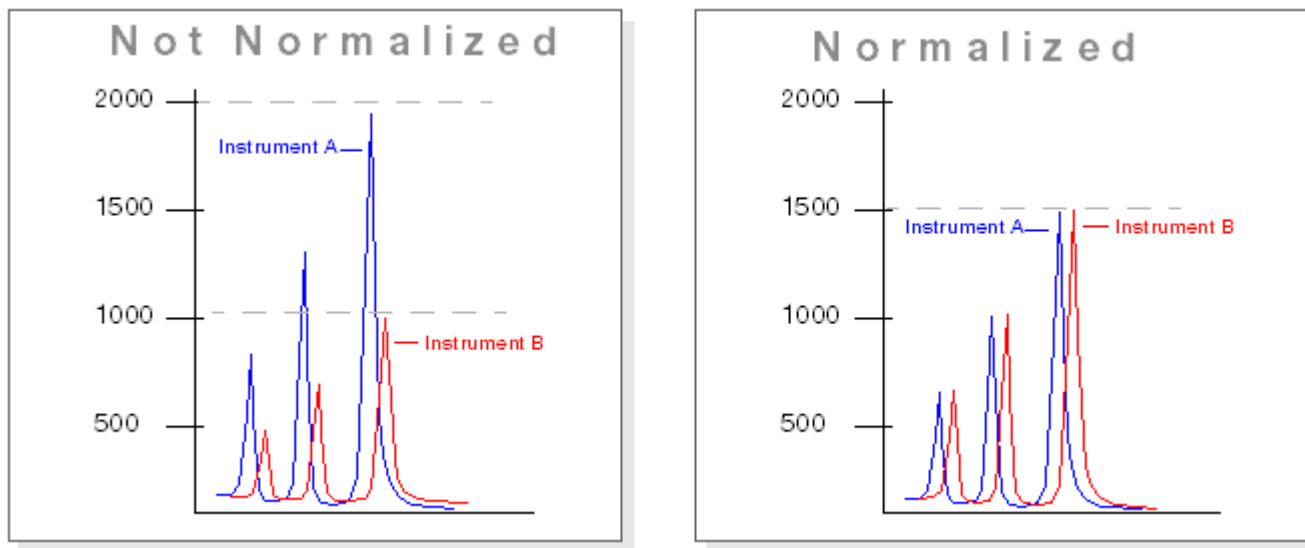
A new HID36\_POP4(xl)\_SO run module (SO=signal optimization) has been optimized to minimize injection variability between capillaries. Enhancements to the run module include the introduction of a minimal amount of polymer into the well before the injection and a higher capillary position in the well during the injection. These changes have been shown to improve peak uniformity across capillaries within an injection.

You can create and use new SO assays to implement the second component of signal optimization.

## Size standard normalization feature

### Overview of the normalization feature

For fragment analysis applications, the software includes an optional normalization feature for use with the GeneScan™ 600 LIZ™ Size Standard v2.0 (GS600 LIZ v2). This feature attenuates signal variations associated with instrument, capillary array, sample salt load, and injection variability between capillaries and instruments. Normalization can be applied during primary analysis of the data.



To use the normalization feature, prepare each sample with the GS600 LIZ v2 size standard, then specify the appropriate normalization size standard for file primary analysis. The GS600 LIZ™ v2 reagent can function as an internal standard for signal-height normalization as well as a size standard for peak sizing.

### When to use the normalization feature

The software provides three normalization size-standard definition files that you can specify for primary analysis of samples prepared with the GS600 LIZ v2 size standard and the G5 and J6 dye sets:

- Fragment (POP-6™ and POP-7™ polymer):
  - GS600LIZ+Normalization
  - GS600(60-600)LIZ+Normalization—For applications that have primer peaks that obscure the 20 and 40-mer peaks of the GS600 LIZ v2 size standard.
- Fragment (POP-4™ polymer):
  - GS600(80-400)LIZ+Normalization
- HID (POP-4™ polymer):
  - GS600(80-400)LIZ+Normalization



# Safety



**WARNING! GENERAL SAFETY.** Using this product in a manner not specified in the user documentation may result in personal injury or damage to the instrument or device. Ensure that anyone using this product has received instructions in general safety practices for laboratories and the safety information provided in this document.

- Before using an instrument or device, read and understand the safety information provided in the user documentation provided by the manufacturer of the instrument or device.
- Before handling chemicals, read and understand all applicable Safety Data Sheets (SDSs) and use appropriate personal protective equipment (gloves, gowns, eye protection, and so on). To obtain SDSs, visit [thermofisher.com/support](http://thermofisher.com/support).

## Symbols on this instrument

Symbols may be found on the instrument to warn against potential hazards or convey important safety information. In this document, the hazard symbol is used along with one of the following user attention words:

- **CAUTION!**—Indicates a potentially hazardous situation that, if not avoided, may result in minor or moderate injury. It may also be used to alert against unsafe practices.
- **WARNING!**—Indicates a potentially hazardous situation that, if not avoided, could result in death or serious injury.
- **DANGER!**—Indicates an imminently hazardous situation that, if not avoided, will result in death or serious injury.

Symbol	English	Français
	Caution, risk of danger Consult the manual for further safety information.	Attention, risque de danger Consulter le manuel pour d'autres renseignements de sécurité.
	Caution, risk of electrical shock	Attention, risque de choc électrique
	Caution, piercing hazard	Attention, danger de perforation



(continued)

Symbol	English	Français
	Caution, hot surface	Attention, surface chaude
	Potential biohazard	Danger biologique potentiel
	On	On (marche)
	Off	Off (arrêt)
	On/Off	On/Off (marche/arrêt)
	Protective conductor terminal (main ground)	Borne de conducteur de protection (mise à la terre principale)
	Terminal that can receive or supply alternating current or voltage	Borne pouvant recevoir ou envoyer une tension ou un courant de type alternatif
	Do not dispose of this product in unsorted municipal waste  <b>CAUTION!</b> To minimize negative environmental impact from disposal of electronic waste, do not dispose of electronic waste in unsorted municipal waste. Follow local municipal waste ordinances for proper disposal provision and contact customer service for information about responsible disposal options.	Ne pas éliminer ce produit avec les déchets usuels non soumis au tri sélectif.  <b>MISE EN GARDE !</b> Pour minimiser les conséquences négatives sur l'environnement à la suite de l'élimination de déchets électroniques, ne pas éliminer ce déchet électronique avec les déchets usuels non soumis au tri sélectif. Se conformer aux ordonnances locales sur les déchets municipaux pour les dispositions d'élimination et communiquer avec le service à la clientèle pour des renseignements sur les options d'élimination responsable.

## Conformity symbols

Conformity mark	Description
	Indicates conformity with safety requirements for Canada and U.S.A.



(continued)

Conformity mark	Description
	Indicates conformity with European Union requirements.
	Indicates conformity with Australian standards for electromagnetic compatibility.

## Safety alerts on this instrument

Additional text may be used with one of the symbols described above when more specific information is needed to avoid exposure to a hazard. See the following table for safety alerts found on the instrument.

English	Français
<b>CAUTION!</b> Hazardous chemicals. Read the Safety Data Sheets (SDSs) before handling.	<b>MISE EN GARDE !</b> Produits chimiques dangereux. Lire les fiches signalétiques (FS) avant de manipuler les produits.
<b>CAUTION!</b> Hazardous waste. Refer to SDS(s) and local regulations for handling and disposal.	<b>MISE EN GARDE !</b> Déchets dangereux. Lire les fiches signalétiques (FS) et la réglementation locale associées à la manipulation et à l'élimination des déchets.
<b>DANGER!</b> Class 3B (III) visible and/or invisible laser radiation present when open and interlocks defeated. Avoid exposure to beam.	<b>DANGER !</b> Rayonnement laser visible ou invisible de classe 3B (III) présent en position ouverte et avec les dispositifs de sécurité non enclenchés. Éviter toute exposition au faisceau.

## Location of safety labels on this instrument

English	French translation	Location on Instrument
<b>WARNING!</b> Class 3B (III) visible and/or invisible laser radiation present when open and interlocks defeated. Avoid exposure to beam.	<b>ATTENTION!</b> Rayonnement laser visible ou invisible de classe 3B (III) présent en position ouverte et avec les dispositifs de sécurité non enclenchés. Éviter toute exposition au faisceau.	Detection cell cover 

(continued)

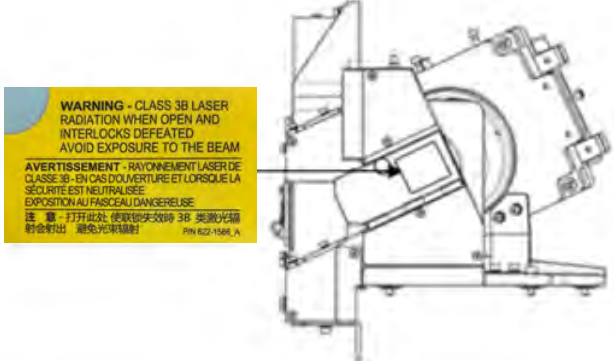
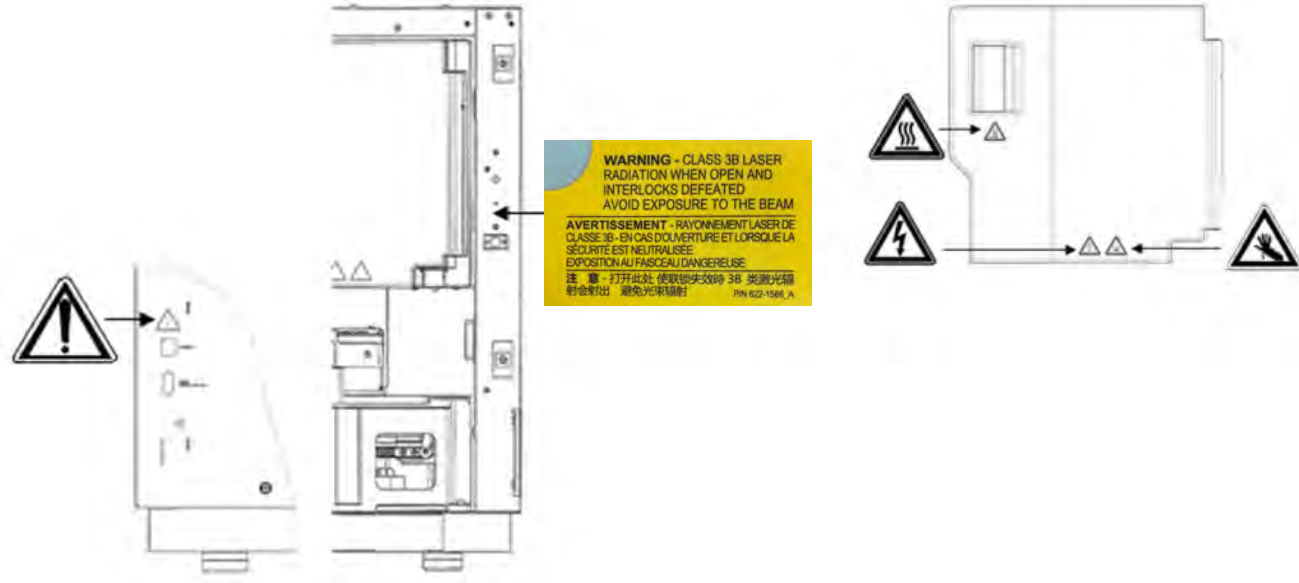
English	French translation	Location on Instrument
 <p><b>WARNING - CLASS 3B LASER RADIATION WHEN OPEN AND INTERLOCKS DEFEATED AVOID EXPOSURE TO THE BEAM</b></p> <p><b>AVERTISSEMENT - RAYONNEMENT LASER DE CLASSE 3B - EN CAS D'OUVERTURE ET LORSQUE LA SÉCURITÉ EST NEUTRALISÉE EXPOSITION AU FASCEAU DANGÉREUSE.</b></p> <p>注意 - 打开此处 使联锁失效时 3B 类激光辐射会射出 避免光束照射 P/N 622-1566_A</p>		
 <p><b>WARNING - CLASS 3B LASER RADIATION WHEN OPEN AND INTERLOCKS DEFEATED AVOID EXPOSURE TO THE BEAM</b></p> <p><b>AVERTISSEMENT - RAYONNEMENT LASER DE CLASSE 3B - EN CAS D'OUVERTURE ET LORSQUE LA SÉCURITÉ EST NEUTRALISÉE EXPOSITION AU FASCEAU DANGÉREUSE.</b></p> <p>注意 - 打开此处 使联锁失效时 3B 类激光辐射会射出 避免光束照射 P/N 622-1566_A</p>		

Figure 49 Front view

Figure 50 Rear panel (left) oven door (right)

## Instrument safety

### General



**CAUTION! Do not remove instrument protective covers.** If you remove the protective instrument panels or disable interlock devices, you may be exposed to serious hazards including, but not limited to, severe electrical shock, laser exposure, crushing, or chemical exposure.



## Physical injury



**CAUTION! Moving Parts.** Moving parts can crush, pinch and cut. Keep hands clear of moving parts while operating the instrument. Disconnect power before servicing.

## Electrical safety



**WARNING! Ensure appropriate electrical supply.** For safe operation of the instrument:

- Plug the system into a properly grounded receptacle with adequate current capacity.
- Ensure the electrical supply is of suitable voltage.
- Never operate the instrument with the ground disconnected. Grounding continuity is required for safe operation of the instrument.



**AVERTISSEMENT ! Veiller à utiliser une alimentation électrique appropriée.** Pour garantir le fonctionnement de l'instrument en toute sécurité :

- Brancher le système sur une prise électrique correctement mise à la terre et de puissance adéquate.
- S'assurer que la tension électrique est convenable.
- Ne jamais utiliser l'instrument alors que le dispositif de mise à la terre est déconnecté. La continuité de la mise à la terre est impérative pour le fonctionnement de l'instrument en toute sécurité.



**WARNING! Power Supply Line Cords.** Use properly configured and approved line cords for the power supply in your facility.



**AVERTISSEMENT ! Cordons d'alimentation électrique.** Utiliser des cordons d'alimentation adaptés et approuvés pour raccorder l'instrument au circuit électrique du site.



**WARNING! Disconnecting Power.** To fully disconnect power either detach or unplug the power cord, positioning the instrument such that the power cord is accessible.



**AVERTISSEMENT ! Déconnecter l'alimentation.** Pour déconnecter entièrement l'alimentation, détacher ou débrancher le cordon d'alimentation. Placer l'instrument de manière à ce que le cordon d'alimentation soit accessible.





## Cleaning and decontamination



**CAUTION! Cleaning and Decontamination.** Use only the cleaning and decontamination methods specified in the manufacturer's user documentation. It is the responsibility of the operator (or other responsible person) to ensure the following requirements are met:

- No decontamination or cleaning agents are used that could cause a HAZARD as a result of a reaction with parts of the equipment or with material contained in the equipment.
- The instrument is properly decontaminated a) if hazardous material is spilled onto or into the equipment, and/or b) prior to having the instrument serviced at your facility or sending the instrument for repair, maintenance, trade-in, disposal, or termination of a loan (decontamination forms may be requested from customer service).
- Before using any cleaning or decontamination methods (except those recommended by the manufacturer), users should confirm with the manufacturer that the proposed method will not damage the equipment.



**MISE EN GARDE ! Nettoyage et décontamination.** Utiliser uniquement les méthodes de nettoyage et de décontamination indiquées dans la documentation du fabricant destinée aux utilisateurs. L'opérateur (ou toute autre personne responsable) est tenu d'assurer le respect des exigences suivantes:

- Ne pas utiliser d'agents de nettoyage ou de décontamination susceptibles de réagir avec certaines parties de l'appareil ou avec les matières qu'il contient et de constituer, de ce fait, un DANGER.
- L'instrument doit être correctement décontaminé a) si des substances dangereuses sont renversées sur ou à l'intérieur de l'équipement, et/ou b) avant de le faire réviser sur site ou de l'envoyer à des fins de réparation, de maintenance, de revente, d'élimination ou à l'expiration d'une période de prêt (des informations sur les formes de décontamination peuvent être demandées auprès du Service clientèle).
- Avant d'utiliser une méthode de nettoyage ou de décontamination (autre que celles recommandées par le fabricant), les utilisateurs doivent vérifier auprès de celui-ci qu'elle ne risque pas d'endommager l'appareil.



## Laser



**WARNING! LASER HAZARD.** Under normal operating conditions, the Applied Biosystems™ 3500/3500xL Genetic Analyzer is categorized as a Class 1 laser product. However, removing the protective covers and (when applicable) defeating the interlock(s) may result in exposure to the internal Class 3 B laser. Lasers can burn the retina, causing permanent blind spots. To ensure safe laser operation:

- Never look directly into the laser beam.
- Do not remove safety labels, instrument protective panels, or defeat safety interlocks.
- The system must be installed and maintained by a Thermo Fisher Scientific Technical Representative.
- Remove jewelry and other items that can reflect a laser beam into your eyes or those of others
- Wear proper eye protection and post a laser warning sign at the entrance to the laboratory if the laser protection is defeated for servicing

Thermo Fisher Scientific Technical Representatives are instructed to:

DO NOT operate the laser when it cannot be cooled by its cooling fan; an overheated laser can cause severe burns on contact.

## Safety and electromagnetic compatibility (EMC) standards

The instrument design and manufacture complies with the following standards and requirements for safety and electromagnetic compatibility.

### Safety (compliance)

Reference	Description
EU Directive 2014/35/EU	European Union “Low Voltage Directive”
IEC 61010-1 EN 61010-1 UL 61010-1 CSA C22.2 No. 61010-1	<i>Safety requirements for electrical equipment for measurement, control, and laboratory use – Part 1: General requirements</i>
IEC 61010-2-010 EN 61010-2-010	<i>Safety requirements for electrical equipment for measurement, control and laboratory use – Part 2-010: Particular requirements for laboratory equipment for the heating of materials</i>
IEC 61010-2-081 EN 61010-2-081	<i>Safety requirements for electrical equipment for measurement, control and laboratory use – Part 2-081: Particular requirements for automatic and semi-automatic laboratory equipment for analysis and other purposes</i>



(continued)

Reference	Description
IEC 60825-1:2014 EN 60825-1:2014	<i>Safety of laser products – Part 1: Equipment classification and requirements</i>
21 CFR 1040.10 and 1040.11 as applicable	U.S. FDA Health and Human Services (HHS) “Radiological health performance standards for laser products” and “Radiological health performance standards for specific purpose laser products”

## EMC

Reference	Description
Directive 2014/30/EU	European Union “EMC Directive”
EN 61326-1	<i>Electrical Equipment for Measurement, Control and Laboratory Use – EMC Requirements – Part 1: General Requirements</i>
FCC Part 15 (47 CFR)	U.S. Standard “Industrial, Scientific, and Medical Equipment”
AS/NZS 2064	<i>Limits and Methods of Measurement of Electromagnetic Disturbance Characteristics of Industrial, Scientific, and Medical (ISM) Radiofrequency Equipment</i>
ICES-001, Issue 3	<i>Industrial, Scientific and Medical (ISM) Radio Frequency Generators</i>

## Environmental design

Reference	Description
Directive 2012/19/EU	European Union “WEEE Directive” – Waste electrical and electronic equipment
Directive 2011/65/EU Commission Delegated Directive 2015/863	European Union “RoHS Directive” – Restriction of hazardous substances in electrical and electronic equipment



## Radio compliance

Reference	Description
Directive 2014/53/EU (as of June 12, 2017)	European Union "RE Directive" - Radio equipment
Contains FCC ID: 2AM8P-3668  Contains IC: 7805A-3668	<p>This device complies with part 15 of FCC Rules and Innovation, Science and Economic Development Canada's licence-exempt RSS(s). Operation is subject to the following two conditions: (1) this device may not cause harmful interference, and (2) this device must accept any interference received, including interference that may cause undesired operation.</p> <p>Le présent appareil est conforme à la partie 15 des règles de la FCC et aux normes des CNR d'Innovation, Sciences et Développement économique Canada applicables aux appareils radio exempts de licence. L'exploitation est autorisée aux deux conditions suivantes : (1) l'appareil ne doit pas produire de brouillage, et (2) l'appareil doit accepter tout brouillage subi, même si le brouillage est susceptible d'en compromettre le fonctionnement.</p> <p>Note: This equipment has been tested and found to comply with the limits for a Class A digital device, pursuant to part 15 of the FCC Rules. These limits are designed to provide reasonable protection against harmful interference when the equipment is operated in a commercial environment. This equipment generates, uses, and can radiate radio frequency energy and, if not installed and used in accordance with the instruction manual, may cause harmful interference to radio communications. Operation of this equipment in a residential area is likely to cause harmful interference in which case the user will be required to correct the interference at his own expense.</p>



## Chemical safety



**WARNING! GENERAL CHEMICAL HANDLING.** To minimize hazards, ensure laboratory personnel read and practice the general safety guidelines for chemical usage, storage, and waste provided below. Consult the relevant SDS for specific precautions and instructions:

- Read and understand the Safety Data Sheets (SDSs) provided by the chemical manufacturer before you store, handle, or work with any chemicals or hazardous materials. To obtain SDSs, see the “Documentation and Support” section in this document.
- Minimize contact with chemicals. Wear appropriate personal protective equipment when handling chemicals (for example, safety glasses, gloves, or protective clothing).
- Minimize the inhalation of chemicals. Do not leave chemical containers open. Use only with adequate ventilation (for example, fume hood).
- Check regularly for chemical leaks or spills. If a leak or spill occurs, follow the manufacturer's cleanup procedures as recommended in the SDS.
- Handle chemical wastes in a fume hood.
- Ensure use of primary and secondary waste containers. (A primary waste container holds the immediate waste. A secondary container contains spills or leaks from the primary container. Both containers must be compatible with the waste material and meet federal, state, and local requirements for container storage.)
- After emptying a waste container, seal it with the cap provided.
- Characterize (by analysis if necessary) the waste generated by the particular applications, reagents, and substrates used in your laboratory.
- Ensure that the waste is stored, transferred, transported, and disposed of according to all local, state/provincial, and/or national regulations.
- **IMPORTANT!** Radioactive or biohazardous materials may require special handling, and disposal limitations may apply.



**AVERTISSEMENT ! PRÉCAUTIONS GÉNÉRALES EN CAS DE MANIPULATION DE PRODUITS CHIMIQUES.** Pour minimiser les risques, veiller à ce que le personnel du laboratoire lise attentivement et mette en œuvre les consignes de sécurité générales relatives à l'utilisation et au stockage des produits chimiques et à la gestion des déchets qui en découlent, décrites ci-dessous. Consulter également la FDS appropriée pour connaître les précautions et instructions particulières à respecter :

- Lire et comprendre les fiches de données de sécurité (FDS) fournies par le fabricant avant de stocker, de manipuler ou d'utiliser les matériaux dangereux ou les produits chimiques. Pour obtenir les FDS, se reporter à la section « Documentation et support » du présent document.
- Limiter les contacts avec les produits chimiques. Porter des équipements de protection appropriés lors de la manipulation des produits chimiques (par exemple : lunettes de sûreté, gants ou vêtements de protection).
- Limiter l'inhalation des produits chimiques. Ne pas laisser les récipients de produits chimiques ouverts. Ils ne doivent être utilisés qu'avec une ventilation adéquate (par exemple, sorbonne).
- Vérifier régulièrement l'absence de fuite ou d'écoulement des produits chimiques. En cas de fuite ou d'écoulement d'un produit, respecter les directives de nettoyage du fabricant recommandées dans la FDS.
- Manipuler les déchets chimiques dans une sorbonne.



- Veiller à utiliser des récipients à déchets primaire et secondaire. (Le récipient primaire contient les déchets immédiats, le récipient secondaire contient les fuites et les écoulements du récipient primaire. Les deux récipients doivent être compatibles avec les matériaux mis au rebut et conformes aux exigences locales, nationales et communautaires en matière de confinement des récipients.)
- Une fois le récipient à déchets vidé, il doit être refermé hermétiquement avec le couvercle fourni.
- Caractériser (par une analyse si nécessaire) les déchets générés par les applications, les réactifs et les substrats particuliers utilisés dans le laboratoire.
- Vérifier que les déchets sont convenablement stockés, transférés, transportés et éliminés en respectant toutes les réglementations locales, nationales et/ou communautaires en vigueur.
- **IMPORTANT !** Les matériaux représentant un danger biologique ou radioactif exigent parfois une manipulation spéciale, et des limitations peuvent s'appliquer à leur élimination.

## Biological hazard safety



**WARNING! BIOHAZARD.** Biological samples such as tissues, body fluids, infectious agents, and blood of humans and other animals have the potential to transmit infectious diseases. Conduct all work in properly equipped facilities with the appropriate safety equipment (for example, physical containment devices). Safety equipment can also include items for personal protection, such as gloves, coats, gowns, shoe covers, boots, respirators, face shields, safety glasses, or goggles. Individuals should be trained according to applicable regulatory and company/ institution requirements before working with potentially biohazardous materials. Follow all applicable local, state/provincial, and/or national regulations. The following references provide general guidelines when handling biological samples in laboratory environment.

- U.S. Department of Health and Human Services, *Biosafety in Microbiological and Biomedical Laboratories (BMBL)*, 5th Edition, HHS Publication No. (CDC) 21-1112, Revised December 2009; found at:  
[www.cdc.gov/labs/pdf/CDC-BiosafetymicrobiologicalBiomedicalLaboratories-2020-P.pdf](http://www.cdc.gov/labs/pdf/CDC-BiosafetymicrobiologicalBiomedicalLaboratories-2020-P.pdf)
- World Health Organization, *Laboratory Biosafety Manual*, 3rd Edition, WHO/CDS/CSR/LYO/2004.11; found at:  
[www.who.int/publications/i/item/9789240011311](http://www.who.int/publications/i/item/9789240011311)



# Documentation and support

## Related Documentation

Document	Publication number
<i>3500/3500xL Genetic Analyzer with 3500 Series Data Collection Software v3.3 Quick Reference</i>	100081365
<i>Polymer Delivery Pump Cleaning Kit RUO Product Information Sheet</i>	4414004

**Note:** For additional documentation, see “Obtaining support” on page 343.

## Customer and technical support

Visit [thermofisher.com/support](http://thermofisher.com/support) for the latest service and support information.

- Worldwide contact telephone numbers
- Product support information
  - Product FAQs
  - Software, patches, and updates
  - Training for many applications and instruments
- Order and web support
- Product documentation
  - User guides, manuals, and protocols
  - Certificates of Analysis
  - Safety Data Sheets (SDSs; also known as MSDSs)

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**Note:** For SDSs for reagents and chemicals from other manufacturers, contact the manufacturer.

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## Obtaining support

For service and technical support:

- Call Toll-Free in US: 1 800 955 6288
- Email [instrumentservices@lifetech.com](mailto:instrumentservices@lifetech.com)

For the latest services and support information for all locations, go to:

[thermofisher.com/support](http://thermofisher.com/support)



At the website, you can:

- Access worldwide telephone and fax numbers to contact Technical Support and Sales facilities
- Search through frequently asked questions (FAQs)
- Search for user documents, SDSs, vector maps and sequences, application notes, formulations, handbooks, certificates of analysis, citations, and other product support documents
- Obtain information about customer training
- Download software updates and patches

## Limited product warranty

Life Technologies Corporation and/or its affiliate(s) warrant their products as set forth in the Life Technologies' General Terms and Conditions of Sale at [www.thermofisher.com/us/en/home/global/terms-and-conditions.html](http://www.thermofisher.com/us/en/home/global/terms-and-conditions.html). If you have any questions, please contact Life Technologies at [www.thermofisher.com/support](http://www.thermofisher.com/support).



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