applied biosystems

Applied Biosystems® 3500/3500xL Genetic Analyzer

with 3500 Series Data Collection Software 3.1

Catalog Number 4405186, 4405187

Publication Number 100031809

Revision B

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

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Contents

About this guide

CAUTION! ABBREVIATED SAFETY ALERTS. Hazard symbols and hazard types specified in procedures may be abbreviated in this document. For the complete safety information, see the "Safety" appendix in this document.

IMPORTANT! Before using this product, read and understand the information in the "Safety" appendix in this document.

Revision history

Revision	Date	Description
B	26 May 2017	Add 'Radio compliance'. Update conformity symbols. Update licensing information.
A	March 2015	New information for version 3.1 software: Change buffer and polymer limits to 14 days. Updates: Information for 96-sample polymer pouches. Instruction to ensure CBC septum is properly seated. New run modules. Corrections: Remove sample limits on buffer. Correct part numbers for 3500/3500xL Sequencing Standards, BigDye® Terminator v1.1 and BigDye® Terminator (BDT) v3.1 Sequencing Standards, 3500/3500xL. Change instruction to seal 384-well plates from film to septum. Update description in "Evaluate fragment install standard data".

1 Instrument and software description

Instrument and software description

Overview

The Applied Biosystems® 3500/3500xL Genetic Analyzer with 3500 Series Data Collection Software 3.1 is a fluorescence-based DNA analysis instrument using capillary electrophoresis technology with 8 or 24 capillaries.

The 8-capillary model (Part no. 4405186) and the 24-capillary model (Part no. 4405187) is shipped with 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

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 (Life Technologies).

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 8 inches (20 cm) of this instrument if you have a patient-worn and/or implanted active medical device.

Instrument interior components

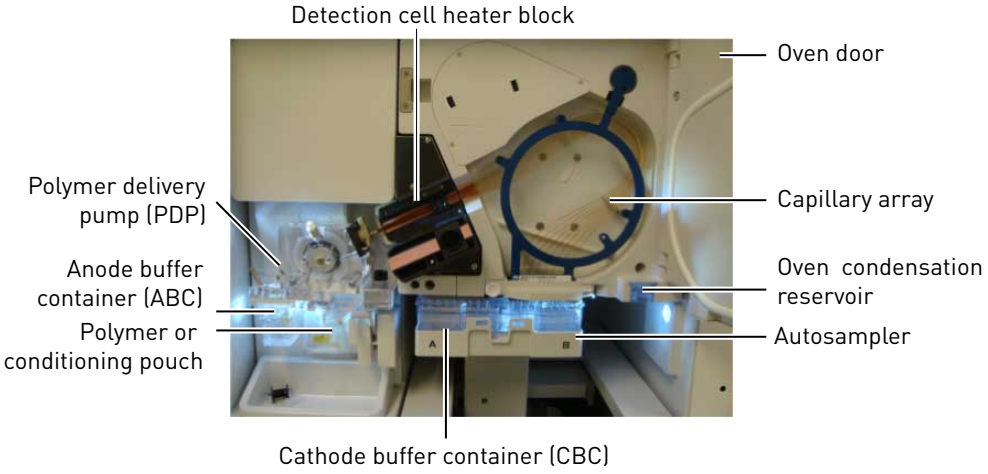


Figure 1 Instrument interior components

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.

Part	Function
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	• **Polymer pouch** – Supplies polymer to the polymer delivery pump. • **Conditioning reagent pouch** – 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.
Radio frequency identification (RFID) (for more information, see Appendix F, "Radio Frequency Identification (RFID) technology").	RFID tags on the following primary instrument consumable labels are detected by read/write units in the instrument interior: • Capillary array • Cathode buffer container (CBC) • POP™ polymer • Anode buffer container (ABC) The instrument reads and tracks the following information: • Lot numbers • Serial numbers • Dates (expiration) • Capacity (usage) 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.

Instrument front panel indicators

Indicator	Status
All lights off	Instrument off
Green light	Idle
Green light (blinking)	Run is in progress **Note:** 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 software, then repeat the run.
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 253).

Instrument and computer requirements

IMPORTANT! Do not modify the instrument hardware or software without notifying Life Technologies. Any modifications must be made by Life Technologies under change control.

Windows® software requirements

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.

We recommend Norton Antivirus, which has been tested and approved for use with the Applied Biosystems® 3500/3500xL Genetic Analyzer with 3500 Series Data Collection Software 3.1.

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 3500 Series Data Collection Software 3.1 is installed. The instrument computer has been assigned a unique name. Changing the name may cause the 3500 Series Data Collection Software 3.1 to malfunction.

Instrument firmware

Instrument firmware is to be updated only by a Life Technologies representative.

Theory of operation

Preparing samples

When DNA samples are prepared for sequencing and fragment analysis on the 3500/3500xL Genetic Analyzer, 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 “Run a spatial calibration“ on page 106.
- Spectral calibration – Generates a matrix for each capillary that compensates for dye overlap and is used to convert the 20-color data into 4-, 5-, or 6-dye data. For more information, refer to “Perform a spectral calibration“ on page 113.

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-color data for each capillary.
- Converts the 20-color 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.

If the autoanalysis functionality has been set up, the system transfers the sample data to a secondary analysis software application for further processing. Alternatively, you can manually transfer the sample data to a secondary analysis software application for further processing.

Materials for routine operation

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

- See Appendix D, "Part numbers"
- Contact your local Life Technologies 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 "Documentation and support" on page 311.

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.

For application-specific reagents, consumables, and run modules, see Appendix B, "Run modules and dye sets".

Buffers

Cat. no.	Description	Storage conditions
4393927	Anode Buffer Container (ABC) 1X running buffer, 4 containers	Store at 2–8°C. The 1X running buffer has been qualified to ship at ambient conditions. For a description of the qualification, visit **lifetechnologies.com/ambientbuffers**.
4408256	Cathode Buffer Container (CBC) 1X running buffer, 4 containers	

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 24.
24-capillary	14 days, 100 injections, or expiry date	

Polymer

Cat. no.	Description	Storage conditions
A26070	POP-4® Polymer (96 samples)	Store at 2–8°C.
4393715	POP-4® Polymer (384 samples)[1]	
4393710	POP-4® Polymer (960 samples)[1]	
A26071	POP-6™ Polymer (96 samples)	
4393717	POP-6™ Polymer (384 samples)	
4393712	POP-6™ Polymer (960 samples)	
A26073	POP-7™ Polymer (96 samples)	
4393708	POP-7™ Polymer (384 samples)	
4393714	POP-7™ Polymer (960 samples)	

[1] The polymer has been validated for HID applications.

IMPORTANT! For the POP-7™ Polymers (Cat. nos. A26073, 4393708, and 4393714), the on-instrument supported limit is 14 days only when the instrument operating temperature is ≤ 25°C. When the instrument operating temperature is > 25°C, the supported limit is 7 days.

Pouch size	Instrument	On-instrument supported limits[1] 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 24.
	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	

[1] 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 conditions
4393718	Conditioning reagent, 1 pouch	Store at 2 to 8°C. After removing from storage, use the pouch within 24 hours.

On-instrument supported limits	Guidelines
Once installed on the instrument, the pouch is good for a one-time use.	Refer to the expiration date on the label. See "Important notice regarding use of consumables that exceed supported limits" on page 24.

Capillary arrays

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

Cat. no.	Description	Storage conditions
4404685	8-Capillary, 50 cm	Ambient temperature
4404689	24-Capillary, 50 cm	
4404683	8-Capillary, 36 cm	
4404685	24-Capillary, 36 cm	

On-instrument limits	Guidelines
160 injections or expiration date listed on packaging and RFID label	Capillary arrays have been verified for use for 160 injections. 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 24. 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.

IMPORTANT! Excessive freeze/thaw cycles or storage at 2 to 8°C may cause hydrolysis into formic acid and formate. Formate ions migrate preferentially into the capillary during electrokinetic injection causing a loss of signal intensity.

Material	Part no.	Storage conditions	Guidelines
Hi-Di™ Formamide (4 5-mL bottles)	4440753	2° to 8°C for ≤ 1 week –15° to –25°C	To minimize freeze-thaw cycles, aliquot the contents from the original bottle into one-time use tubes.
Hi-Di™ Formamide (25-mL bottle)	4311320		

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:

Life Technologies 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 Life Technologies product warranty or service plan. Customer use of expired consumables is at customer's own risk and without recourse to Life Technologies. 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 Life Technologies 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 Life Technologies representative if you have further questions.

Overview of the 3500 Series Data Collection Software 3.1

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: Sizecalling

Dashboard

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

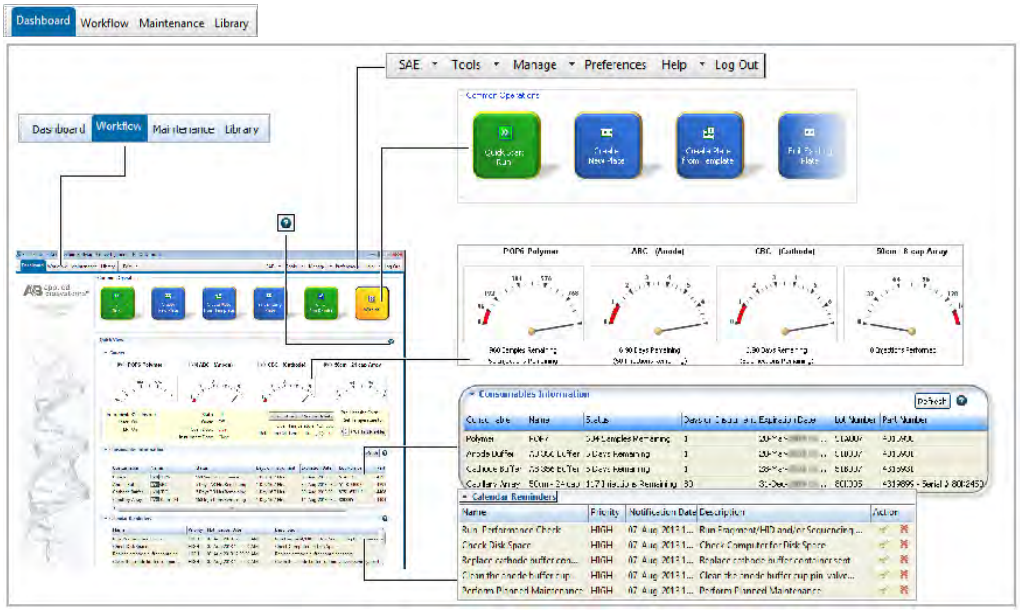


Figure 2 Dashboard overview

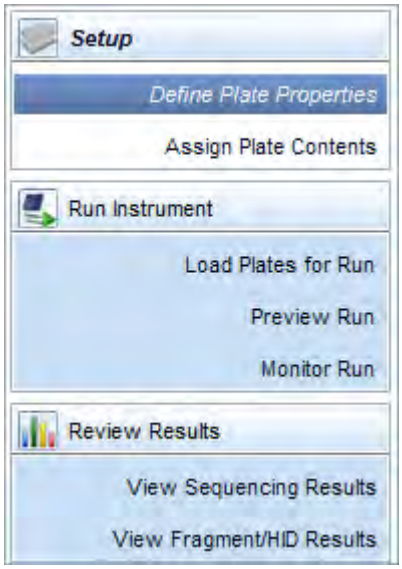
The Dashboard gives you quick access to the information and tasks you need to set up and run:

- **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.

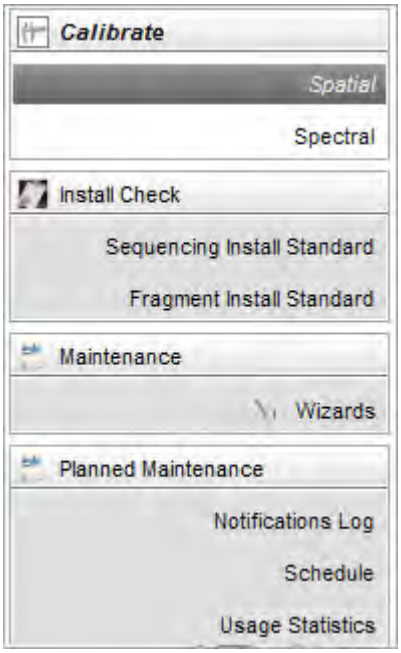
You can click **Dashboard** or any other tab item at any time to advance from the Workflow.

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.

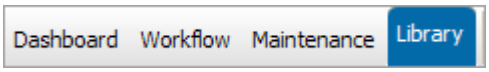
You can click **Main Workflow** or **Dashboard** or select any other menu item at any time to advance from the Maintenance workflow.

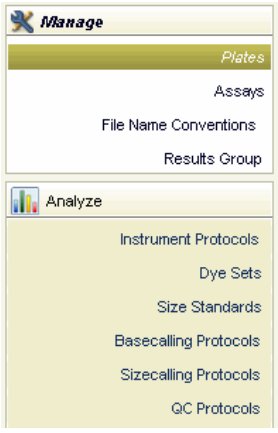


The Maintenance workflow is described in Chapter 9, "Maintain the Instrument".

Library workflow

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





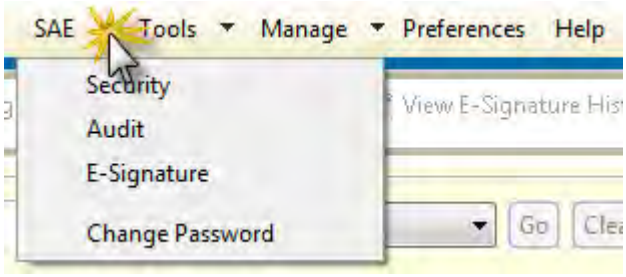
The Library contains items that you manage plates, assays, file name conventions, and results groups that you use to acquire and process data.

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

SAE menu

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

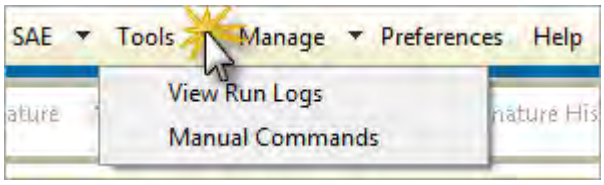
Select **SAE** in the menu bar to access:



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

Tools menu

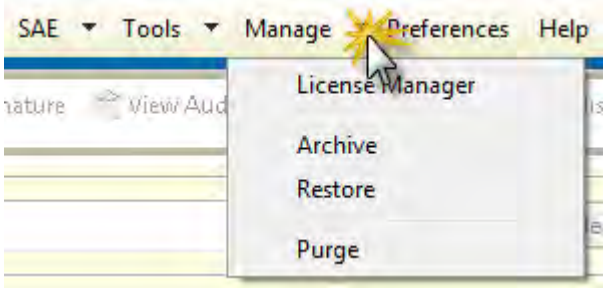
Select **Tools** in the menu bar to access:



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

Manage menu

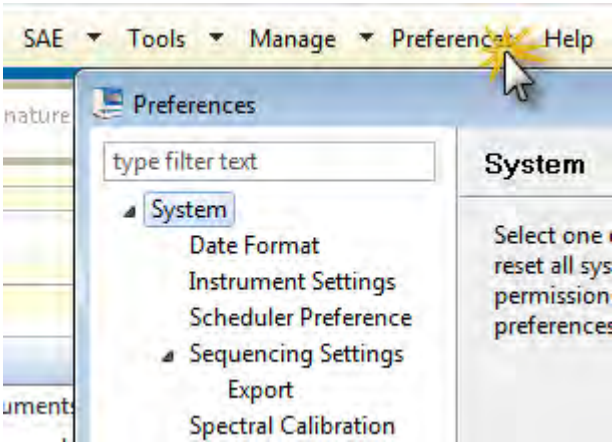
Select **Manage** in the menu bar to access:



- **Archive**, **Restore**, and **Purge** functions
- **License Manager** to renew the software license

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 3500 Series Data Collection Software 3.1 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 3500 Series Data Collection Software 3.1 is installed. The instrument computer has been assigned a unique name. Changing the name may cause the software to malfunction.

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2 Start the system

Workflow

Power on the computer (do not log in), then power on the instrument (see "Start the computer and instrument" on page 31)

▼

When the green front panel indicator stops blinking, log in to Windows® operating system, then start the software (see "Start the software" on page 32)

▼

"Check calendar reminders" on page 34

▼

"Check consumables status" on page 35

▼

"Replenish consumables" on page 37

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 3500 Series Data Collection Software 3.1 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 18.

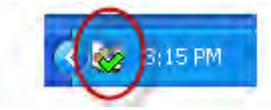
   b. If desired, press the Light button to turn on the interior light.
   c. Check the instrument status. Ensure the green status light is on and not flashing before proceeding. See indicator descriptions in "Instrument front panel indicators" on page 18.

6. Log on to the Windows® operating system.

Start the software

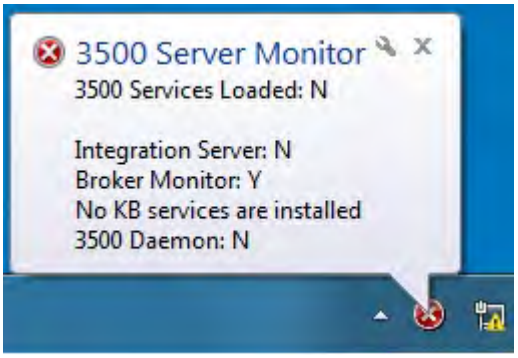
Step one: Start the Server Monitor

1. After you log on to the Windows® operating system, wait ~1 to 2 minutes.
2. Look in the Windows® taskbar at the bottom right of the desktop.



   If the Server Monitor icon is displayed, go to "Step two: Start the 3500 Series Data Collection Software 3" on page 33 below.

3. Select ▸ **Programs** ▸ **Applied Biosystems** ▸ **3500** ▸ **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 3" on page 33 below.

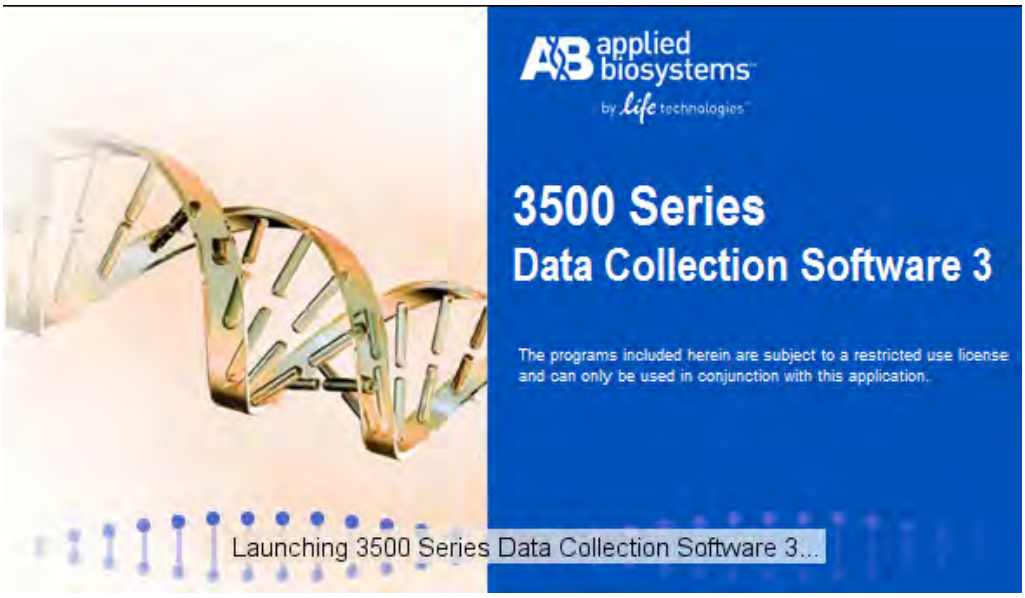


IMPORTANT! If the Server Monitor icon does not change to , you cannot start the software. See "Software troubleshooting — general" on page 263 for more information.

Step two: Start the 3500 Series Data Collection Software 3

Select **Start** ▸ **Programs** ▸ **Applied Biosystems** ▸ **3500** ▸ **3500**.

The 3500 Series Data Collection Software 3.1 splash screen is displayed for a few seconds, then the 3500 Series Data Collection Software 3.1 **Login** dialog box opens.



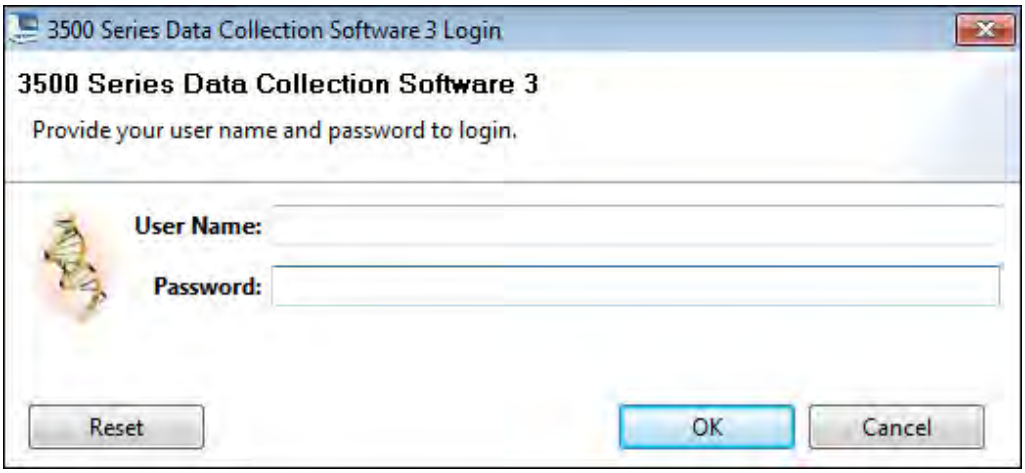
Step three: Log in

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

In the 3500 Series Data Collection Software 3.1 **Login** dialog box:

Enter your **User Name** and **Password**, then click **OK**. See your 3500/3500xL Genetic Analyzer system administrator for log in information.

Note: For information on creating user accounts, see Chapter 8, "Use Security, Audit, and E-Sig functions (SAE Module)".



Check system status in the Dashboard

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

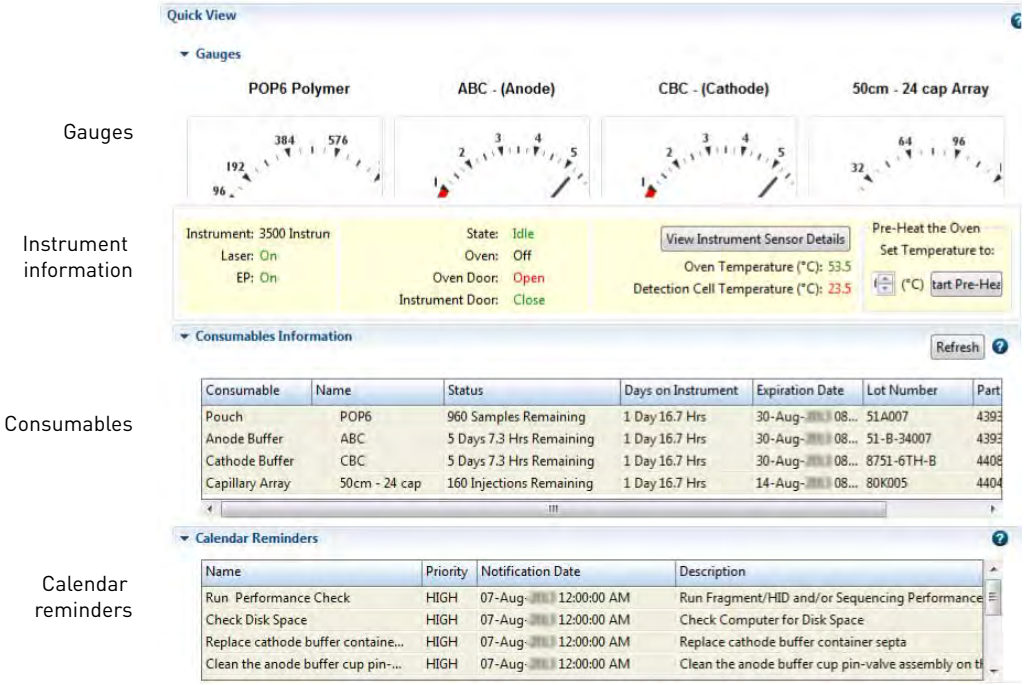
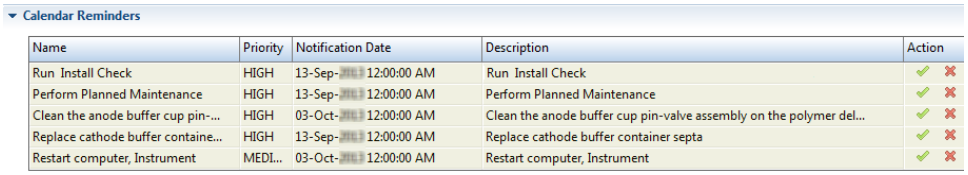


Figure 3 Dashboard

Check calendar reminders

The **Calendar Reminders** section displays reminders for the tasks listed in the schedule (see "As-Needed instrument maintenance tasks" on page 228). You can set the time to trigger calendar reminders in **Preferences**.

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



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 230.

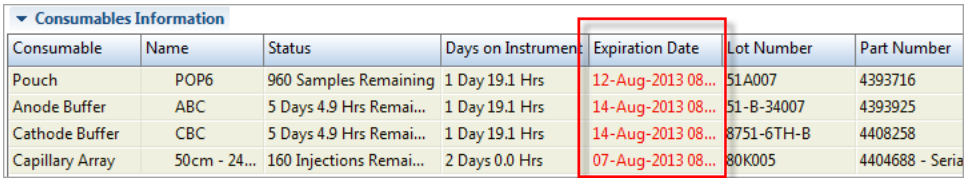
3. Perform any daily, monthly, or quarterly tasks that are not listed in the Calendar Reminders pane (see "Maintenance schedule" on page 225).

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).

Consumable	Name	Status	Days on Instrument	Expiration Date	Lot Number	Part Number
Pouch	POP6	960 Samples Remaining	1 Day 19.6 Hrs	23-Aug-[redacted] 08...	[redacted]	[redacted]
Anode Buffer	ABC	5 Days 4.4 Hrs Remai...	1 Day 19.6 Hrs	30-Aug-[redacted] 08...	[redacted]	[redacted]
Cathode Buffer	CBC	5 Days 4.4 Hrs Remai...	1 Day 19.6 Hrs	30-Aug-[redacted] 08...	[redacted]	[redacted]
Capillary Array	50cm - 24...	160 Injections Remai...	2 Days 14.6 Hrs	15-Aug-[redacted] 08...	[redacted]	[redacted]

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.



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 - Seria

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 21 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 two days before the polymer should be replaced.

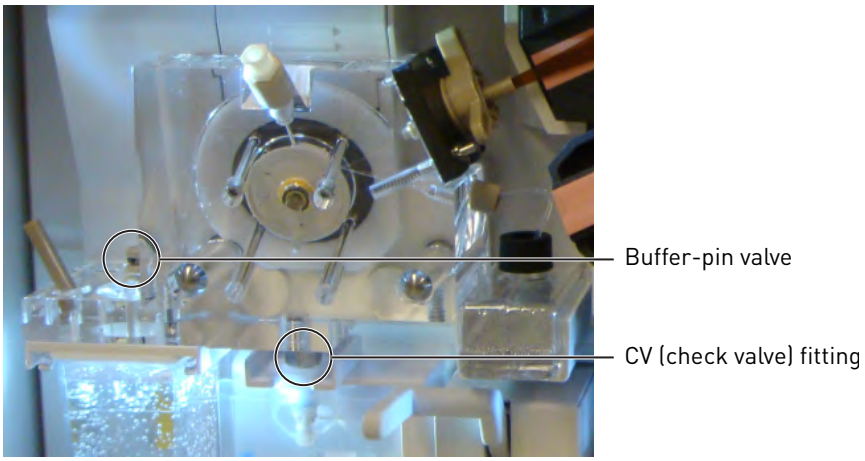
How the polymer sample and injection counters calculate usage

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. Inspect the instrument interior.
2. Wipe any spills.
3. Check for leaks around the Buffer-Pin Valve, check valve, and array locking lever.



4. Remove dried residue and ensure that the array locking lever is pushed securely in place.

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:

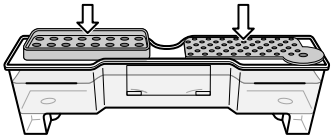
- "Replenish polymer or change polymer type" on page 235

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

- "Install the anode buffer container (ABC)" on page 231
- "Install the cathode buffer container (CBC)" on page 232
- "Fill capillary array with fresh polymer" on page 236
- "Install or change the capillary array" on page 237

Ensure proper installation of CBC septa

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

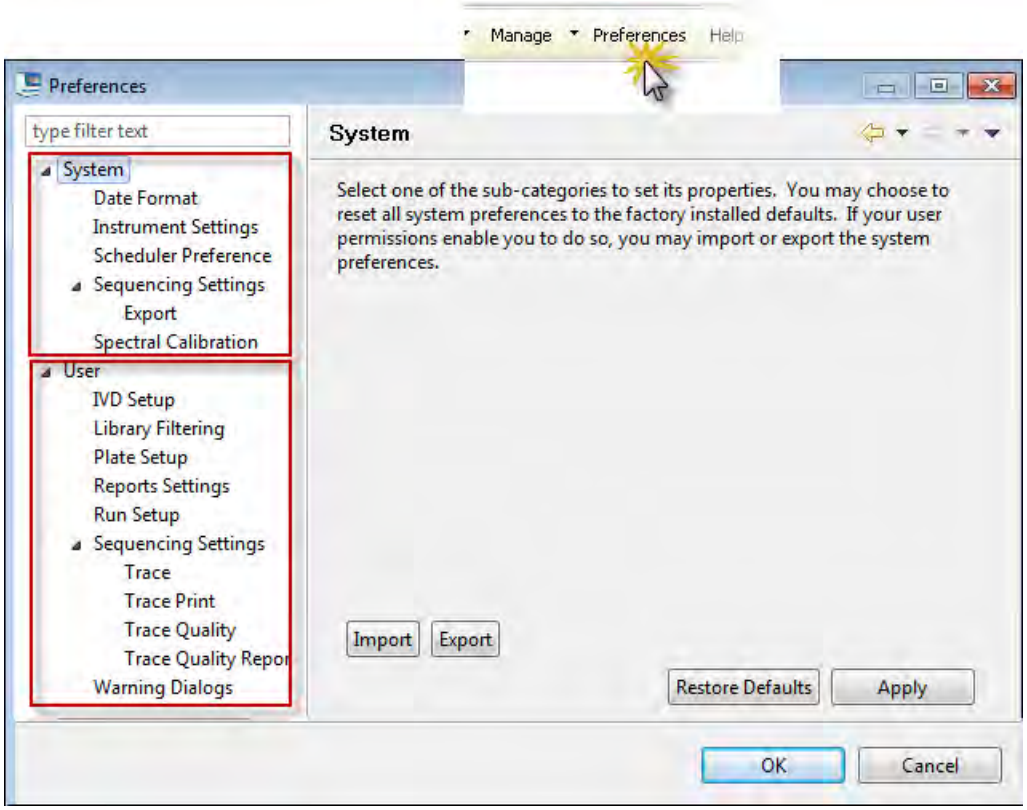


IMPORTANT! Look at the CBC from the side and ensure there is no gap between the container and the lip of the septum.

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, 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 77.

System preferences

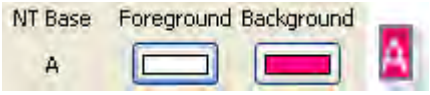
In the **Preferences** dialog box, click a system preference, select a setting, then click **Apply** to save the preference.

System preference	Sets
Date Format	Date and time format for the software.
Instrument Settings	• Instrument name (appears in the **Dashboard**, reports, file name conventions, instrument sensor details, view sequencing results.) **Note:** If you have multiple instruments, you can assign each instrument a unique instrument name. • 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. • Number of runs to preserve in the **Run Log** (accessed by selecting **Tools ▸ View Run Logs**).
Scheduler Preference	Time for calendar reminders to be displayed in the Dashboard (see "Check calendar reminders" on page 34).
Spectral Calibration	Number of allowed borrowing events for spectral calibration (see "What you see during a spectral calibration" on page 118).
Sequencing Settings Export	Default file types for files exported during a sequencing run. Exported files are stored in the same directory as the .ab1 files: • *.annotation.txt — Information from the Annotation tab in the sequencing trace view such as data collection time, run time start finish • *.phd.1, *.scf - Sequencing files • *.fsta, *.qual, *.seq - Reference files - specify Entire Sequence or Post-trim Sequence Only

User preferences

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

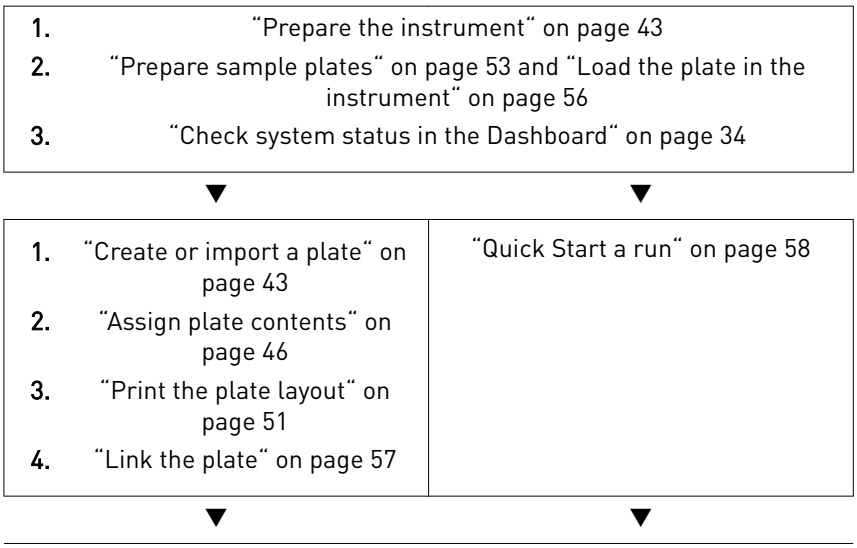
User preference	Sets
IVD Setup Workflow	Not supported.
Library Filtering	Default filter for items displayed in the **Open Plate from Library** dialog box, the **Plates** library, and the **Assays** library. You can set the filter to include only one application type, 8- and/or 24-capillary-specific items, 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. Example: To exclude only items named "ABC", enter ABC . To exclude items named "ABCDE", enter ABC* . To exclude items named "123ABC", enter *ABC . You can disable filters in each location to display all items.
Plate setup	Default settings for plate name.
Reports Settings	Default font and text size and custom logo in reports. **Note:** You can override this setting in each report view.

User preference	Sets
Run Setup	• Default storage location for data files in file name conventions and results groups. **Note:** You can override this setting in file name conventions and results groups. • **Pause After Last Injection** — When enabled, allows reinjection of the last injection by pausing after the last injection is complete (before completing the run).
Sequencing Settings Trace	Default settings for color representation of nucleotide and quality value bars in the **Trace View** in **View Sequencing Results**: • **NT (nucleotide) Base Color** — 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.  • **Pure Base and Mixed Base QV Colors** — Sets the colors and ranges for pure and mixed base QVs (quality values) displayed in the **Trace View**:  **a.** Click a pure base or mixed base color bar to select a new color. **b.** Place the mouse pointer over a slider, then drag to set a new range. We recommend that you set the following ranges for QVs: – 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).
Sequencing Settings Trace Print	Settings for sequencing trace reports: Type of trace data, specific print settings, and Y-Scale.
Sequencing Settings Trace Quality	Quality ranges for: • **QC report** — Trace Score and CRL • **Plate report** — Trace Score Set colors and ranges: **a.** Click a color bar to select a new color. **b.** Place the mouse pointer over a slider, then drag to set a new range. 

User preference	Sets
Sequencing Settings **Trace Quality Report**	Content and formatting used in QC, Plate, Trace Score, CRL, QV20+, and Signal Strength reports: • **Sort data** — Sort data in **Trace Score**, CRL, QV20+, and **Signal Strength Reports** based on Run Name or Capillary Number. • **Signal based on** — Base signal in QC and **Signal Strength Reports** based on Average Raw Signal Intensity or Average Raw Signal to Noise Ratio. • **Display well image by** — Specify the thumbnail option for Plate Reports: Wider thumbnail without file name or Smaller thumbnail without file name.
Warning Dialogs	Suppress warning messages for deleting an injection or exporting a library item.

3 Set up and run

Setup workflow



1. "Load plates for run and create the injection list" on page 59
2. "Review and modify the injection list in Preview Run" on page 63
3. "Start the run from Preview Run" on page 64
4. "Check sequence or sample quality and re-inject samples" on page 67

Prepare the instrument

1. In the **Dashboard**, check consumables status "Check consumables status" on page 35). Ensure that:
   - Consumables are not expired
   - Adequate injections remain for consumables
2. Ensure that buffer levels are at the fill lines ("Check buffer fill levels" on page 37).
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). Preheating 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 239).

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 (sequencing examples shown). Plate template names reflect the run module associated with the plate. The run module contains data collection settings.

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...

Appendix Appendix B, "Run modules and dye sets" lists the run time and size range collected for each run module.

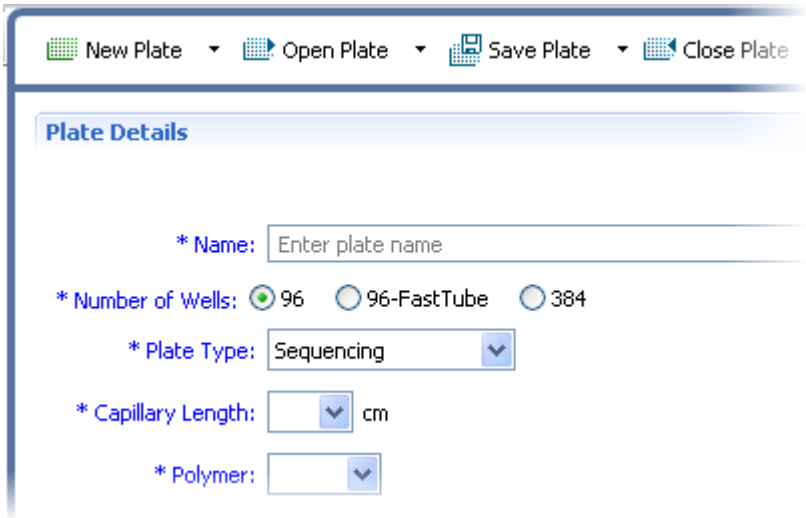
You can also create your own templates. In addition to defining plate parameters, a plate template can also contain a list of the appropriate assays for an application. For more information, see "Create a plate template" on page 80.

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. For more information, see "Create a plate from a template" on page 44.

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**.



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 145.

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 46.

Import a plate

1. Do either of the following:
   - Create a plate on another 3500 Series Data Collection Software 3 computer, then export (see "Import and export a plate" on page 80).
   - Create a plate import file (see "Create a plate import file" on page 79.

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:

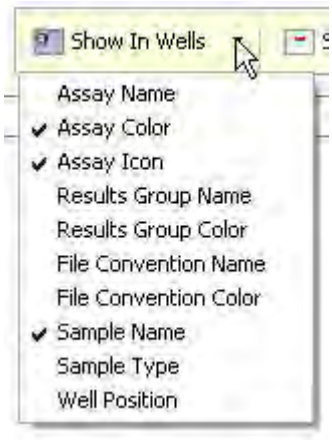
- **Sample names and sample types** (required) — Identifies the well positions of each sample for data collection and processing.
- **Assay** (required) — Specifies the parameters that control data collection and primary analysis (basecalling or sizing). All named wells on a plate must have an assigned assay. For more information on assays, see "Assays library" on page 147.
- **Filename convention** (*optional*) — Specifies file naming. For more information, see "File name convention overview" on page 150.
- **Results group** (*optional*) — Specifies sample data file storage. For more information on assays, see "Results Group overview" on page 155.

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 4 shows the Plate View of the Assign Plate Contents screen.



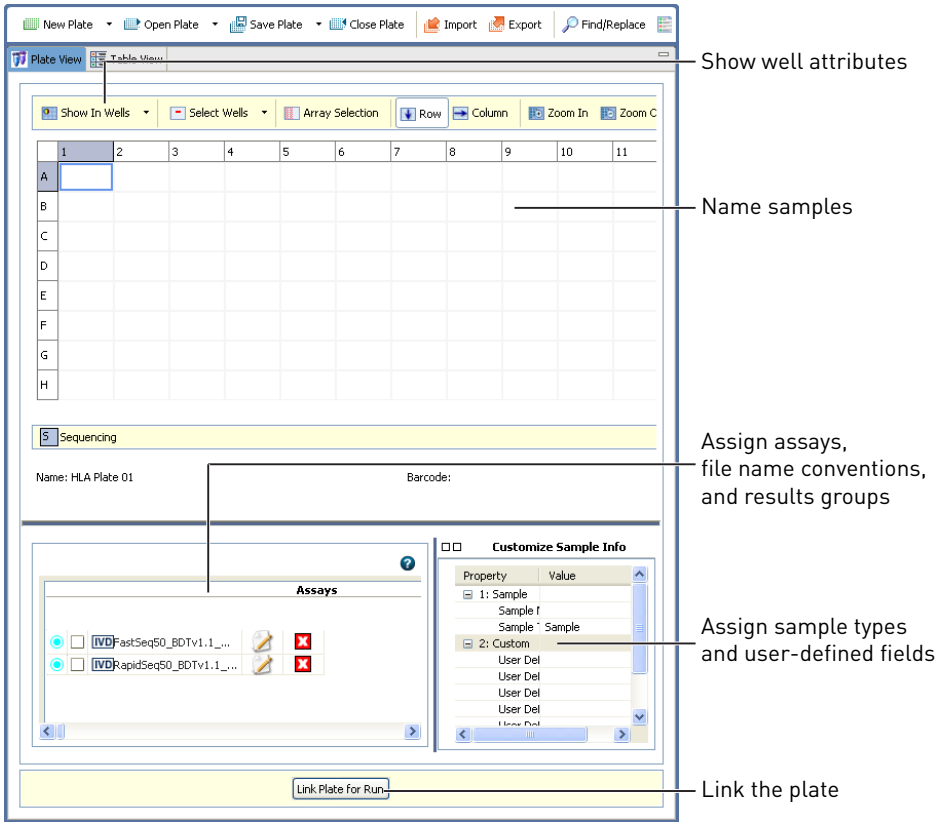
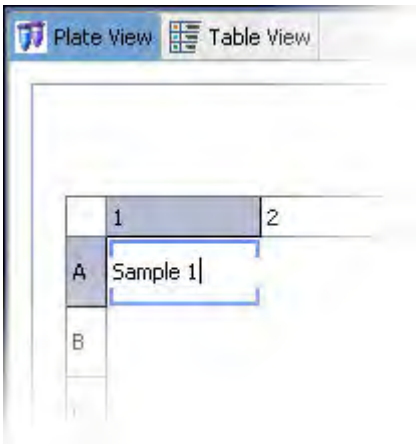


Figure 4 Assign plate Contents

Name samples and assign sample types in the plate view

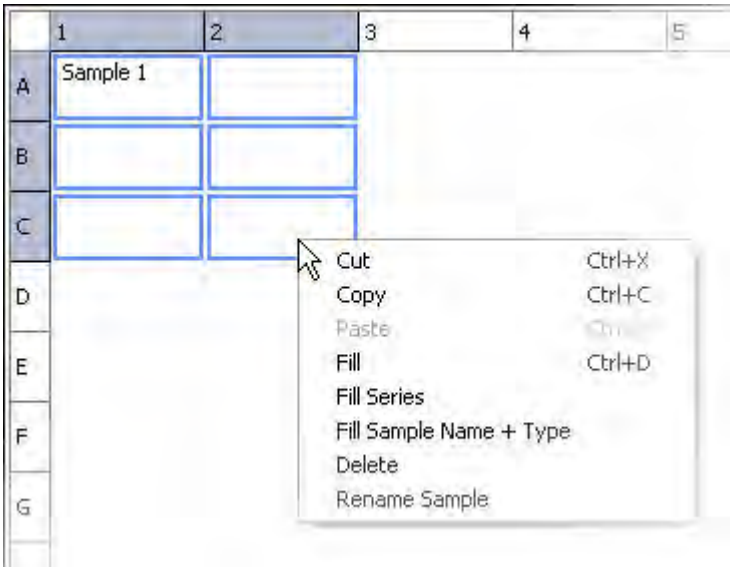
Note: For other ways to name samples, see "Name samples in the plate view" on page 74 and "Use the table view" on page 76.

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.



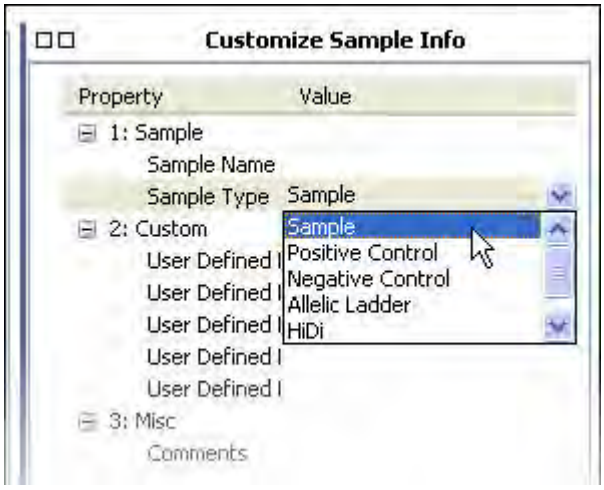
Note: To use Fill Series, type a number as the last character of the named well. The number will increment for each well in the series.

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

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

5. In the Plate View, click-drag to select the wells of interest.

6. Specify the **Sample Type** for the selected wells, then press **Enter**.

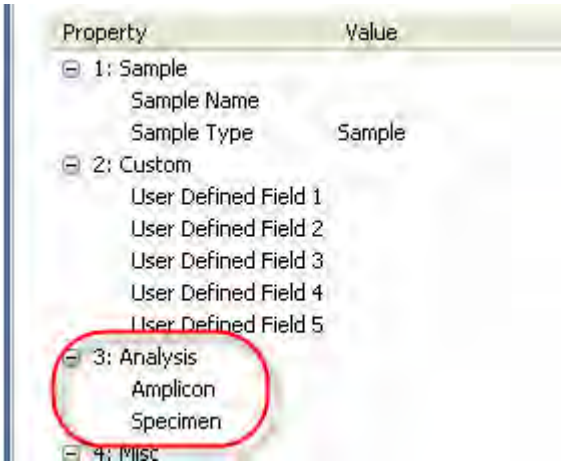


7. (*Optional*) Specify **User Defined Fields** and **Comments**. User Defined Fields contain additional attributes you can assign to a plate and are displayed only in Table View.

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.

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



9. Repeat steps step 6 through step 8 to assign the Sample Type for all named wells.

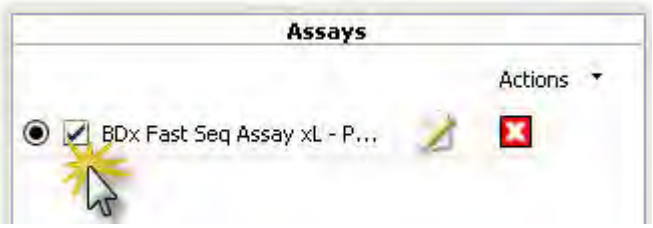
10. Go to "Assign assay, file name convention, and results group in the plate view" on page 50

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 78.

1. Select the wells for which to specify an assay.

2. Select the checkbox next to the assay name to assign the assay to the selected wells.



3. Repeat for file name conventions and results group.

4. Select **Save Plate**.

5. Go to "Print the plate layout" on page 51.

How file location in file name conventions and results groups work

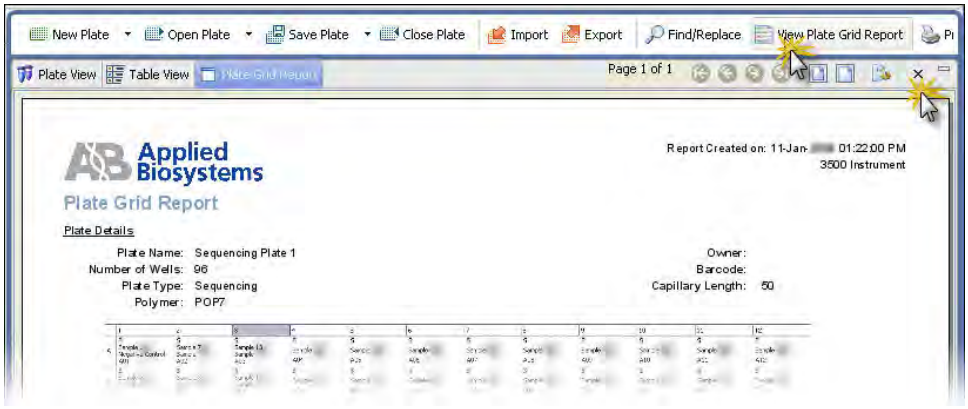
If you do not specify a file name convention, data files are named in this format: `<sample name>_<well>`.

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 39).

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 **CutePDF Writer** as the printer.
4. Close the report.
5. Go to "Prepare and load sample plates" on page 51.

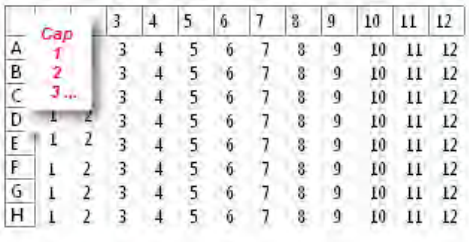
Prepare and load sample plates

IMPORTANT! Do not use warped or damaged plates.

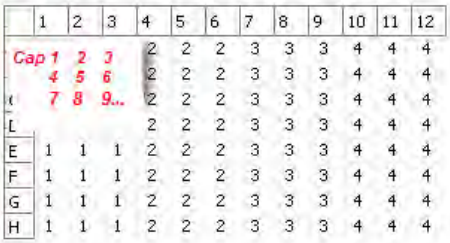
Capillary-to-plate mapping

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

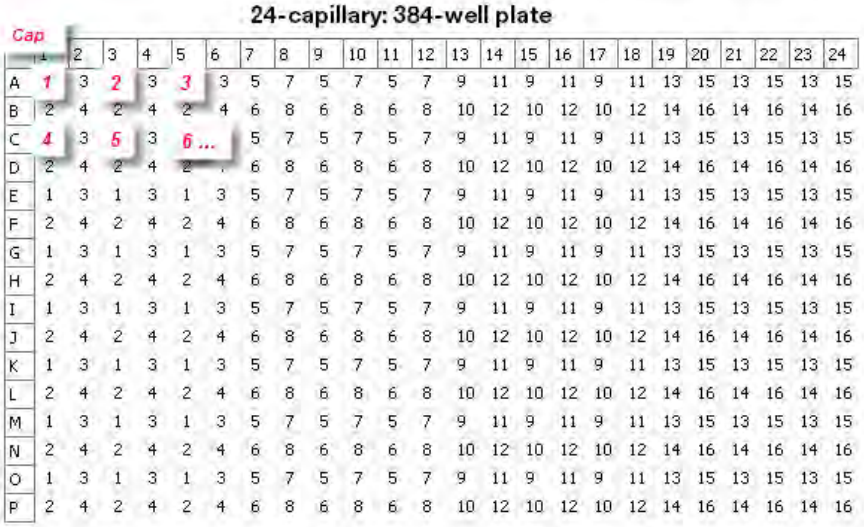
8-capillary: 96-well plate



24-capillary: 96-well plate



24-capillary: 384-well plate



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

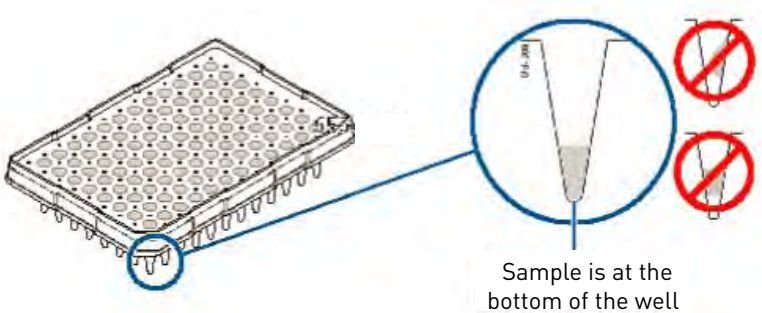
For a 24-capillary instrument, create a results group that specifies an injection folder, then select this results group for all injections on the plate.

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 161.

Prepare sample plates

1. Pipet samples into the plate according to the plate layout (see "Print the plate layout" on page 51).
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.

   
   Sample is at the bottom of the well

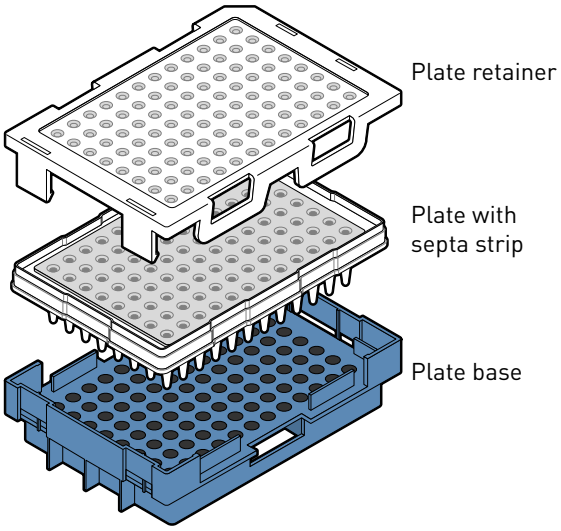
4. Store the plate on ice and protected from light until you prepare the plate assembly and load the plate in the instrument.

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 standard plates. Using the wrong plate base may affect performance. See Appendix D, "Part numbers" for plate assembly specifications and part numbers.



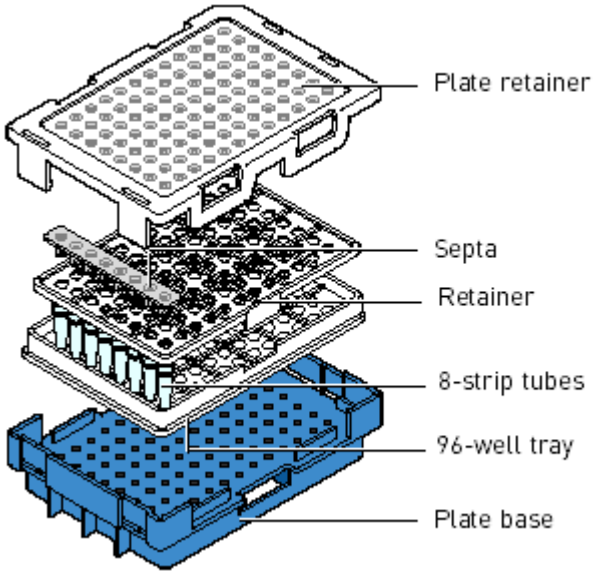
1. Align the holes in the septa strip with the wells of the plate (general purpose supply), then firmly press down on the plate until the septa clicks in to position.
2. Place the plate into the plate base.
3. Snap the plate retainer (cover) onto the plate, septa, and plate base.
4. Verify that the holes of the plate retainer and the septa strip 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 strip 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, "Part numbers" for plate assembly specifications and part numbers.



1. Place the tubes in the 96-well tray.
2. Place the retainer on the tubes.
3. Align the holes in the septa strip with the retainer, 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.
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.

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

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, "Part numbers" for plate assembly specifications and part 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.

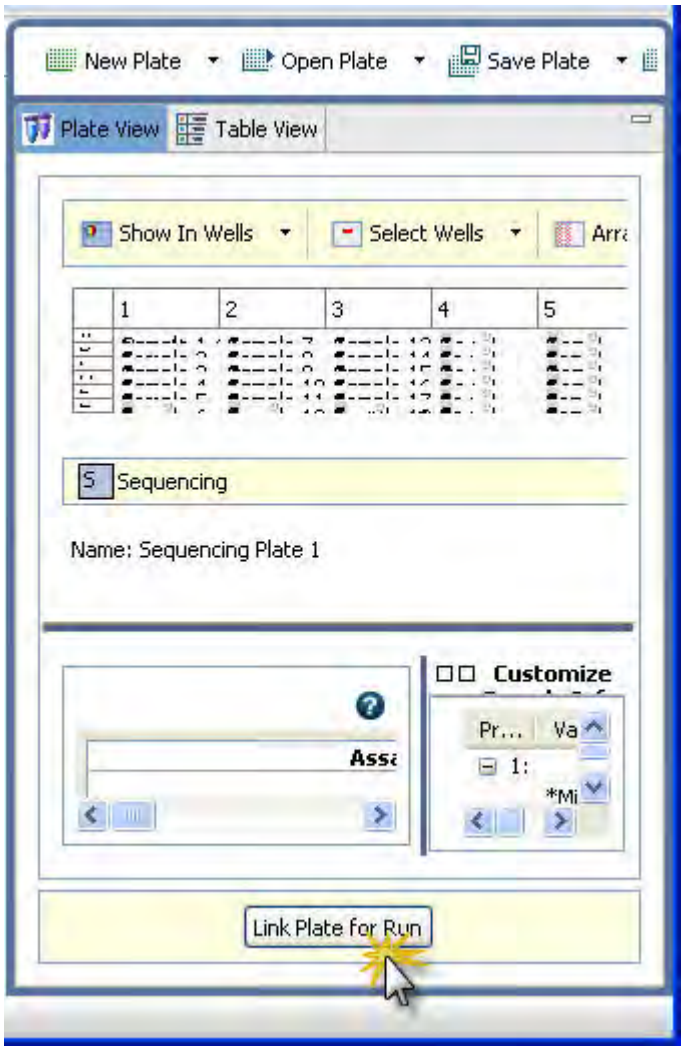
Load the plate in the instrument

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 59.

Quick Start a run

Load the plate in the instrument before proceeding (see "Load the plate in the instrument" on page 56).

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 56) and link the plate ("Link the plate" on page 57) before proceeding.

1. Access the **Load Plates for Run** screen (Figure 5) 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).

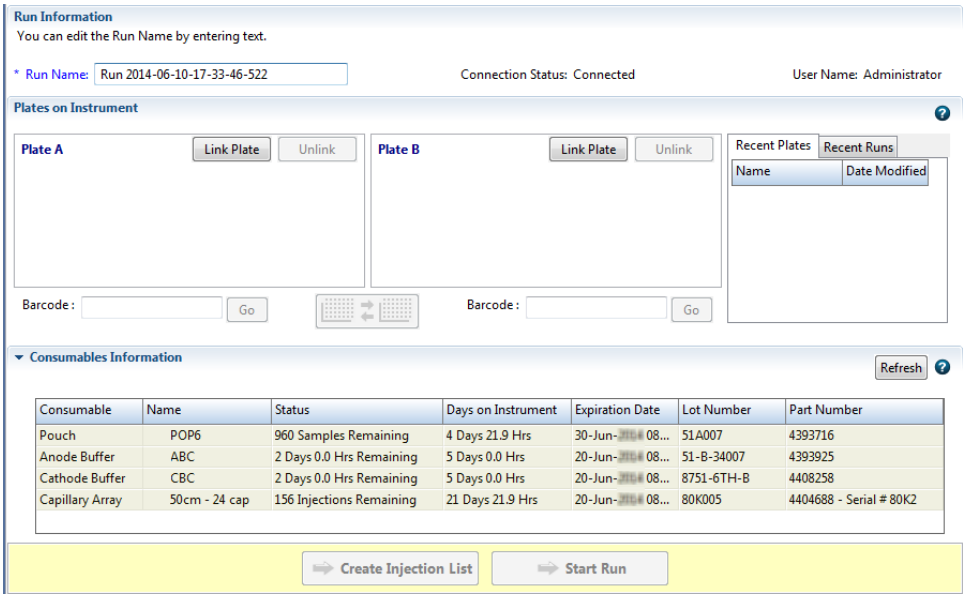


Figure 5 Load Plates for Run

4. If needed, click **Unlink**, then follow the steps in "Link a plate (if a plate is not linked)" on page 61.

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 and modify the injection list in Preview Run" on page 63.
   - **Start Run**— Displays the Monitor Run screen. Go to "Monitor the run" on page 65.

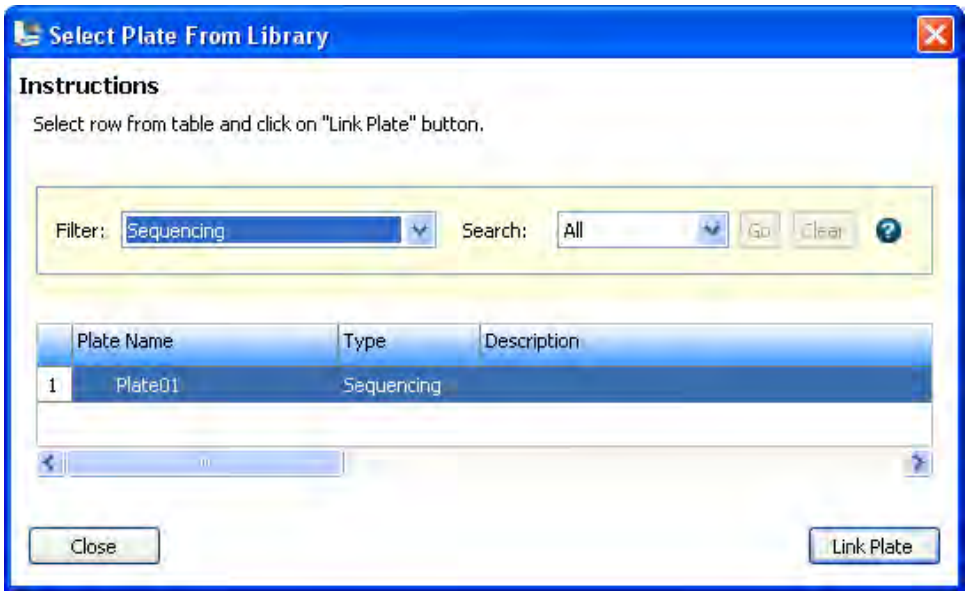
   Note: If an install check for the run application type (Sequencing or Fragment) has not been performed, a message is displayed and the run does not start.

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 and modify the injection list in Preview Run" on page 63
   - Click **Start Run**, then go to "Monitor the run" on page 65

   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 and modify 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 6) 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.

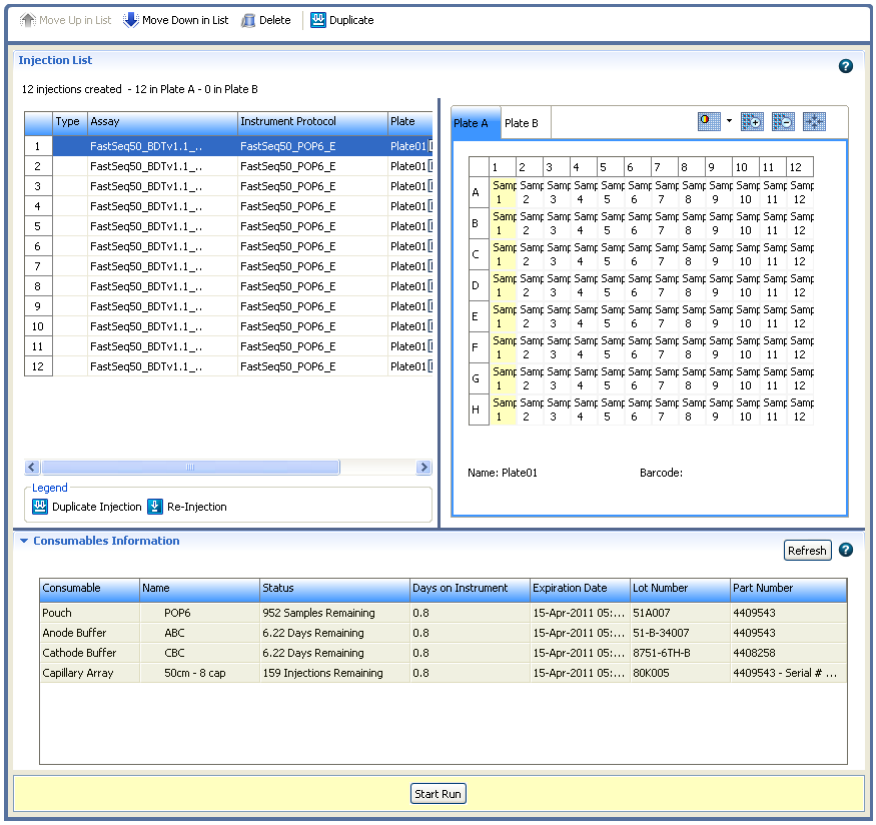


Figure 6 Preview Run screen

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.

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.

Monitor the run

The **Monitor Run** screen (Figure 7) 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.

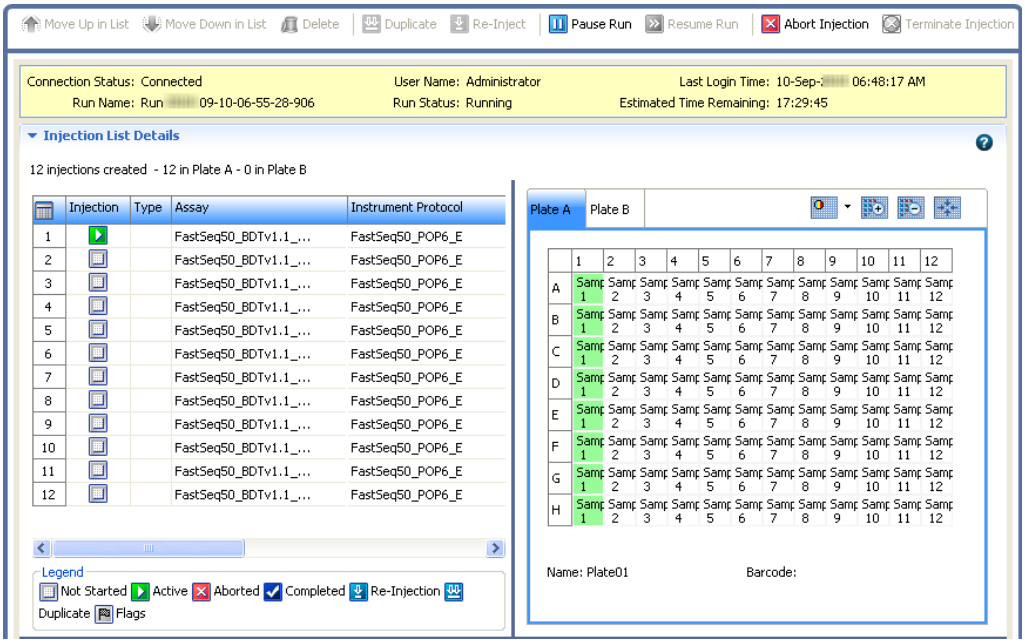
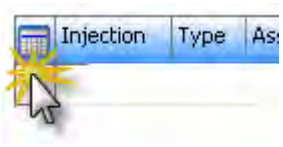


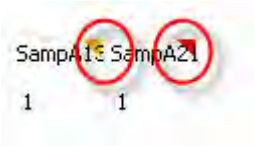
Figure 7 Monitor Run screen

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

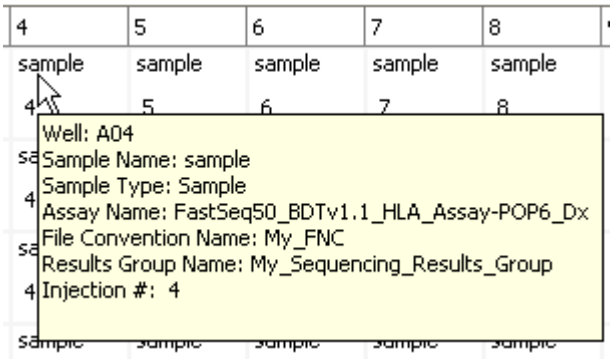


2. *(Optional)* Specify the attributes and/or display sample details:
   - Click the icon above the plate to specify the attributes to display in the plate view. In addition to the attributes available in **Preview Run**, a **Flag** attribute is available.

   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.

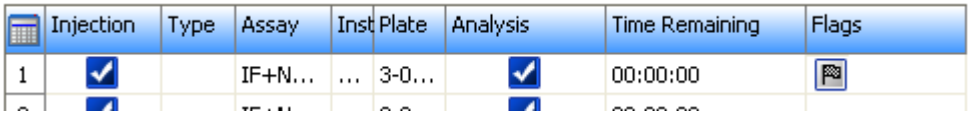


   - Place the mouse pointer over a well to display sample details.

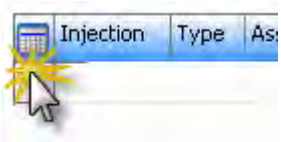


Check sequence or sample quality and re-inject samples

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 🏁.

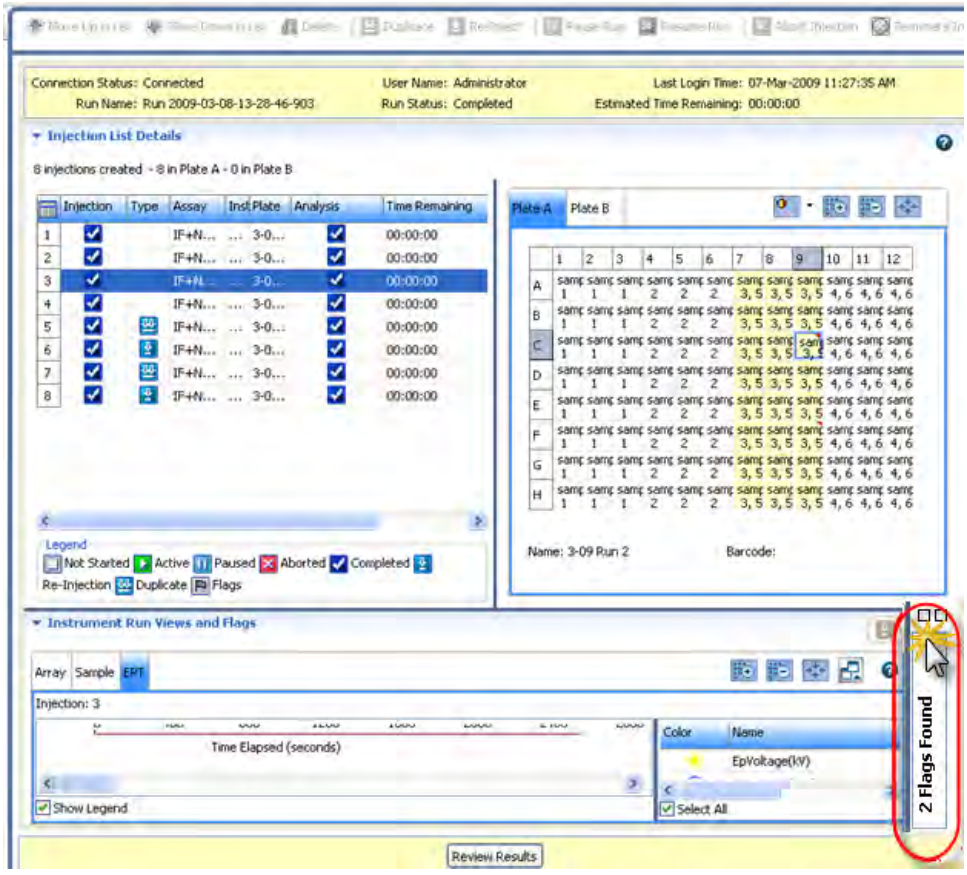


Note: If the **Injection**, **Analysis**, or **Flag** columns are not displayed, you can click the Table Settings button, then show them in the injection list.

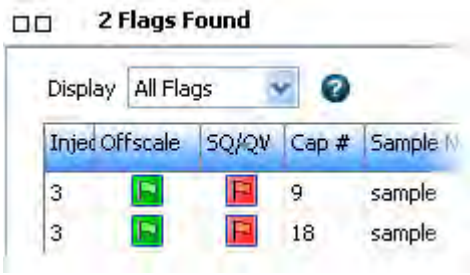


Check sequence or sample quality

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.

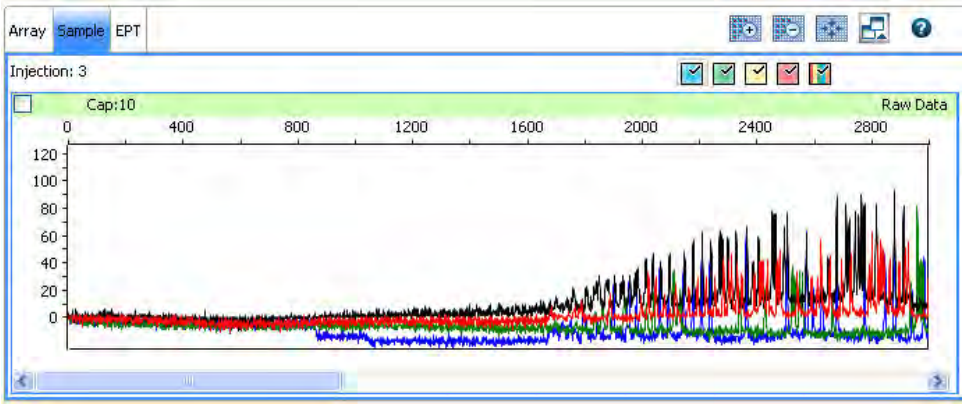
   - All samples passed
   - At least one sample is in the suspect range and requires review
   - At least one sample is offscale or is in the fail range

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. **Note:** In the **View Results** 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 180.
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 186. **IMPORTANT!** 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 39.

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

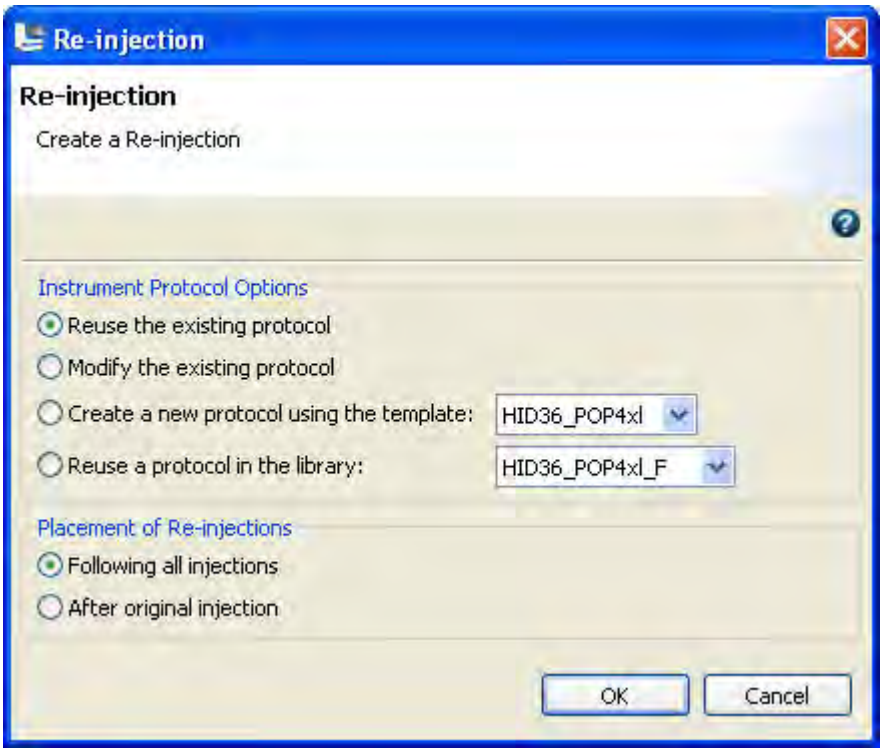
   Note: Re-inject is dimmed if you select an injection that contains more than one results group, or if you select flags in the flags table that correspond to samples with different results groups. To enable Re-inject, select samples that specify the same results group.

To collect data for all wells in an injection	1. Select the injection in the injection list. 2. Click **Re-inject**.
To collect data for only specific wells **Note:** You can also re-inject specific samples in **Review Results**.	1. Select the injection. 2. Select in the array view the capillary that corresponds to the well or sample of interest (see "Array view" on page 82) 3. Click **Re-inject**.
To collect data for only samples that contain flags	1. Select the samples in the flag table (see "Check sequence or sample quality" on page 67) 2. Click **Re-inject**.

   Note: If you are running an HID plate, see "Re-inject HID allelic ladder samples" on page 71.

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.



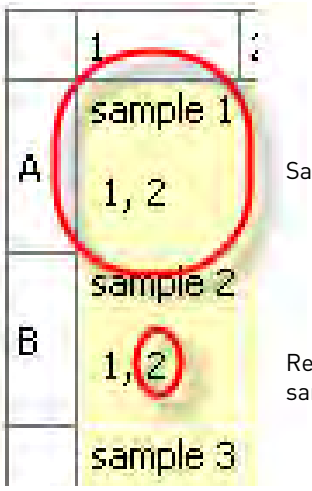
If you select a protocol other than the original

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.



Sample 1 selected for re-injection

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.

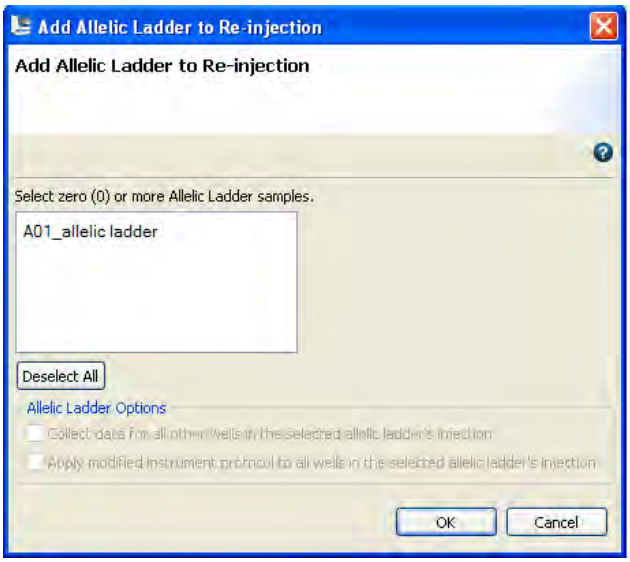
Re-inject HID allelic ladder samples

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 163)
- 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.



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 69.

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 4, "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.

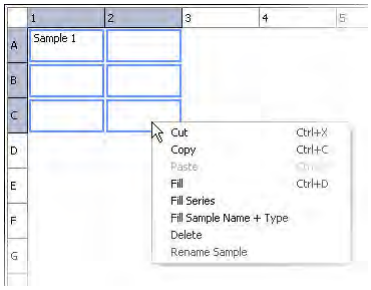
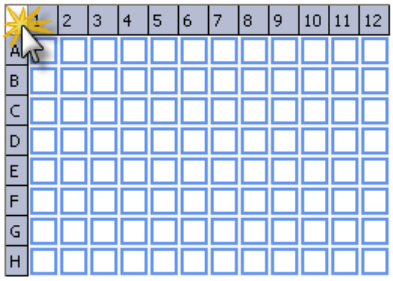
  IMPORTANT! You can stop the current injection only when the front panel indicator is blinking green. If you click **Abort** when the front panel indicator is solid green, the physical injection is already completed (although the software is still processing the information) and a message is displayed 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

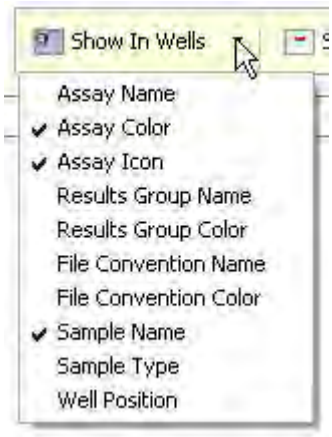
Name samples in the plate view

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

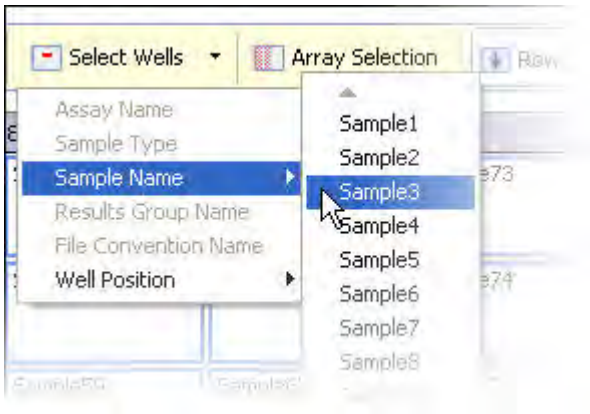
To name one sample	• Click a well, then type a sample name directly into the field, then press **Enter**. *or* • Copy and paste a name from another well. To set the direction for the cursor when you press **Enter**: Click Row to set the Enter key to move the cursor vertically to the next row. Click Column to set the Enter key to move the cursor horizontally to the next column.
To name multiple samples	• Click a named well. • Click-drag multiple wells. • 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). You can also copy and paste sample names. 
To name all wells at one time	• Select all wells. • Select assays, file name conventions, and results group for the plate. • Enter name and select sample type (in the **Customize Sample Info** pane) for the whole plate. 

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.



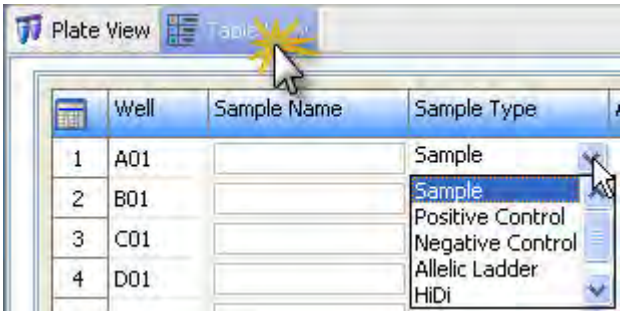
3. Click **Zoom In**, **Zoom Out**, and **Fit** as needed.

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

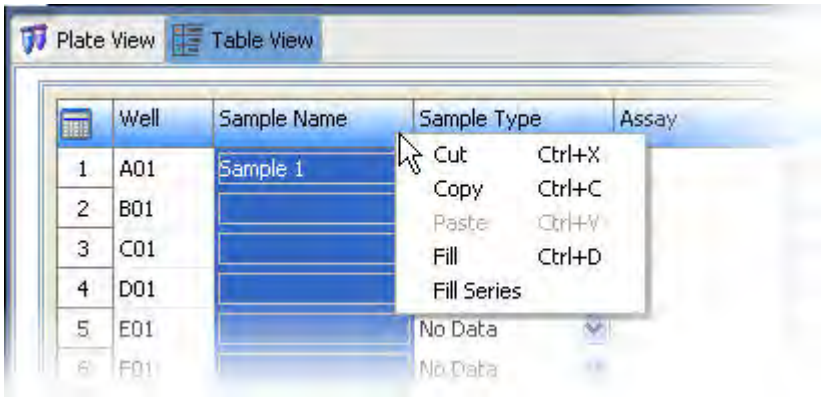
1. Click **Table View**.



2. Click the **Sample Name** field, then type a name.
3. 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 77 below).

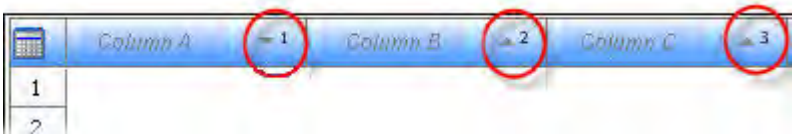


Sort by one or multiple columns

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

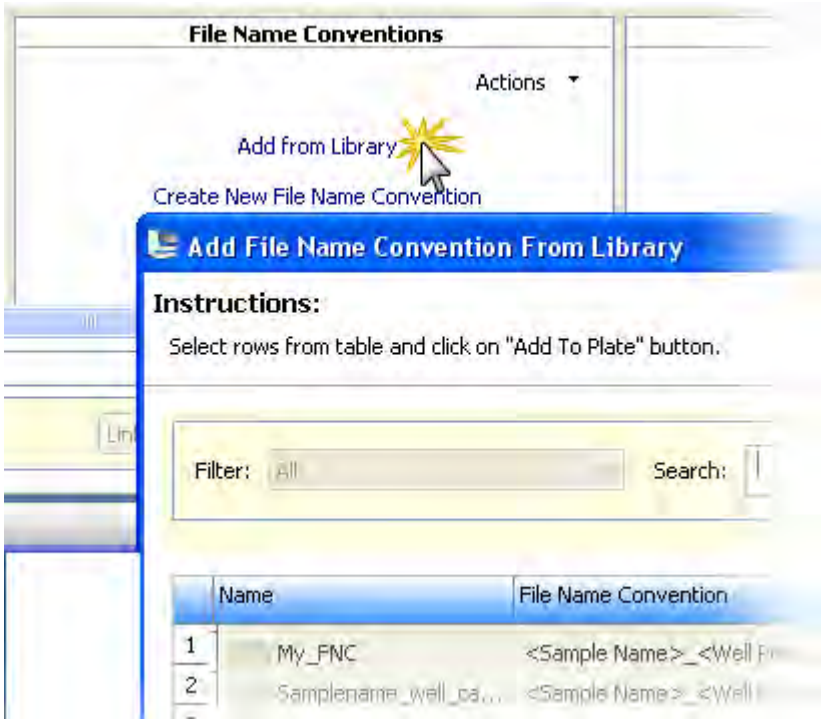
Click the **Table Settings** button, then specify the columns to show or hide.

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 3500 Series Data Collection Software 3.1 allows you to import plate information from files that you create in an application other than the 3500 Series Data Collection Software 3.1. To create a template for importing plate information, set up a plate in the 3500 Series Data Collection Software 3.1, then export it to create a file that contains the correct header and column information for importing:

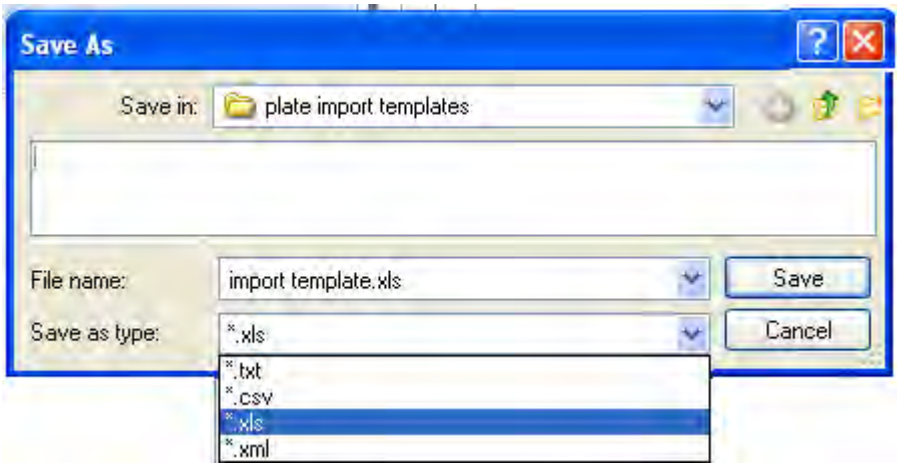
1. In the **Dashboard**, click **Create Plate from Template**.

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**.

5. 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 46.

6. Select a file type for the plate import template.



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

8. 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
7	A01							

Create a plate import file

1. Open a plate import template (see "Create a plate import template" on page 78.

2. Save the plate import template under a new name.

3. 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 3500/3500xL Genetic Analyzer instrument. See "Import and export a library entry" on page 144.
- **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

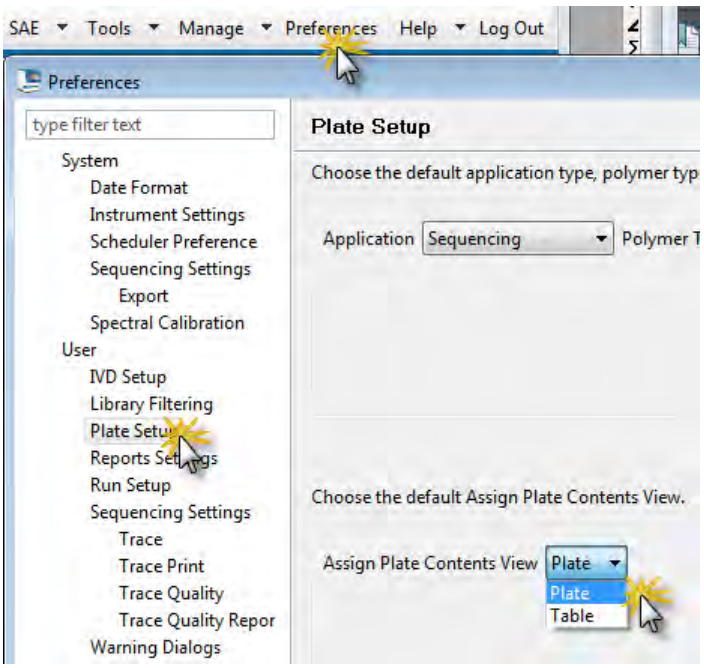
A plate template contains default settings that you can edit when you create a plate from the template.

1. Create a plate (see "Create a new plate" on page 146).
2. (*Optional*) Add sample names and sample types (see "Name samples and assign sample types in the plate view" on page 48).
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 78).

   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 **CutePDF Writer** as the printer, to save the report to .pdf.

More features in Monitor Run

Review the **Instrument Run** views

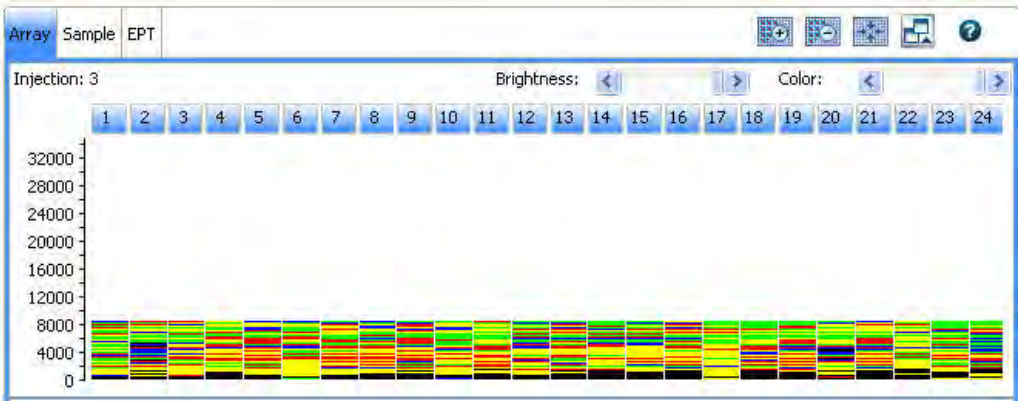
Select an injection, then click an instrument run view tab. As needed:

- 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.

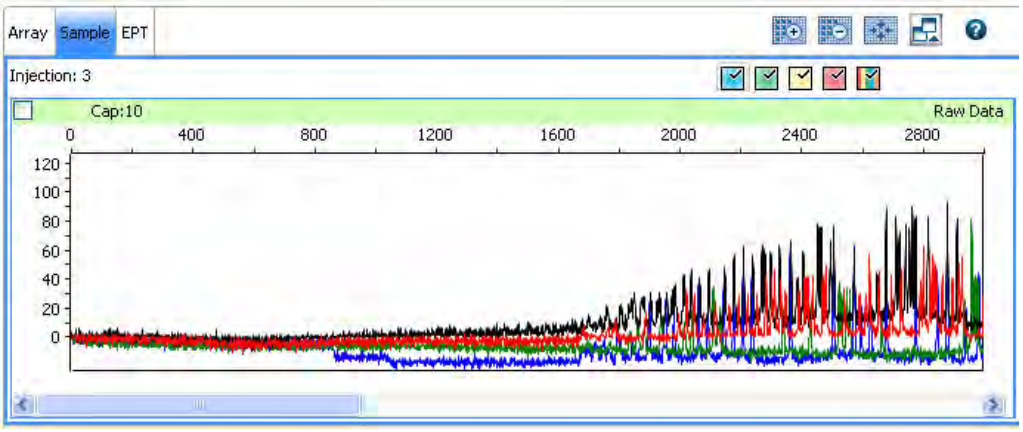
Array view

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.



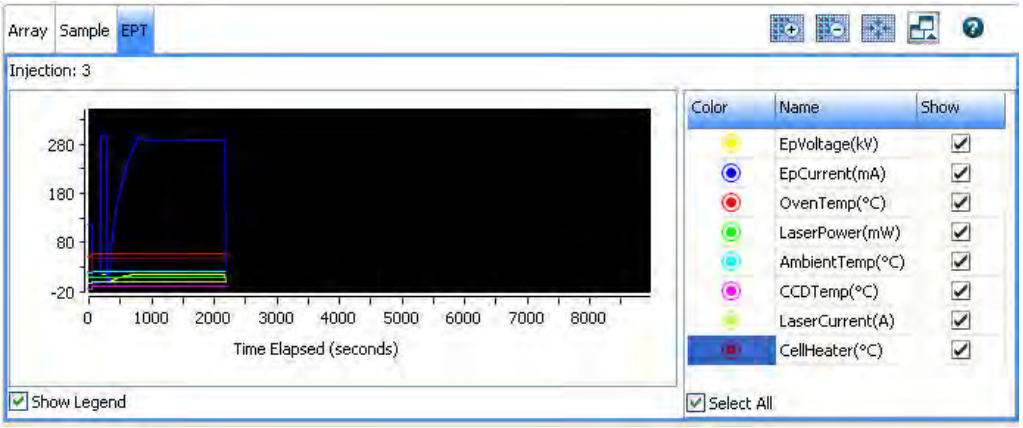
Sample view

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.



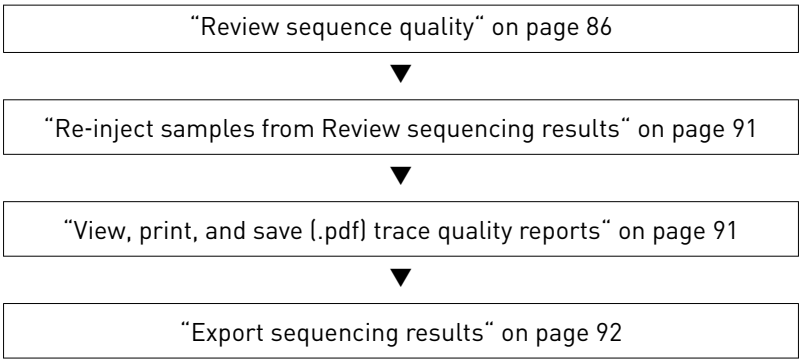
EPT view

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.



4 Review sequencing results

Workflow



Access the View Sequencing Results screen

Access the View Sequencing Results screen from:

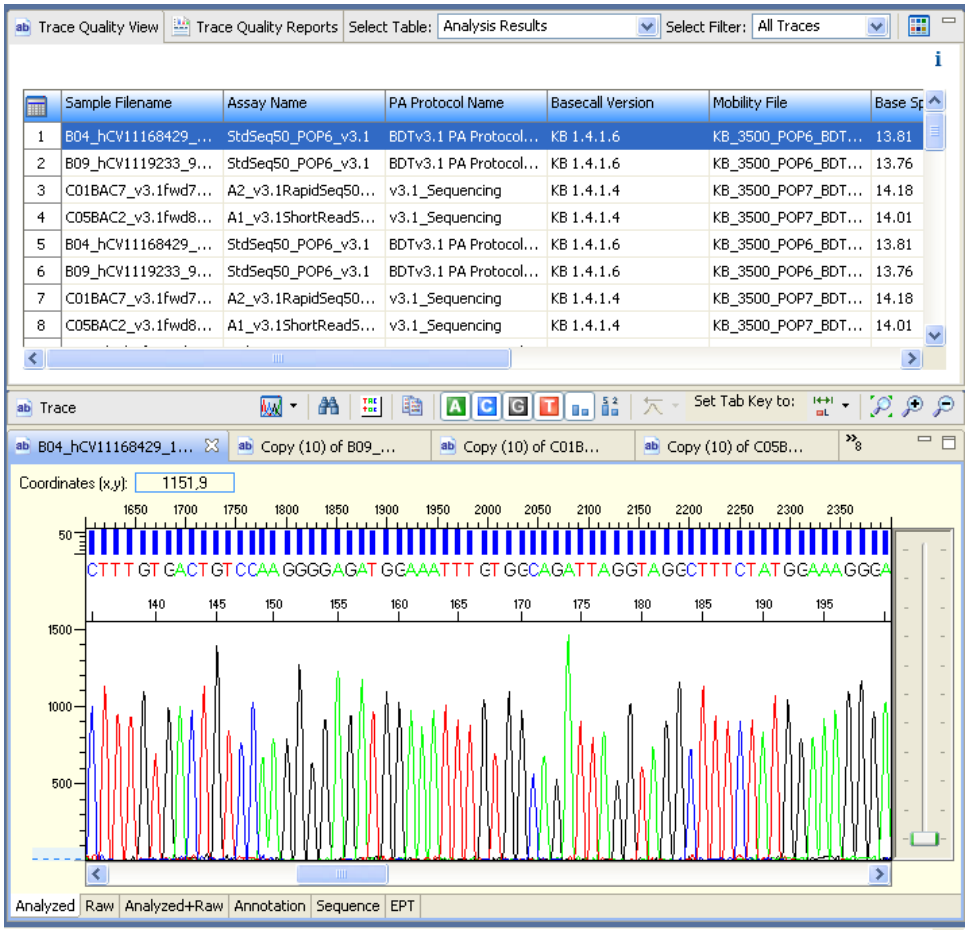
- The Monitor Run screen by clicking **Review Results**.
- The navigation pane by selecting **View Sequencing Results**.
- The Dashboard by clicking **View Run Results**.

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.



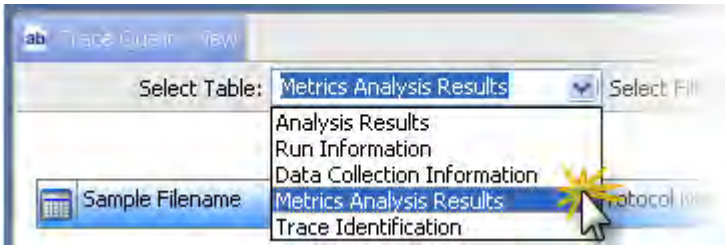
Review previously run sequencing samples

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.



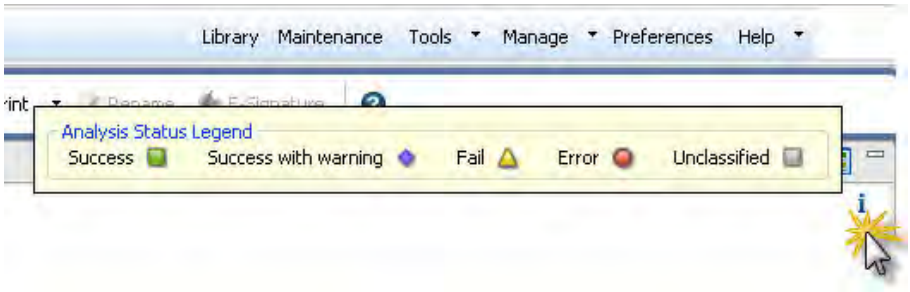
2. Click the **Table Settings** button, then specify the columns to show or hide.

3. Double-click column headers to sort columns. Multi-column sorting is supported (see "Sort by one or multiple columns" on page 77).

4. Review the results:

Result	Description
Trace Score	The average basecall quality value (QV) of bases in the clear range sequence of a trace. The *clear range* 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 bases with an average Quality Value (QV) ≥20. In addition to evaluating the QV of a base call, the software considers the QV of adjacent bases within a ±20-bp moving average 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 20, 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 values ≥20.
Trace Score Quality CRL Quality QV20 Quality	Pass/fail/check determined by the settings in the **Basecalling protocol QV Settings** tab.
PUP Score	A measure of noise calculated as the ratio of the fluorescence signal of the highest secondary peak to the fluorescence signal of the main called base.

5. Review warnings:
   a. Scroll to the right of the **Metric Analysis** table to display the Warning column.
   b. Display the **Analysis Status** legend.



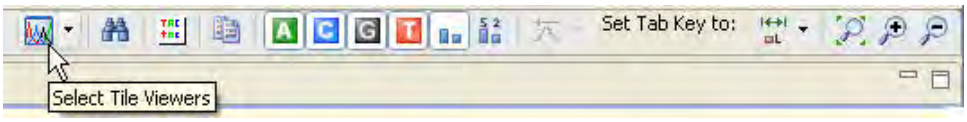
c. Review warnings:

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

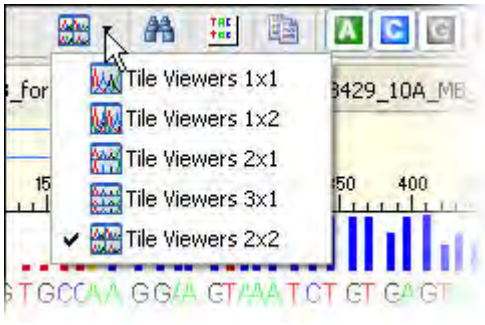
6. (*Optional*) Click **Minimize** and **Restore** to collapse and expand the samples table.

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.

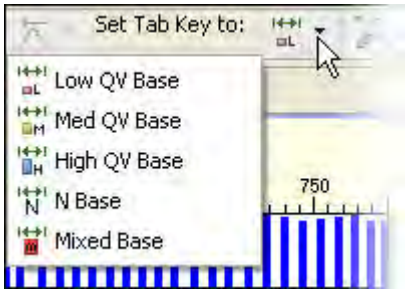


3. (*Optional*) Modify trace display:
   - Use the **Tile Viewer** options to display up to four traces at a time.

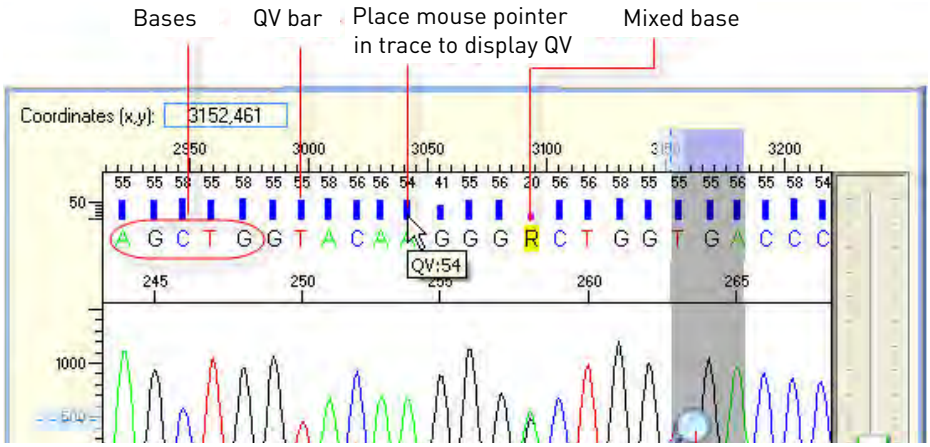


   - Set trace colors in **Preferences** (see "Overview" on page 38).

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



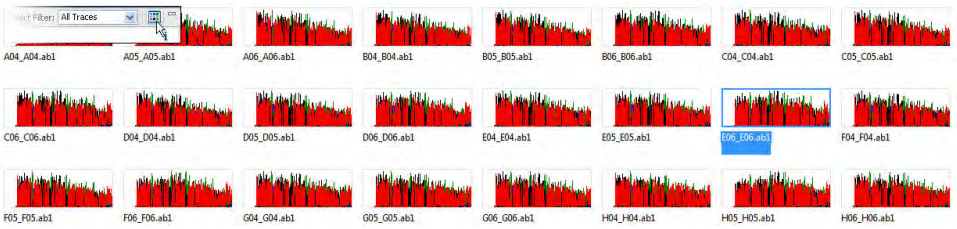
5. Review traces: press **Tab** to review bases from left to right in a trace. Press **Shift +Tab** to move right to left.



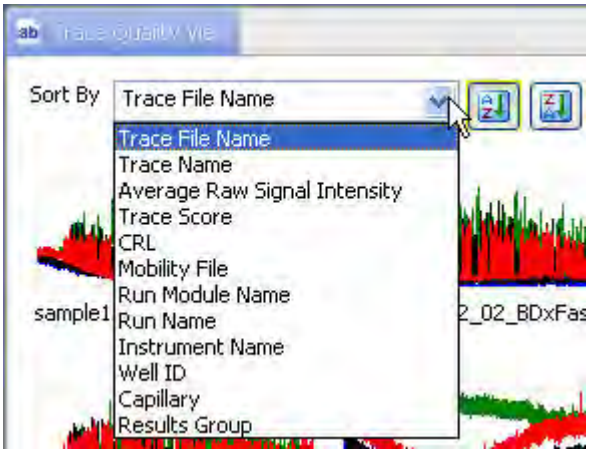
6. Click the tabs at the bottom of the trace pane for different views of the data.

Display thumbnails

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



2. Sort as needed.



3. To compare signal across all samples on a plate, select **Uniform Y Scaling**.

4. 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 38):

- 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.
- For mixed bases, quality values greater than 20 are rare.
- 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

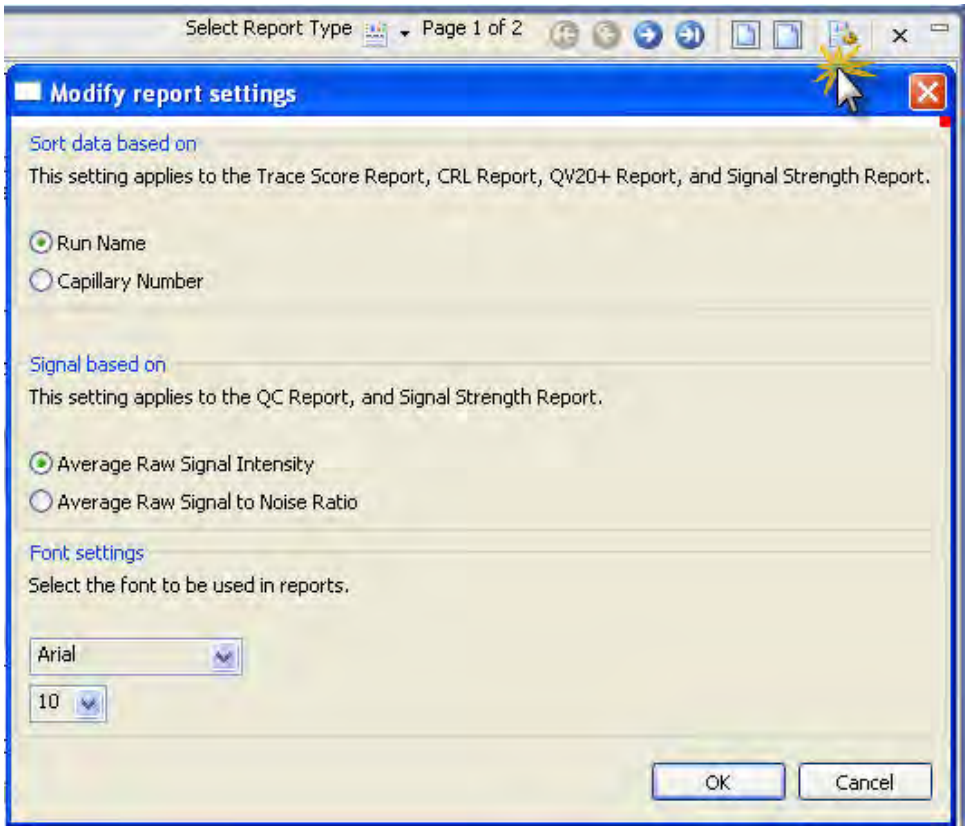
Before the run completes, select a sample with suspect or failing flags, then click **Re-inject**. For information on making a re-injection before a run completes, see "Re-inject samples from the Monitor Run screen" on page 69.

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 38).

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 38).



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 **CutePDF Writer** as the 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

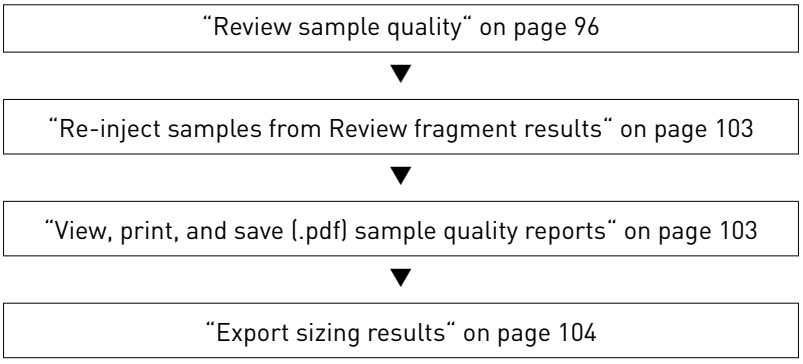
1. Filter the table of interest.
2. Select an export option: Results, Reports, or Traces.
3. Select the export options and the location for the export file, then click **OK**. The file(s) are exported to the specified location with the following naming conventions:
   - **Results** — `export_ReportName`.txt
   - **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).

5 Review fragment/HID analysis results

Workflow



Access the View Fragment/HID Results screen

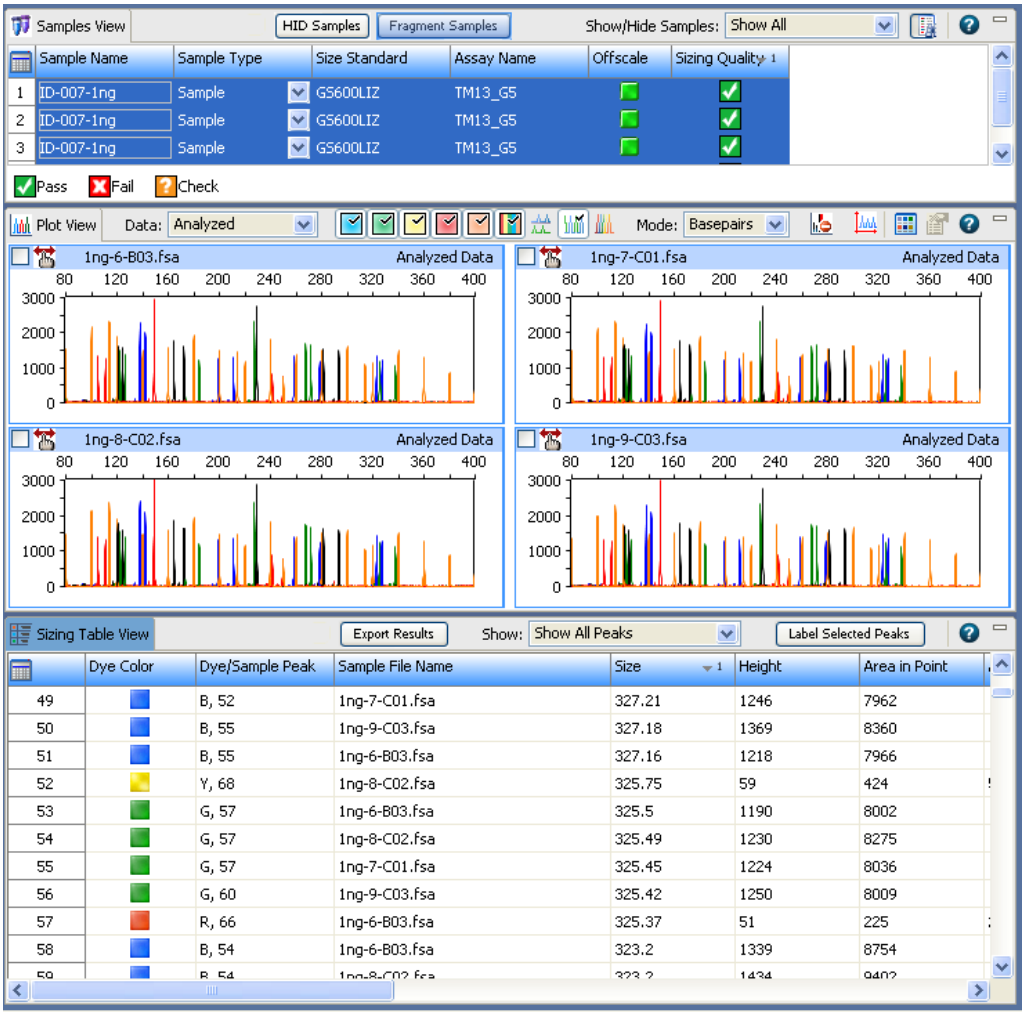
Access the View Fragment Results screen from:

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

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.

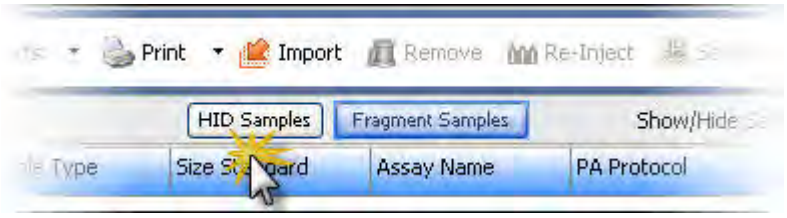


Review previously run fragment analysis/HID samples

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.

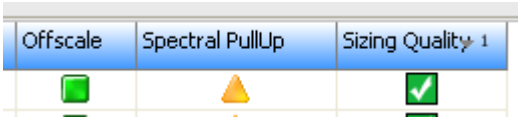
By default, the Fragment Samples view is selected. If you are importing HID files, click **HID Samples**.



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 77).



Flag/ Symbols	Description
Offscale	At least one data point in the analysis range has saturated the CCD camera. **Note:** In the Monitor Run screen, an offscale sample is flagged with .
Spectral Pull-Up (fragment analysis only)	At least one peak contains a pull-up peak. A *pull-up peak* is identified when the peak height of the minor peak is ≤X% of and within ±Y data point of the major peak, where X and Y are values you specify.
Broad Peak (HID analysis only)	At least one peak exceeds the Broad Peak threshold. Broad peaks affect Sizing Quality. See Chapter 7, "Manage library resources". **Note:** 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.
Normalization Limit	• — Sample was collected with a normalization size standard, sample Normalization Factor is within range. — Sample was collected with a normalization size standard, sample Normalization Factor is not within range. **No Data** — Normalization is enabled, but Sizing Quality is . **NO** — Sample was not collected with a normalization size standard. **N/A** — Sample was not collected on a 3500/3500xL Genetic Analyzer instrument. For more information, see "Review normalized data" on page 98. **Note:** If the Sizing Quality is , normalization is not applied, even if the Normalization Factor is within the normalization range.
SQ: Sizing Quality	The Sizing Quality is in the Fail or Suspect range. Place the mouse pointer over a flag to display the Sizing Quality value for the sample.

3. 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.

4. (*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 normalization factor for each sample. The normalization factor is used as a multiplier to adjust the peak height of the sample peaks relative to the GS600 LIZ® V2 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 Normalization Factor is within the normalization range. Ensure that you use the normalization size standard appropriate for your application.

How normalization is applied

To normalize, the software:

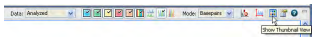
1. Determines if the data was collected on the 3500/3500xL Genetic Analyzer instrument.
2. Determines if the sample was collected with a normalization size standard definition file (normalization is enabled).
3. If normalization is enabled, the software calculates a Normalization Factor for the sample using multiple size standard fragments. The Normalization Factor is calculated by dividing the Normalization Target by the observed average peak height of the size standard fragments in the samples.
4. Compares the sample Normalization Factor to the thresholds (set in the instrument protocol).
5. If the calculated Normalization Factor is within the Normalization Factor range, multiplies the peak heights of the sample by the calculated Normalization Factor.
6. If the calculated 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 Normalization Factor is 5, the software applies a Normalization Factor of 3.0).
7. Indicates the normalization state of the sample in the Normalization Limit column in the Samples View.

Normalization factor in secondary analysis

If normalization is applied in the 3500 Series Data Collection Software 3.1, the calculated 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 3.1 (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 or 6-dye sample, you must manually select the fifth or sixth dye. It is not automatically selected when you switch to a 5-dye or 6-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 100).

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

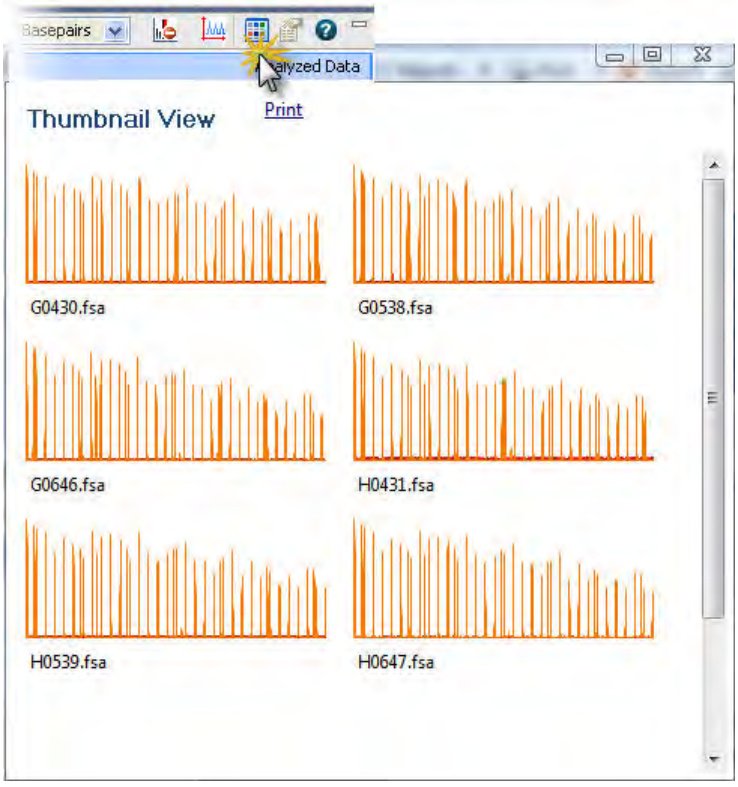
1. Select samples in the samples view to display the plots.
2. Click (Plot Settings) in the plot view toolbar, then select the **Labels** tab.

3. Label peaks:

If you have ...	Then ...
Already specified default labeling preferences	1. Select **Show Peak Labels**. 2. Click **Label Peaks**. 3. Click **Apply**. IMPORTANT! You must open **Plot Settings** each time you access the **View Results** screen, then click **Label Peaks**. Labeling settings are not automatically applied when you access **View Results**, or when you click **Apply**.
Not specified default labeling preferences	1. In **Labels to Show**, select the needed labels. 2. In **Labeling Options**: • Select **Show Peak Labels**. • To label all peaks with the selected labels, click **Label Peaks** (make sure **All** is selected). • To label selected peaks, select the category from the **Label Peaks** list (**Height**, **Area**, **Size**), specify the range to label for the selected category (for example, if you select Height, specify the height range of the peaks to label), then click **Label Peaks**. • Select **Retain Labels**. 3. Click **Save to Preferences** to save these settings for future use. You can change preferences at any time. 4. Click **Apply**.

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:

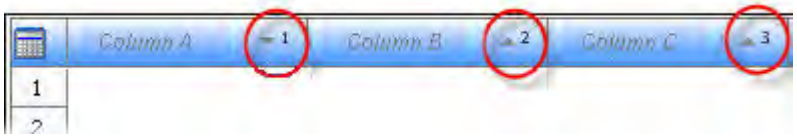
1. In the **Sample Name** column, select the samples to rename, or click the Sample Name column header to select the entire column.
2. Click **Rename**.
3. In the **Search** field, enter the sample name to change.
4. In the **Rename** field, enter the new name.
5. Click **Search**, then click **Rename**.

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 77).
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

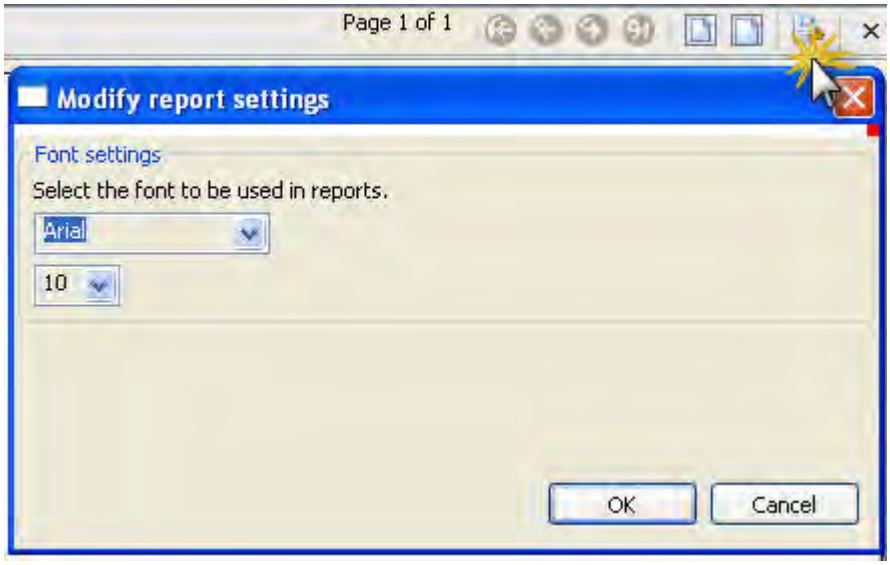
1. Click (Plot Settings) in the plot view toolbar.
2. Select **Overlay Sizing Curve** in the Display tab.

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 69.

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 102). 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)

6 Run calibrations and install checks

Section 6.1 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:

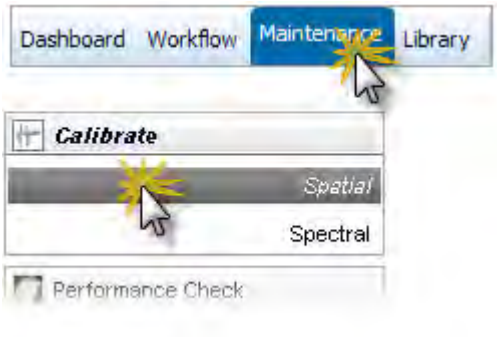
- Remove or replace the capillary array.
- Replace the capillary when it expires.

  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 3500 Series Data Collection Software 3.1.

1. Preheat the oven if you will be selecting the **Fill** option for the calibration (fill the array with polymer).
2. Access the **Spatial Calibration** screen.

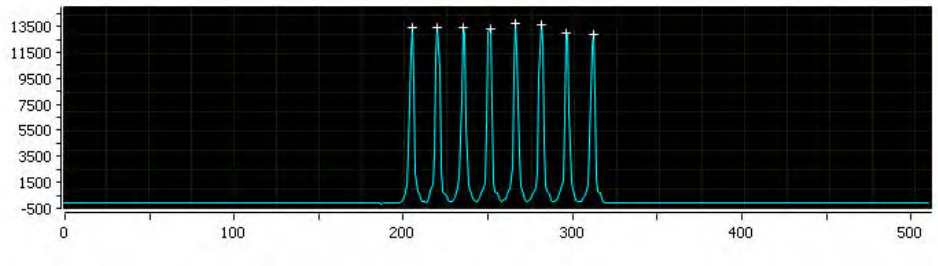


   Note: The screen does not display results unless you have previously performed a spatial calibration.
3. Select **No Fill**, or select **Fill** to fill the array with polymer before starting the calibration.
4. Select **Perform QC Checks**.
5. Click **Start Calibration**.

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)	• 8-cap: 6400 RFU • 24-cap: 3000 RFU
Individual peak height	Peak height	1000 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 **Spatial QC Check** error message is displayed if:

- The average peak height or individual peak height is below the threshold
- Uniformity or capillary spacing exceeds the threshold

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).

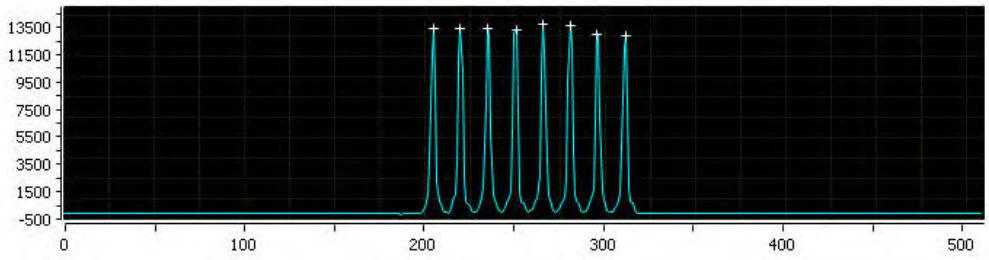
2. If the results meet the criteria above, click **Accept Results**.

   If the results do not meet the criteria above, the **Accept** button is dimmed. Go to "Spatial calibration troubleshooting" on page 272.

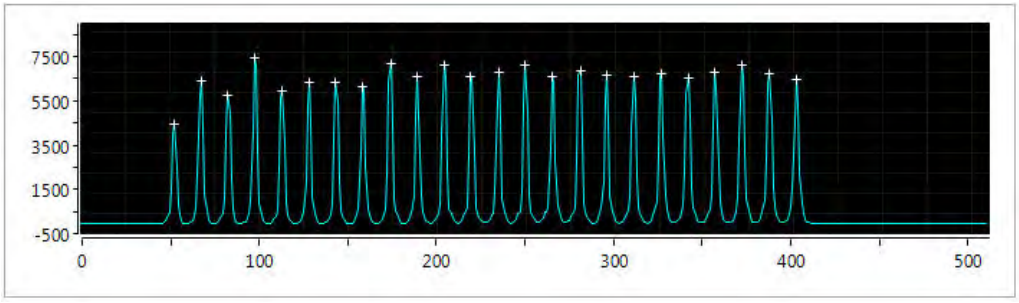
IMPORTANT! Do not log off or close the software before clicking Accept Results. Spatial calibration results are not saved until you click Accept Results.

Example spatial profiles

8-capillary spatial



24-capillary spatial



Export spatial calibration results

1. Click **Export Results**.

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 **CutePDF Writer** as the 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 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 123.

Estimated run time

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	≤30

Prepare for spectral calibration

Before you begin

If you have not already done so, perform a spatial calibration (see "Run a spatial calibration" on page 106).

Prepare the instrument

1. In the **Dashboard**, check consumables status "Check consumables status" on page 35). Ensure that:
   - Consumables are not expired
   - Adequate injections remain for consumables
2. Ensure that buffer levels are at the fill lines ("Check buffer fill levels" on page 37).
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). Preheating 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 239).

Prepare the spectral calibration standard

Prepare the matrix standard appropriate for your application as described in the product insert. See Appendix D, "Part numbers" for part numbers.

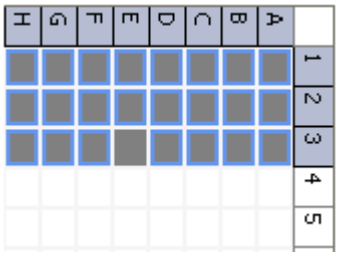
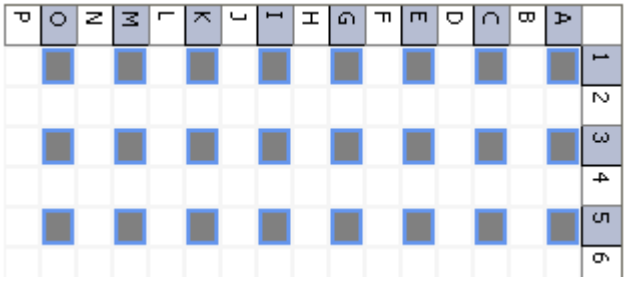
If peaks are offscale for G5, F, and E5 dye sets, dilute the matrix standard and repeat the calibration.

Prepare the standard plate

IMPORTANT! Do not use warped or damaged plates.

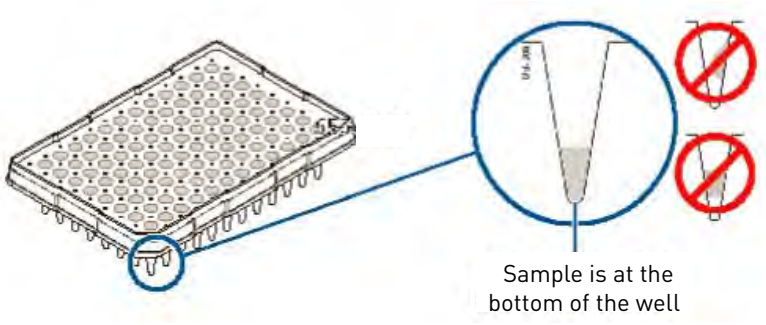
1. Load the standards in any injection position in the plate. The example below shows injection position 1, but you can specify the starting well for an injection position.

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

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

2. Briefly centrifuge the plate containing 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 54.

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.

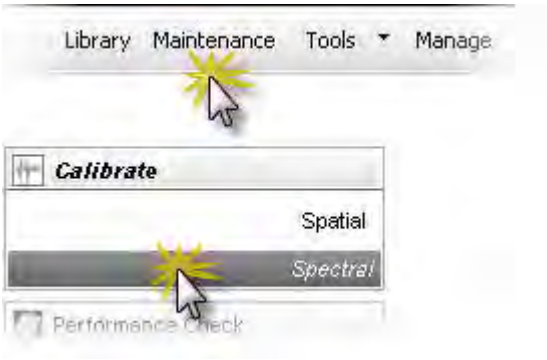
3. Close the instrument door to initialize the instrument.

Perform a spectral calibration

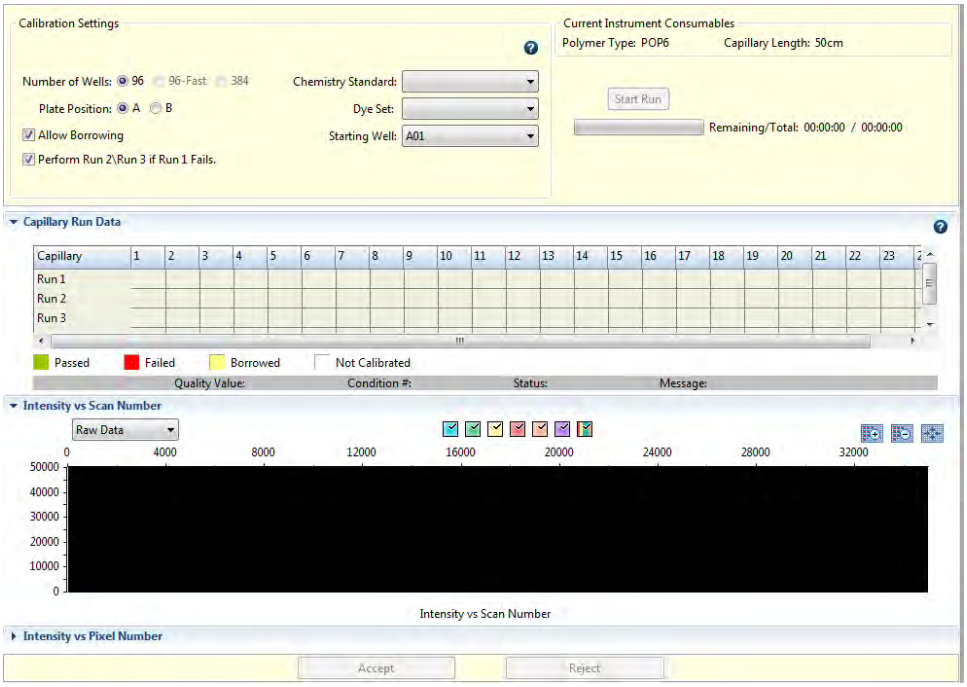
IMPORTANT! Do not change E-Signature settings during a spectral calibration.

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
BigDye® Terminator (BDT) v1.1 Sequencing Standards, 3500/3500xL	E	Sequencing
BigDye® Terminator (BDT) v1.1 Matrix Standards Kit, 31xx and 3500	E	Sequencing
BigDye® Terminator (BDT) v3.1 Sequencing Standards, 3500/3500xL	Z	Sequencing
BigDye® Terminator (BDT) v3.1 Matrix Standards Kit, 3500/3500xL	Z	Sequencing
DS-32 Matrix Standard	F	Fragment analysis
DS-02 Matrix Standard	E5	Fragment analysis
DS-33 Matrix Standard	G5	Fragment analysis
DS-36 Matrix Standard	J6	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 118.

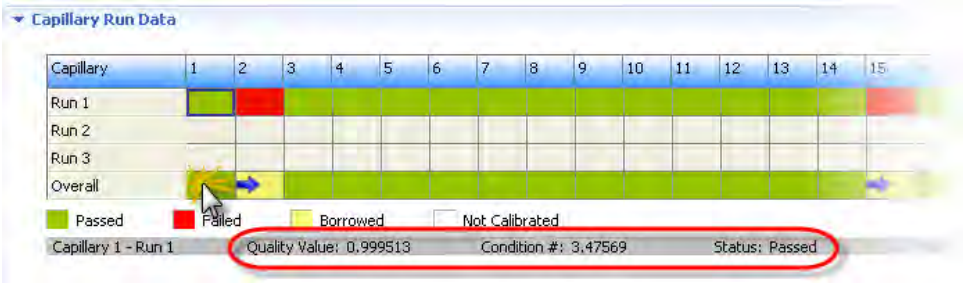
7. Click **Start Run**. The following occurs:
   - If you used the default setting "**Perform run 2 and 3 if run 1 fails**", the instrument sets up three injections (see "What you see during a spectral calibration" on page 118 for information on the number of injections performed).
   - The **Capillary 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 109.



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 peak(s) causes 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 (see "Evaluate the spectral calibration data" on page 116).

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)
E	0.95	5.5
E5	0.95	6.0
F	0.95	8.5
G5	0.95	13.5
J6	0.95	8.0

Dye Set	Quality Value Minimum	Condition Number Maximum
Z	0.95	5.5

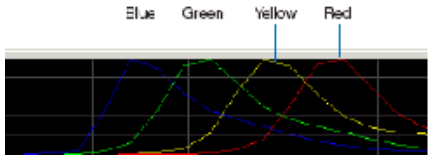
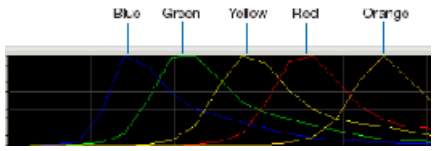
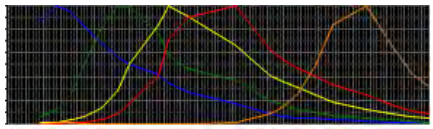
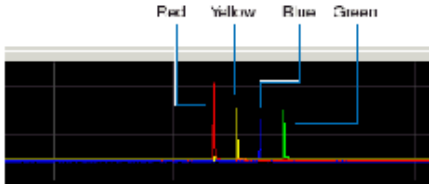
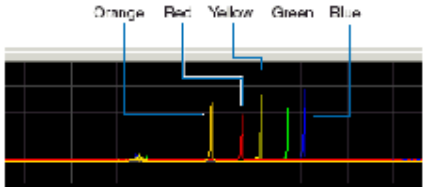
Evaluate the spectral calibration data

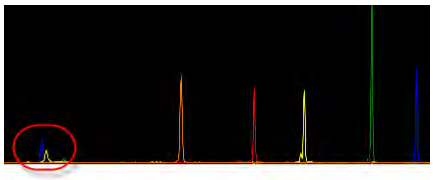
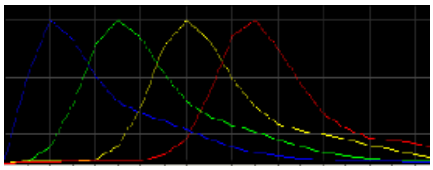
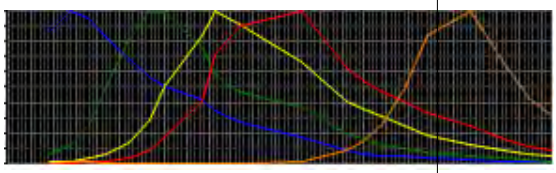
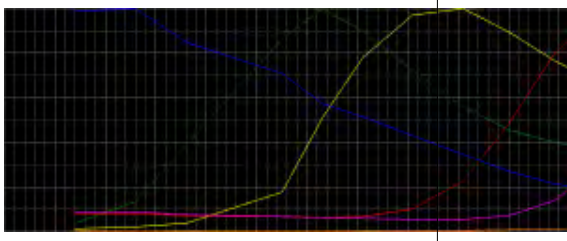
IMPORTANT! Do not accept a spectral calibration until you examine the data for all capillaries.

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	
	Fragment analysis: • 4-dye: red-yellow-green-blue • 5-dye: orange-red-yellow-green-blue	

Attribute	Acceptance Criteria	Example
Extraneous peaks in the raw data profile (intensity vs scan)	None **Note:** The E5 profile may include extraneous peaks outside the matrix peak region, which can be ignored.	E5: 
Peak morphology in the spectral profile (intensity vs pixel)	• No gross overlaps, dips, or other irregularities • Peaks separate and distinct • Peak apexes are separate and distinct (the tails will overlap)	
	Note: 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).	 

3. As needed, zoom on the spectral profile traces to determine if the data meet the criteria (see "Zoom on data" on page 99).
4. If the data for all capillaries meet the criteria above, click **Accept Results**.
5. If any capillary data does not meeting the criteria above, click **Reject Results**, then go to "Spectral calibration troubleshooting" on page 273.

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  .

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.

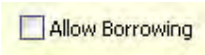
Capillary information sharing

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

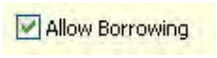
When Borrowing is *disabled,* all capillaries must pass (meet the spectral Quality Value and Condition Number limits) for the calibration to pass.



Injection 1	• The software evaluates the Quality Value and Condition Number of all capillaries. • If all capillaries pass, the calibration is complete, and injections 2 and 3 are not performed. • If any capillaries fail, injection 2 is performed.
Injection 2	• 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. • If all capillaries now pass, the calibration is complete and injection 3 is not performed. • If the same capillary fails in both injection 1 and 2, injection 3 is performed.
Injection 3	• 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. • If all capillaries now pass, the calibration passes. • If the same capillary fails in injection 1, 2, or 3, the calibration fails.

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:



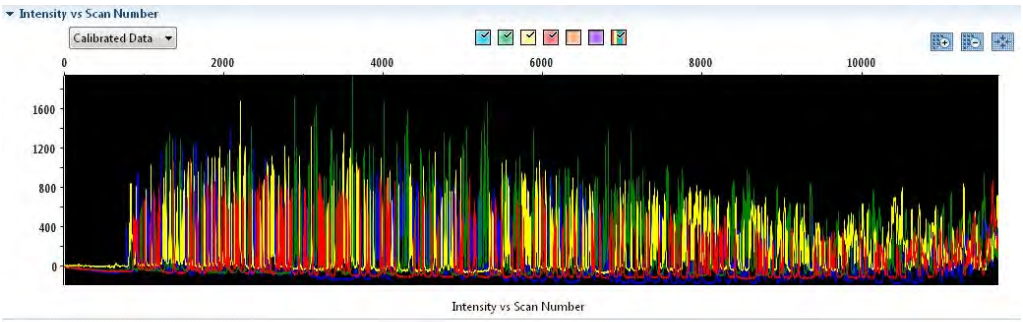
- 8-capillary instruments – One adjacent-capillary borrowing event allowed
- 24-capillary instruments – Up to three adjacent-capillary borrowing events allowed (the number of allowed borrowing events can be decreased in Preferences).

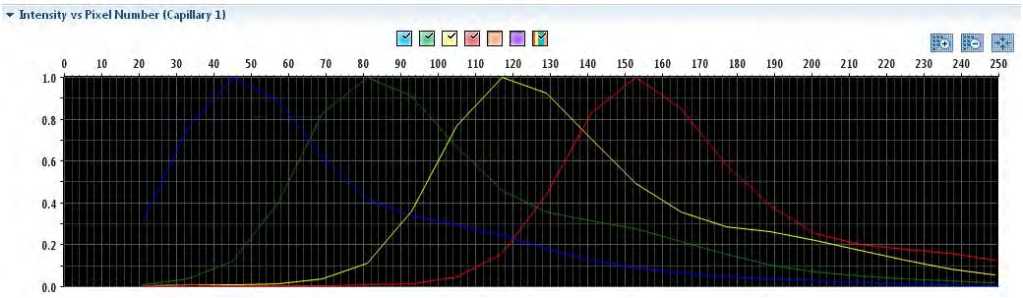
The software identifies a borrowed capillary with an arrow pointing from the capillary from which the data is borrowed.

Injection 1	• The software evaluates the Quality Value and Condition Number of all capillaries. • If all capillaries pass, the calibration is complete, and injections 2 and 3 are not performed. • If any capillaries fail, the software borrows from an adjacent capillary. • If, after borrowing, >1 or > 3 capillaries fail, injection 2 is performed.
Injection 2	• 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. • If all capillaries pass, the calibration is complete and injection 3 is not performed. • If, after borrowing, >1 or > 3 capillaries from injection 1 or 2 do not pass, injection 3 is performed.
Injection 3	• 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. • If all capillaries now pass, the calibration passes. • If after borrowing, >1 or > 3 capillaries from injection 1, 2, or 3 do not pass, the calibration fails.

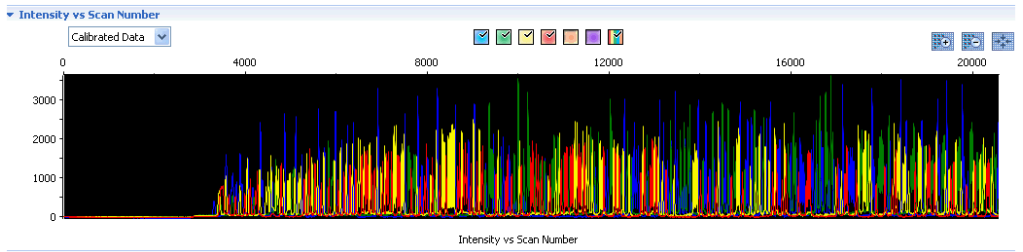
Example spectral calibration data

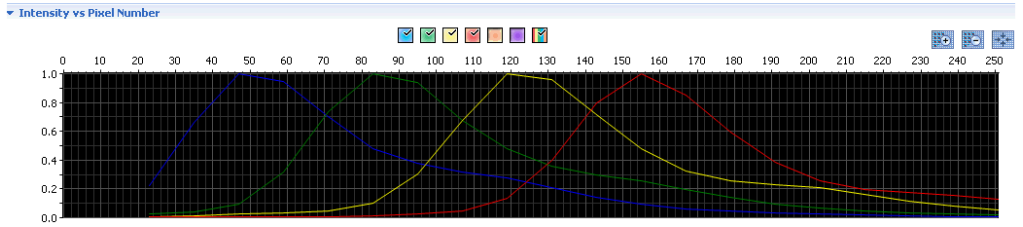
Dye Set E created from Sequencing Standard



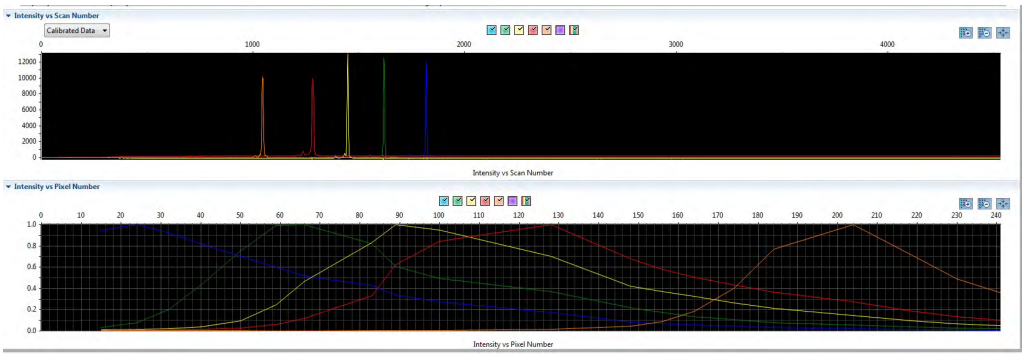


Dye Set Z created from Sequencing Standard

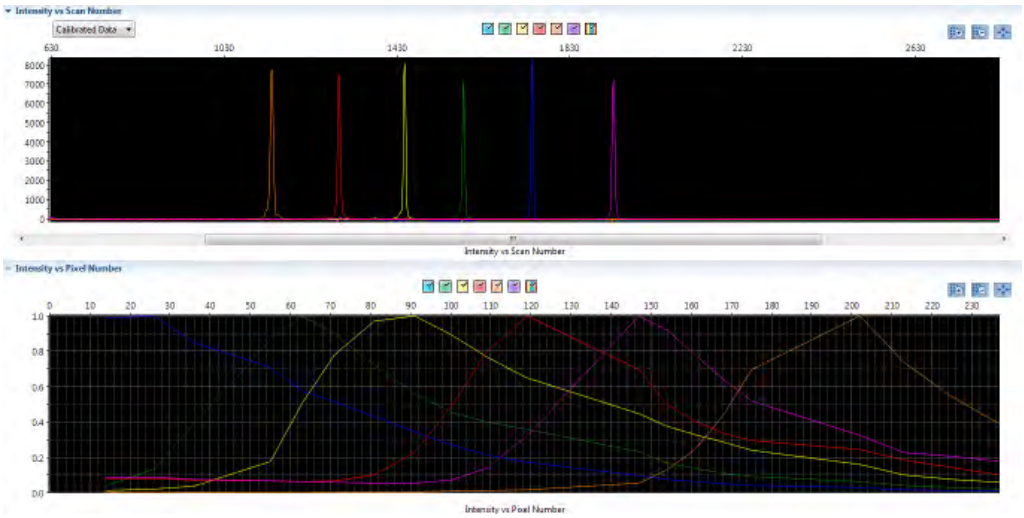




Dye Set G5 created from Matrix Standard Set DS-33



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 **CutePDF Writer** as the 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 6.2 Run an install check

Run a Sequencing install check

When to perform a sequencing install check

If an install check was 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 123) for E or Z dye set.

Estimated run time

- General sequencing (BDTv3.1 on POP-7™ polymer): ~1 hour
- MicroSeq® ID: 2 hours
- BDTv1.1POP6: ~2.5 hours

Prepare for the sequencing install check

Before you begin

If you have not already done so, perform a spectral calibration (see "Perform a spectral calibration" on page 113).

Prepare the instrument

1. In the **Dashboard**, check consumables status "Check consumables status" on page 35). Ensure that:
   - Consumables are not expired
   - Adequate injections remain for consumables
2. Ensure that buffer levels are at the fill lines ("Check buffer fill levels" on page 37).
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). Preheating 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 239).

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, "Part numbers" for part numbers.

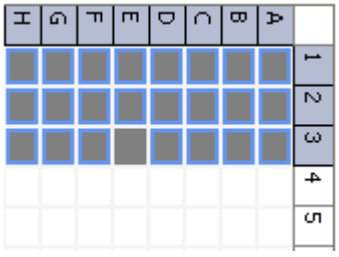
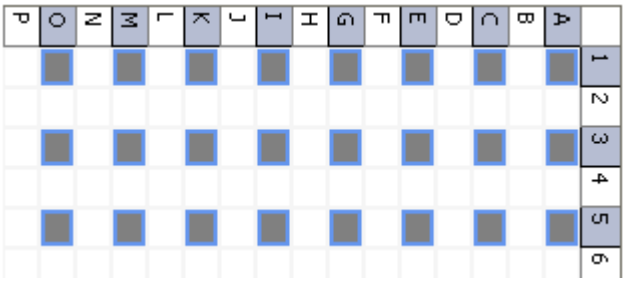
Note: For the BigDye® Direct DNA PCR Amplification/ Clean-up/Cycle Sequencing kit, use the v3.1 Sequencing Standard.

Prepare the standard plate

IMPORTANT! Do not use warped or damaged plates.

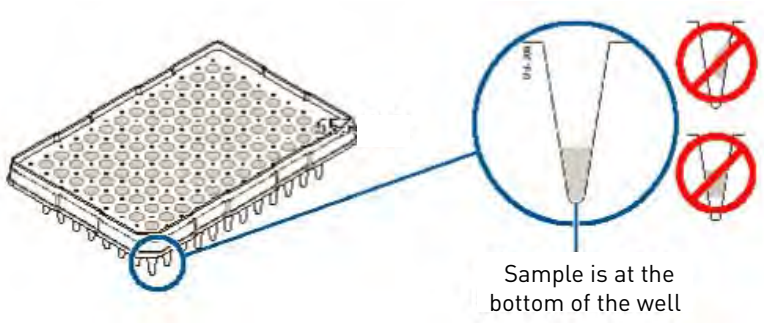
1. Load the standards in any injection position in the plate. The example below shows injection position 1, but you can specify the starting well for an injection position.

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

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

2. Briefly centrifuge the plate containing 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 54.

Load the plate in the instrument

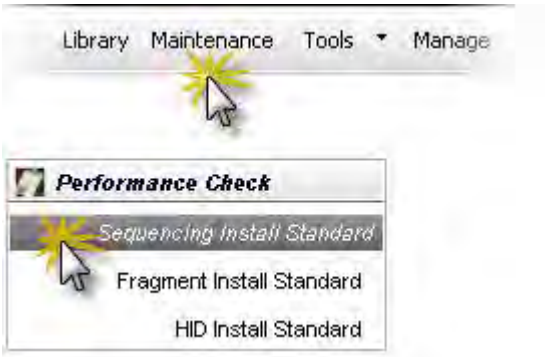
1. Click the Tray button on the front panel to move the autosampler to the front position, then open the instrument door.

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 Check** 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.

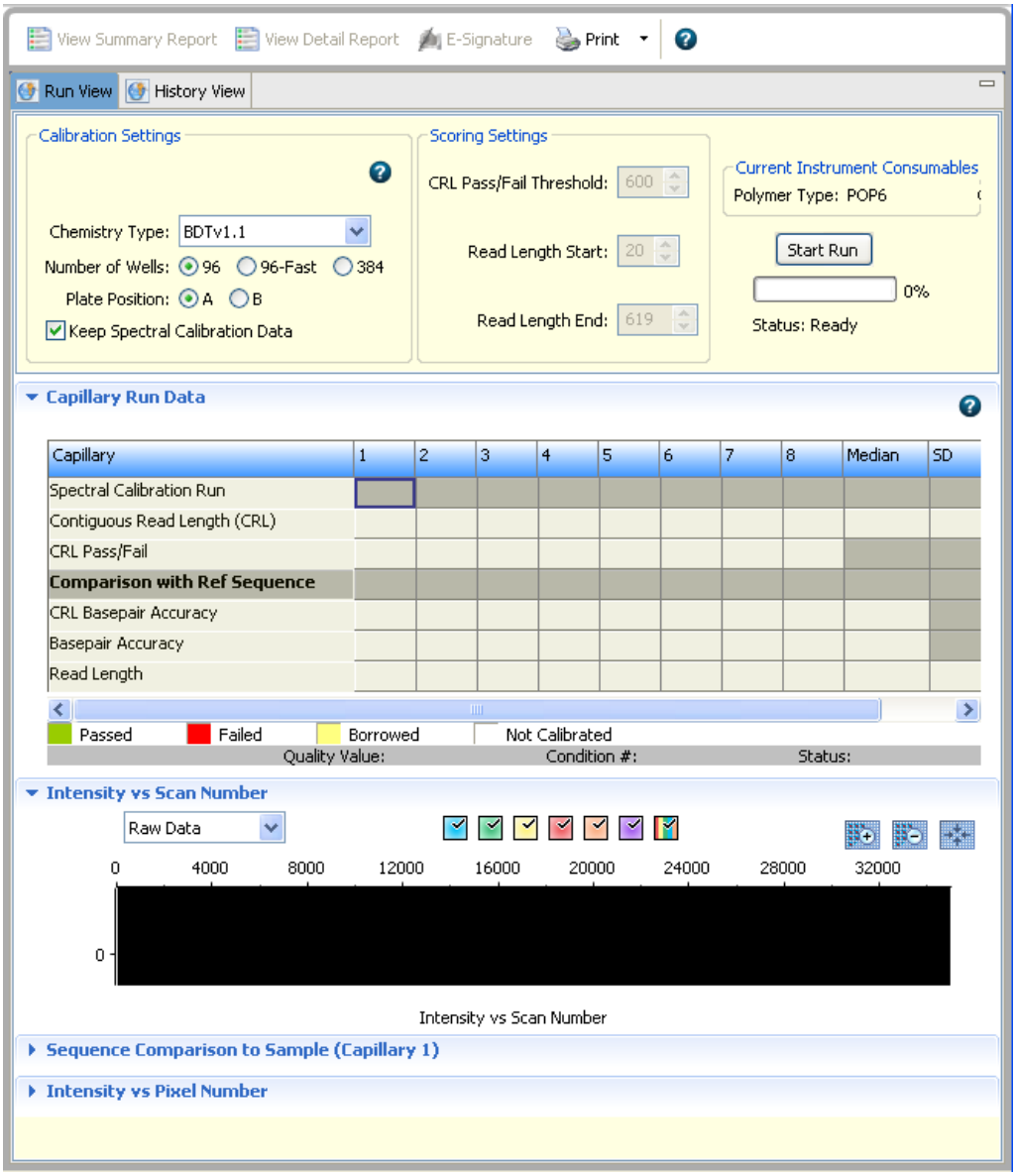
   Note: If you navigate away from the **Install Check** screen after you start the install check, the starting well may be reset to A01. This is a display issue only; the starting well you specify is used for the install check.

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 **Keep Spectral Calibration Data** option is checked on the screen. If you decide to uncheck the option, create a separate spectral calibration from the **Maintenance** menu.

6. Click **Start Run**.

IMPORTANT! Do not accept a sequencing installation standard run until you examine the data.



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 8) updates 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.

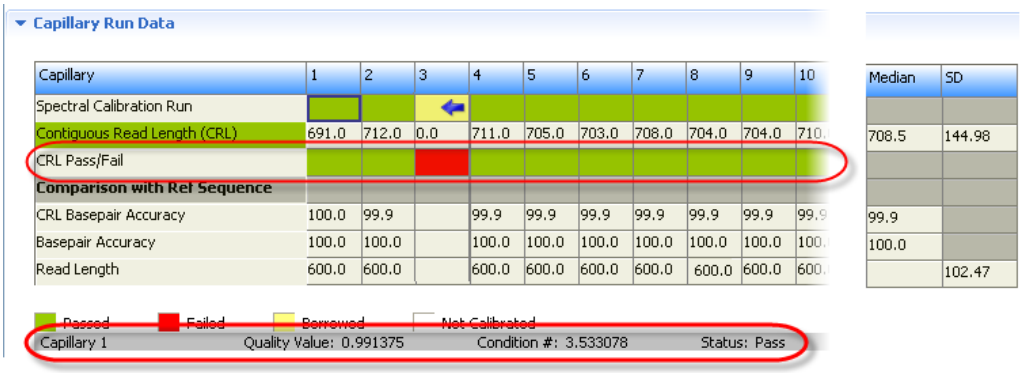


Figure 8 Capillary Run Data

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 115).

Borrowing is automatically enabled: 1 borrowing event is allowed for 8-capillary instruments, up to 3 borrowing events for 24-capillary instruments. For more information, see "Spectral calibration with Borrowing enabled" on page 119. The number of borrowing events can be decreased (see "System preferences" on page 39).

Thresholds used by the software for pass/fail are:

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.

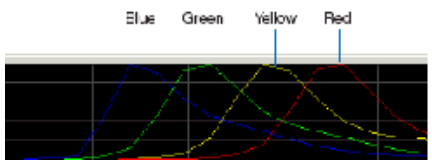
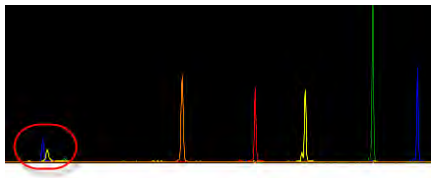
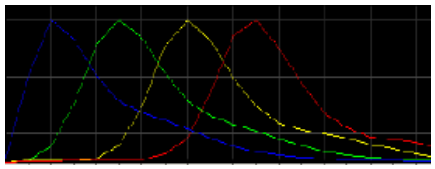
Result	Description
Contiguous Read Length (CRL)	The longest uninterrupted segment of bases with an average Quality Value (QV) ≥20. In addition to evaluating the QV of a base call, the software considers the QV of adjacent bases within a ±20-bp moving average to determine a contiguous read length based on quality values: the software starts from the 5′ end and calculates the average QV across a moving window size of 20, sliding 1 bp at a time, to the 3′ end. The resulting longest contiguous segment is determined as the CRL.
CRL Pass/Fail	• **BDTv1.1** – Capillaries with a CRL <600 bp fail. • **BDTv3.1 (General Sequencing)** – Capillaries with a CRL <500 bp fail. • **MicroSEQ® ID** – Capillaries with a CRL <600 bp fail.
For information only – The alignment of the base-called sample sequence with the known reference of the sequencing install standard is used to calculate the following results.	
CRL **Basepair Accuracy**	CRL accuracy is determined by base-pair 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).
Read Length	The length of read (in bases) at which base calling accuracy is ≥ 98.5%. The read length value for this information is derived from basecall-accuracy, not from quality value.
Basepair Accuracy (Read Length Accuracy)	Basepair Accuracy calculates the percent of accurate basecalls in the known reference sequence of the sequencing install standard: • BDTv1.1: 20 to 619 bp • BDTv3.1 (General Sequencing): 40 to 539 bp • MicroSEQ® ID: 20 to 619 bp
CRL Median and SD	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 **Note:** The E5 profile may include extraneous peaks outside the matrix peak region, which can be ignored.	E5: 
Peak morphology in the spectral profile (intensity vs pixel)	• No gross overlaps, dips, or other irregularities • Peaks separate and distinct • Peak apexes are separate and distinct (the tails will overlap)	

3. (*Optional*) Review the CRL 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 239), 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**.

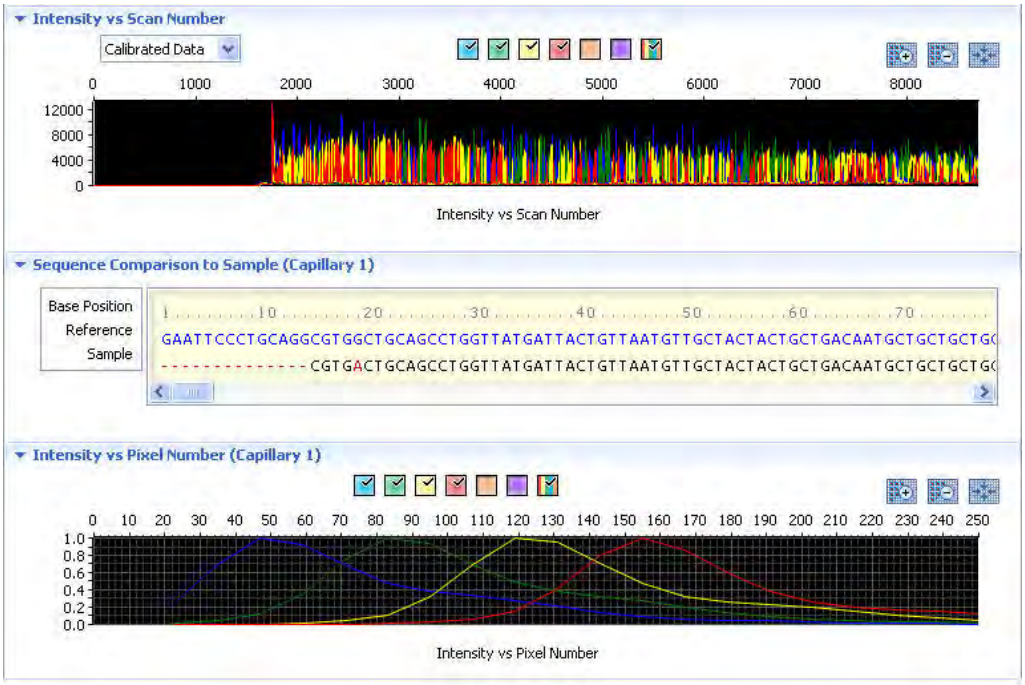
5. If the data for the required number of capillaries do not meet the criteria above (at least 7 capillaries for 8-capillary instruments, at least 22 capillaries for 24-capillary instruments):

   a. (*Optional*) If you want to generate a report for the failed calibration, click **View Report** before you click **Reject Results**. To save the report electronically, select **CutePDF** as the printer.

b. Click **Reject Results**. For troubleshooting information, see "Sequencing install standard troubleshooting" on page 275.

IMPORTANT! If you reject results, the spectral calibration is not saved.

Example sequencing install check 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 Check** 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**.
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 **CutePDF Writer** as the 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 **CutePDF Writer** as the 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 was 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

30 minutes

Prepare for the fragment/HID install check

Before you begin

If you have not already done so, perform a spectral calibration (see “Perform a spectral calibration“ on page 113).

Prepare the instrument

1. In the **Dashboard**, check consumables status "Check consumables status" on page 35). Ensure that:
   - Consumables are not expired
   - Adequate injections remain for consumables
2. Ensure that buffer levels are at the fill lines ("Check buffer fill levels" on page 37).
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). Preheating 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 239).

Prepare the fragment/HID install check standard

Prepare the standard as described in the product insert. See Appendix D, "Part numbers" for part numbers.

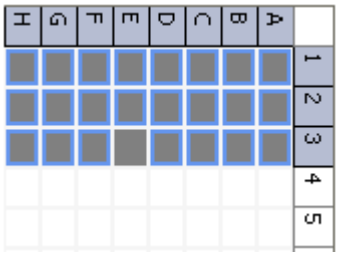
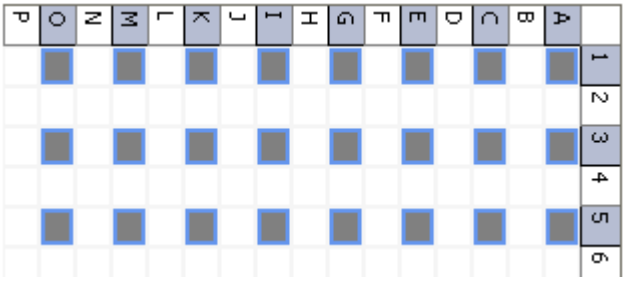
- Fragment analysis: DS-33 GeneScan Installation Standards with GeneScan™ 600 LIZ® Size Standard v2.0
- HID: AmpFℓSTR® Identifiler® Allelic Ladder

Prepare the standard plate

IMPORTANT! Do not use warped or damaged plates.

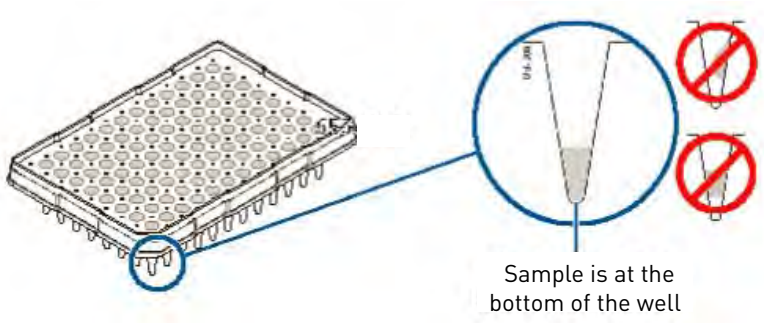
1. Load the standards in any injection position in the plate. The example below shows injection position 1, but you can specify the starting well for an injection position.

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

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

2. Briefly centrifuge the plate containing 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 54.

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.

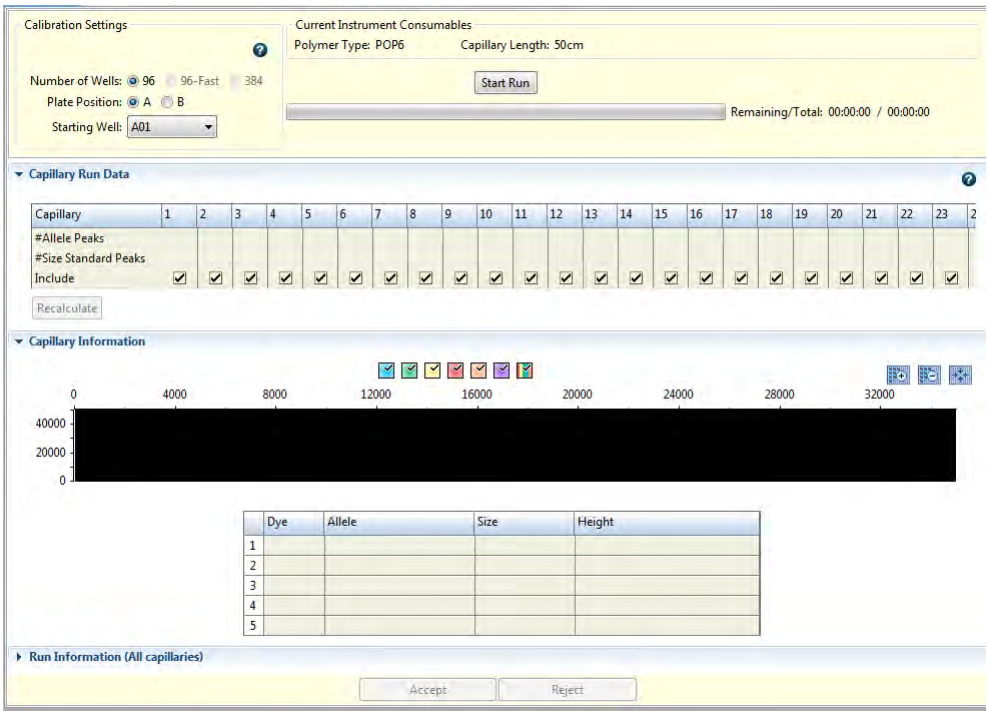
Perform the fragment/HID install check

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.



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 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.

5. Click **Start Run**.

What you see during a fragment install check

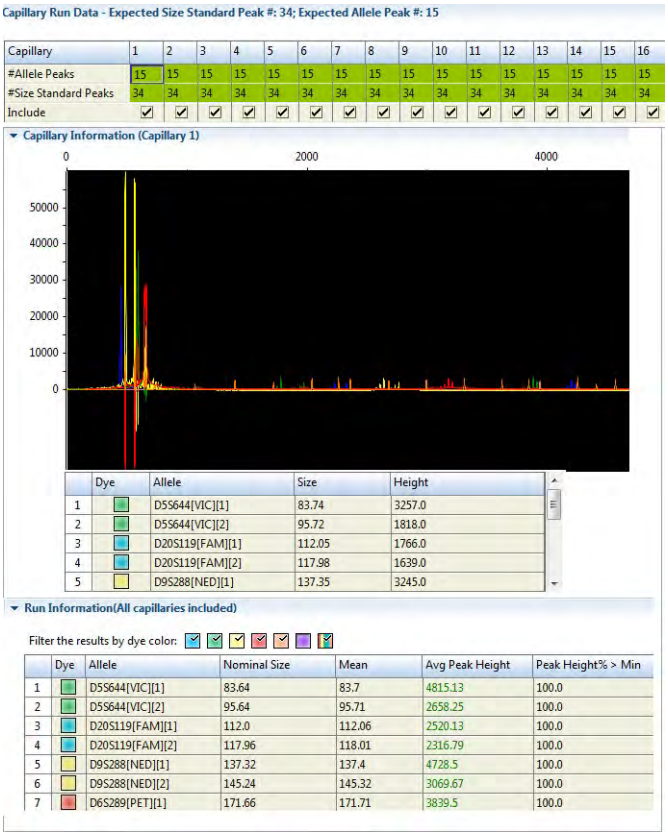
The instrument performs one run and indicates the number of observed allele and size standard peaks.

The **Capillary Run Data** display updates 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.

Number of peaks per capillary

Plot and allele size/height for selected capillary

Allele results for all capillaries



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):

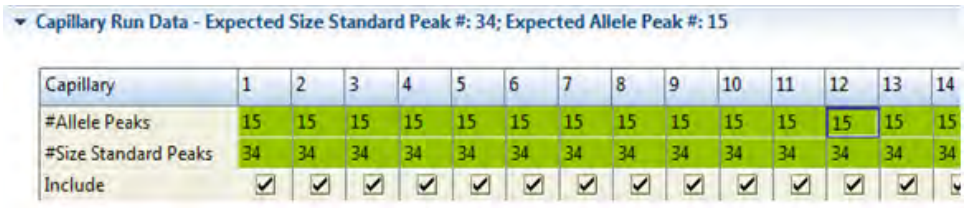
Fragment Analysis	HID Analysis
All markers between ±0.4 bp or ±0.5 bp of nominal size for the allele	• All markers except TH01: ±0.7 bp of nominal size for the allele • TH01: – Seven markers are ±0.7 bp of nominal size for the allele – Three markers are ±0.5 bp of nominal size for the allele

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 thresholds below pass.

Result	Description	Threshold
Min Peak Height	Minimum of peak heights for observed allele peaks of the included capillaries.	• Fragment: >175 RFU • HID: >400 RFU
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. Review the data for failed alleles as described below.	
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

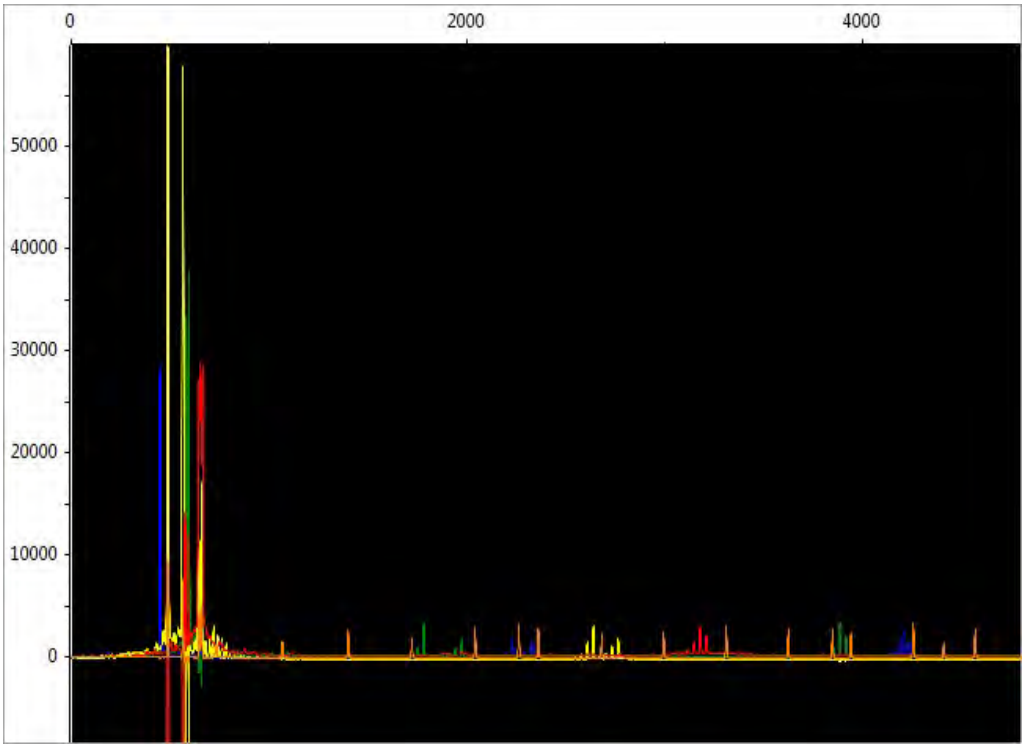
1. Examine the number of size standard and allele peaks found for each capillary.



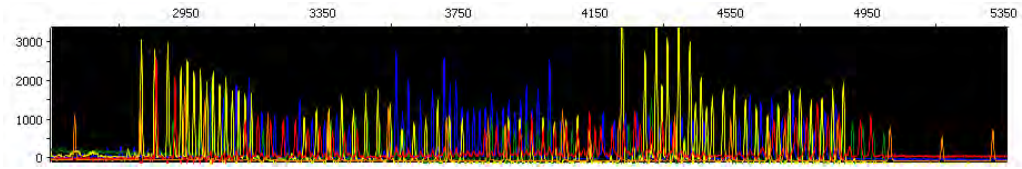
2. If all capillaries pass, click **Accept Results**.

   If any capillaries fail, the **Accept Results** button is dimmed. Evaluate the raw data for failed capillaries to determine if the install check can be accepted with the failed capillaries. If the run is acceptable, the software allows you to deselect capillaries and recalculate results.

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 Check** 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**.
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 **CutePDF Writer** as the 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 **CutePDF Writer** as the printer.
4. Specify a name and location for the report.

7 Manage library resources

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 3500 Series Data Collection Software 3.1 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.

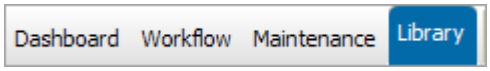
Entries in the library may be flagged with the following symbols:

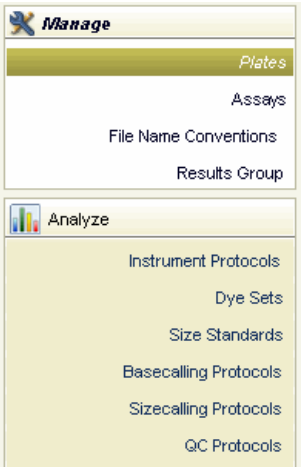
- Factory-provided. Cannot be edited or deleted.
- Template.
- Locked. If the SAE module is enabled on your system, a locked item can be unlocked and modified by the user who created it, the administrator, or another user with unlock permissions. For information, see Chapter 8, "Use Security, Audit, 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 207.

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 207.

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 207.

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 207.

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 3500 Series Data Collection Software 3.1 instruments:

- **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 8, "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 206.

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 207.

Plate templates

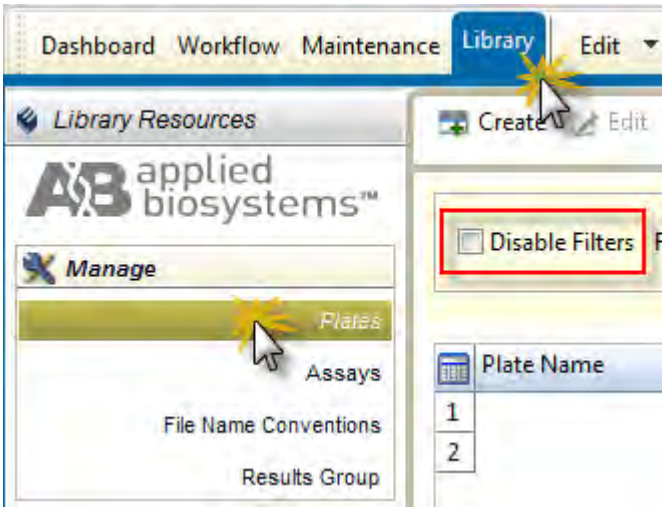
The Plates library includes templates that specify the appropriate application type, polymer, and capillary length. You can use these template to create new plates. To create your own templates, see "Create a plate template" on page 80.

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 3500 Series Data Collection Software 3.1 (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.



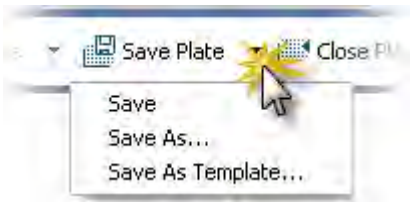
   The list of items in the library may be filtered based on the library filtering user preference. Click **Disable Filters** to show all items in the list.

2. Click **Create**. The software switches to the Workflow tab.

3. To create a new plate, specify settings ("Define plate properties" on page 147).

   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
Plate Details	
Name	Plate name. Names must be unique.
Number of Wells	• **96 well** — For standard 96-well plates standard reaction plates and 8-strip standard tubes with retainers. • **96 Fast tube** — For Fast 96-well plates and Fast 8-strip tubes with retainers. • **384 well** — For 384-well plates (24-capillary instruments only)
Plate Type	Sequencing, Fragment, or Mixed (Seq+Frag).
Capillary Length and Polymer	Capillary length and polymer type with which the plate will be used.
Owner, **Barcode**, **Description** (optional)	Optional text entries. You can use these entries to search for plates in the **Plates** library and in run logs (**Tools** ▸ **View Run Logs**).
Autoanalysis	Settings to communicate with secondary analysis software. For information, refer to 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:

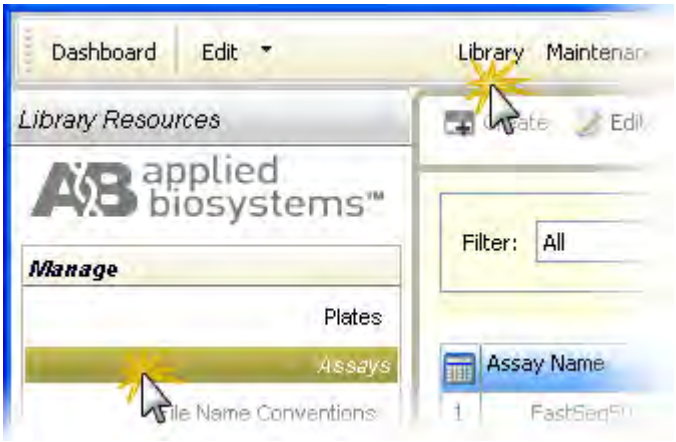
- One or more instrument protocols appropriate for the sample type/dye set for which the assay will be used
- A primary analysis protocol that depends on your application:
  - **Sequencing** — Basecalling protocol
  - **Fragment** — Sizecalling protocol
  - **HID** — QC protocol

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 207.

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 9) are described in "Assay settings" on page 149.

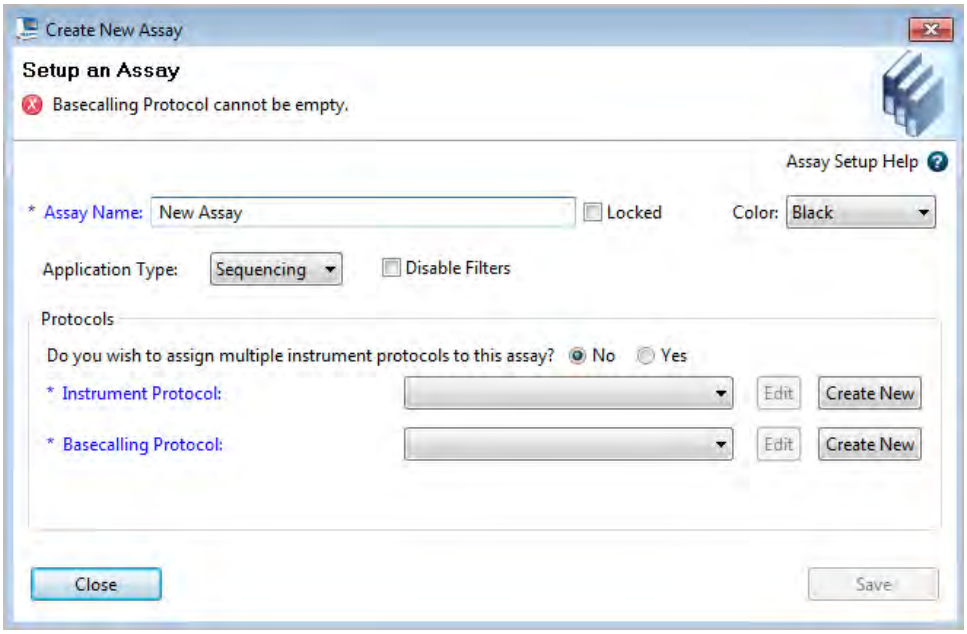
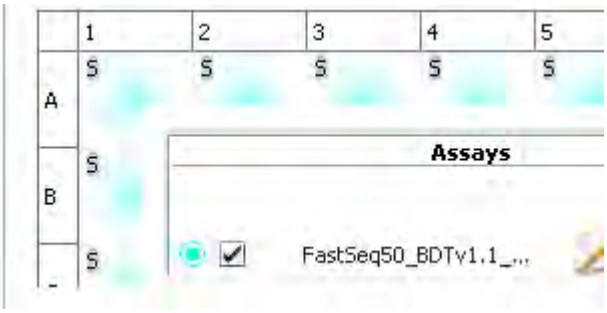
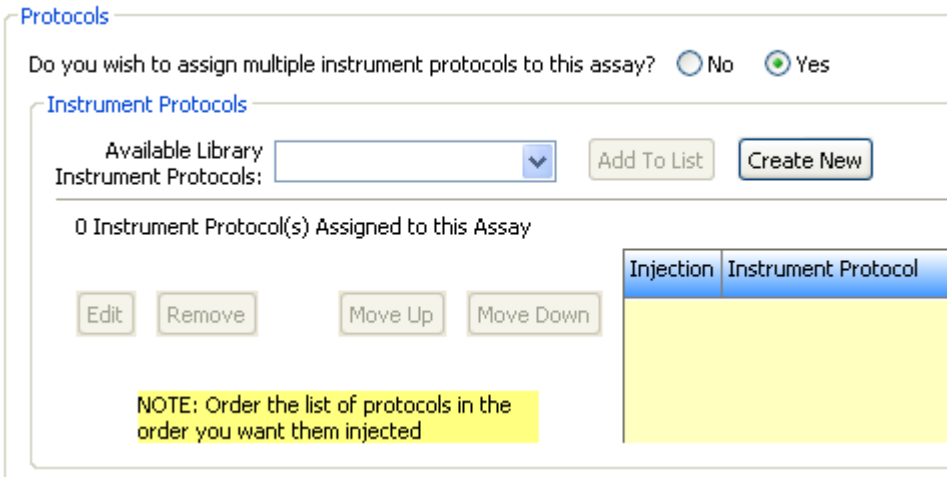


Figure 9 Create new assay

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 **Assign Plate Contents** screen (if **Assay Color** is selected for **Show In Wells**). 
Application Type	**Sequencing** or **Fragment**.

Setting	Description
Do you wish to assign multiple instrument protocols to this assay?	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. 
Instrument Protocol	Instrument protocol for data collection. For information, see "Instrument protocol settings" on page 166.
Basecalling Protocol (sequencing)	Protocol for basecalling, trimming, and quality determination. For information, see "Basecalling protocol - Analysis settings" on page 179.
Sizecalling Protocol (fragment analysis)	Protocol for primary analysis (peak detection and sizing) and quality determination. For information, see "Sizecalling protocol - Analysis settings" on page 183 .
QC Protocol (HID)	Protocol for primary analysis (peak detection and sizing) and quality determination. For information, see "QC protocols library (primary analysis - HID)" on page 187 .

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 38.)
- **Fragment analysis** — .fsa
- **HID** — .hid

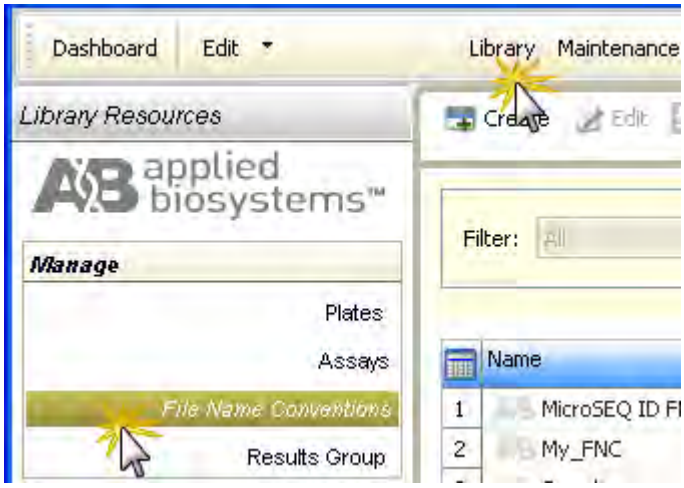
Note: The file location specified in a file name convention is used only if a results group is not specified for a well.

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 207.

Create a new file name convention

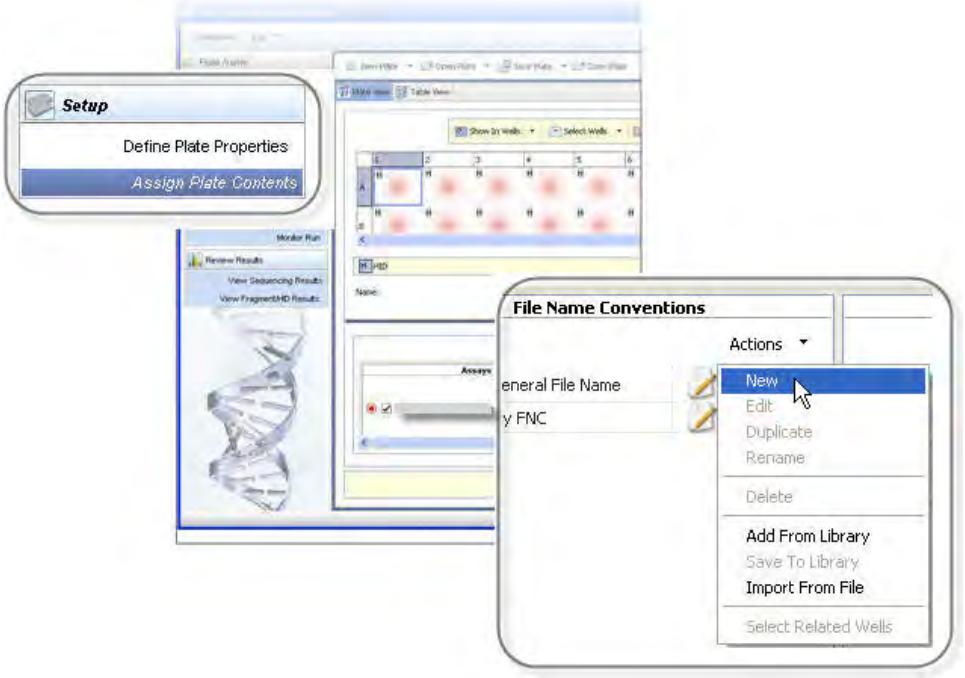
If factory-provided file name conventions do not suit your needs, you can create new file name conventions:

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



2. Click **Create**.

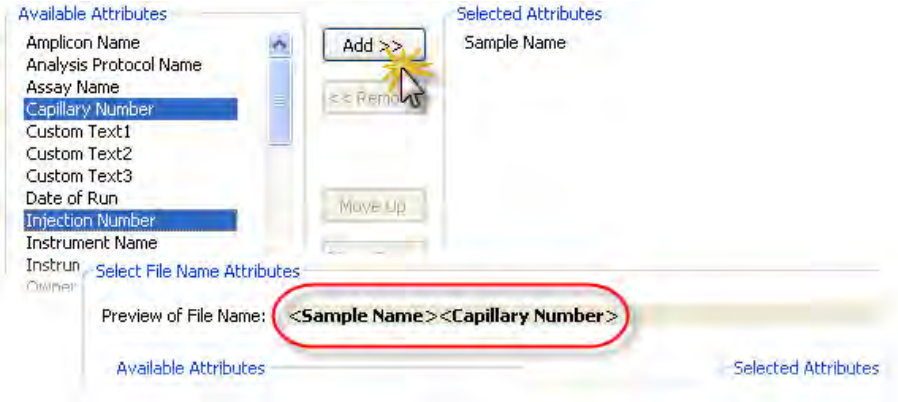
   Note: You can also create a file name convention from the **Assign Plate Contents** screen.



3. In the **Create New File Name Conventions** dialog box (Figure 10), select attributes and delimiters ("File name convention settings" on page 153).

   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**.

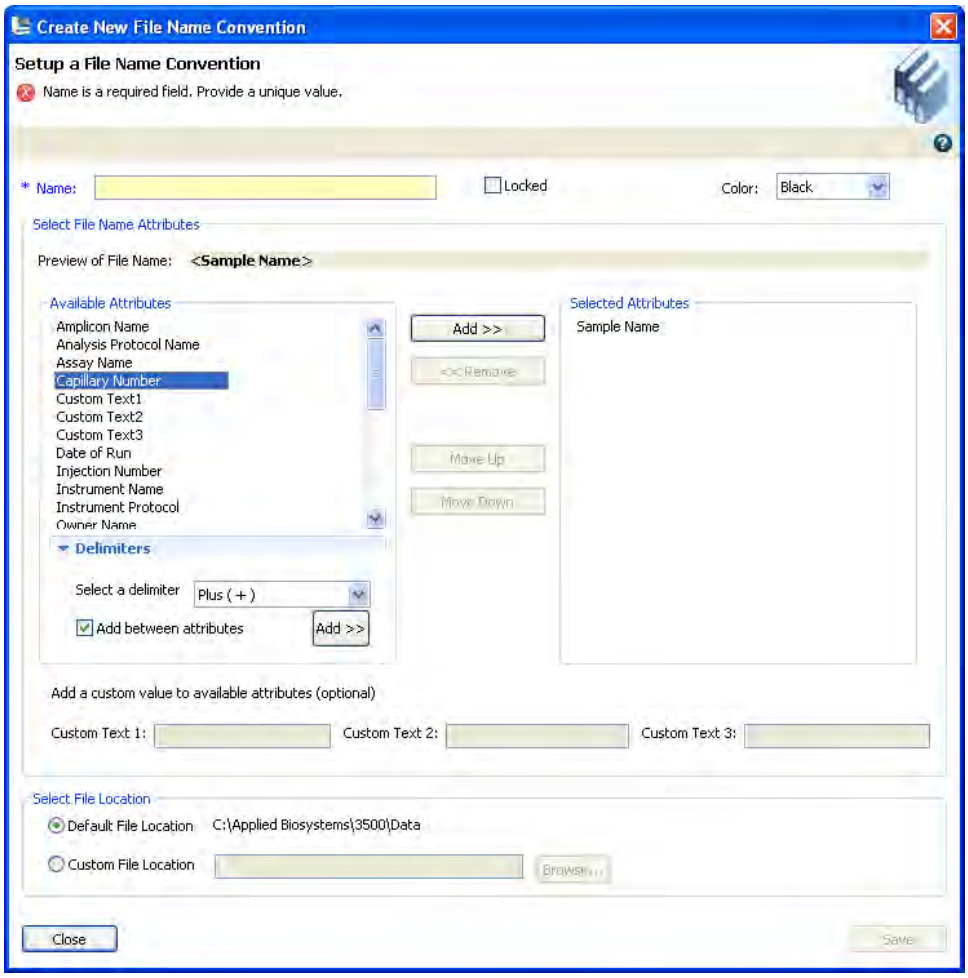
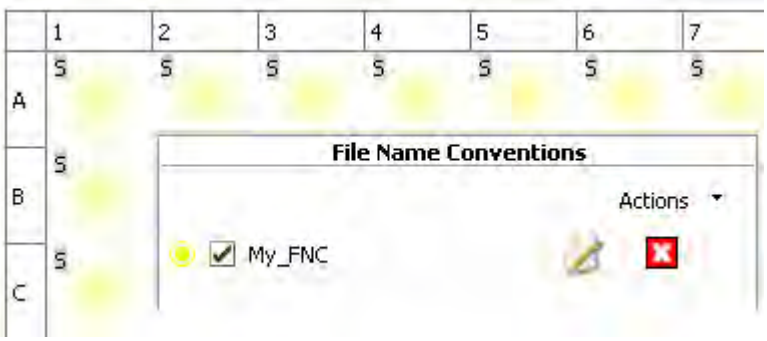


Figure 10 Create new File Name convention

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.

Setting	Description
Color	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). 
Preview of name	Interactively displays the attributes you select.
Available attributes	• Amplicon Name (from Customize Sample Info in sequencing assays) • Analysis Protocol Name (primary analysis protocol) • Assay Name • Capillary Number • Custom Text fields (≤3) • Date of Run • Injection Number • Instrument Name • Instrument Protocol • Owner Name (plate owner) • Plate Name • Polymer Type • run name • Sample Type • Specimen Name (from Customize Sample Info in sequencing assays) • Time of Run (run start time) • Unique Time Stamp Integer - (numeric string in milliseconds that does not correspond to the current time) • User-defined Fields (up to 5; specified in "Assign plate contents" on page 46) • User Name (available only when security is enabled in the SAE module) • Well Position
	IMPORTANT! 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.
Delimiters	Symbols you can include in the file name: Dash (-), Dot (.), Underscore (_), Plus (+), Dollar ($).

Setting	Description
Custom text	Text to display for the custom text attribute fields.
File location	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.

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 207.

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

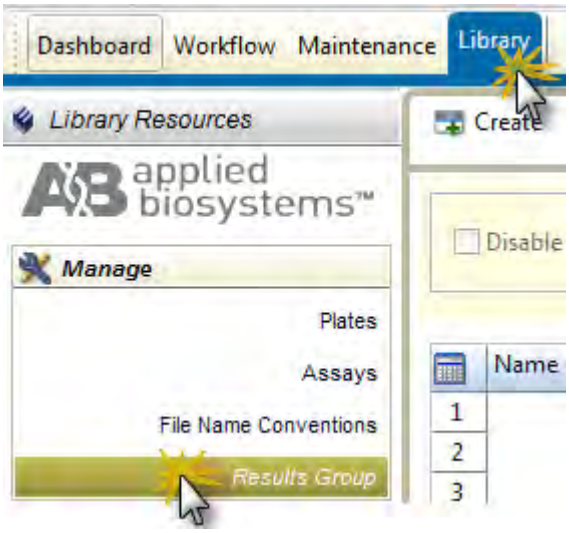
Note: Run HID validation studies to determine the required number of allelic ladders for your application.

See "Results Group example 3: store one allelic ladder per run folder (8-capillary instruments)" on page 163 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 11 on page), select attributes and delimiters (“Results group settings“ on page 158).

   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.

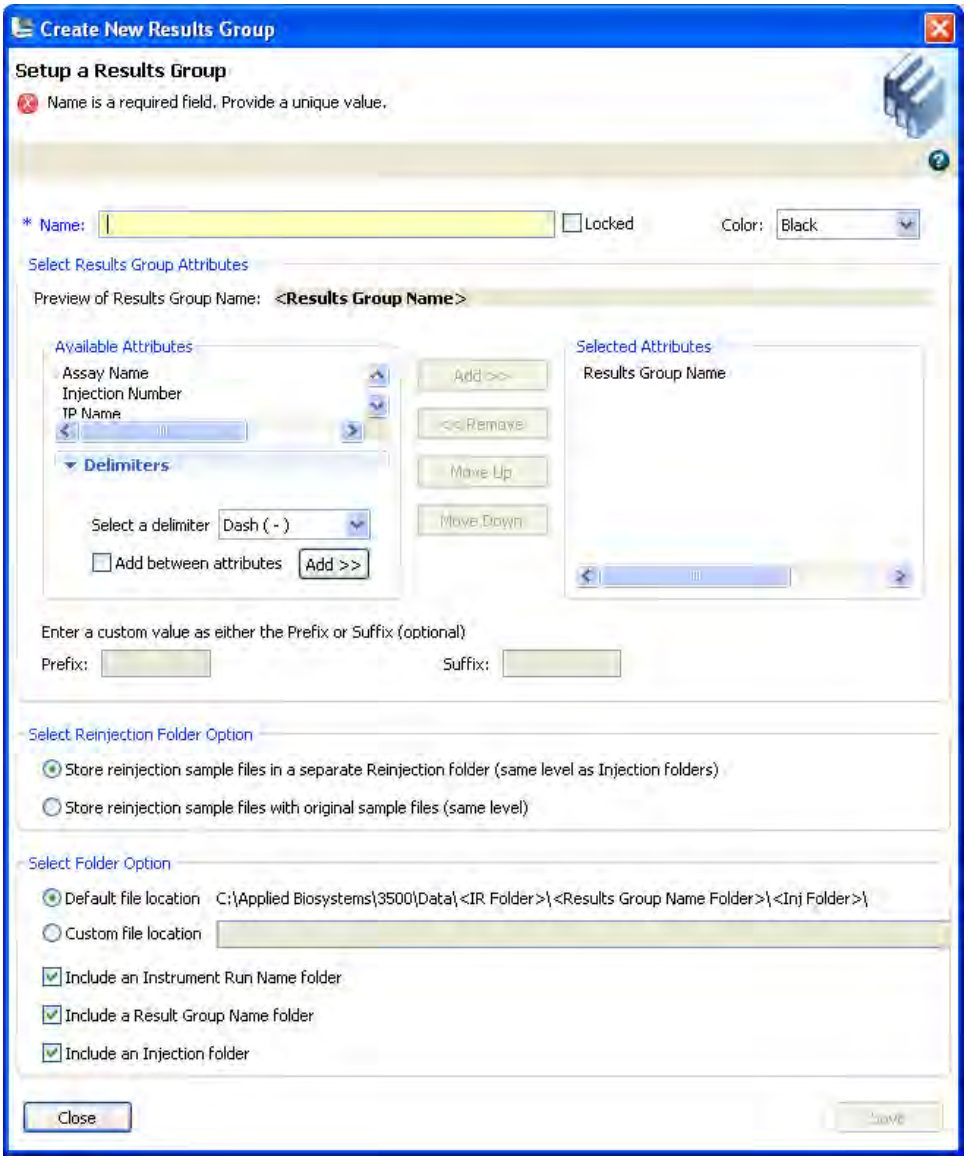
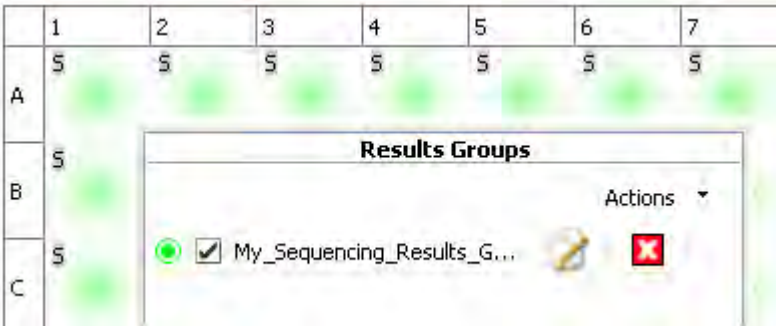


Figure 11 Create New Results Group

Results group settings

Setting	Description
Name	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.
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.

Setting	Description	
Color	Color code for the results group when it is displayed in the **Assign Plate Contents** screen (if **Results Group Color** is selected for **Show In Wells**). 	
Preview of name	Interactively displays the attributes you select.	
Available attributes	• **Results Group Name** (required) • **Assay Name** • **Injection Number** • **IP Name** (instrument protocol) • **Logged-in User Name** (available only when security is enabled in the SAE module)	• **PA Protocol Name** (primary analysis=basecalling protocol) • **Plate Name** • **Prefix** • **Start Instrument Run Date**/time Stamp • **Suffix**
Delimiters	Symbols you can include in the results group name: Dash (-), Dot (.), Underscore (_), Plus (+), Dollar ($).	
Prefix/suffix text	Text to display for the prefix or suffix text attribute fields.	
Select re-injection folder option	• Store reinjection sample files in a separate reinjection folder (same level as injection folders). • Store reinjection sample files with original sample files (same level).	
Select folder option	Location: • Default file location (specified in **Preferences** ▸ **User** ▸ **Run Setup**) • Custom location Sub-folder options: • Include an instrument run name folder (run name can be user-defined in the Load Plates for Run screen) • Include a results group name folder • Include an injection folder	

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 12 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 13 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.

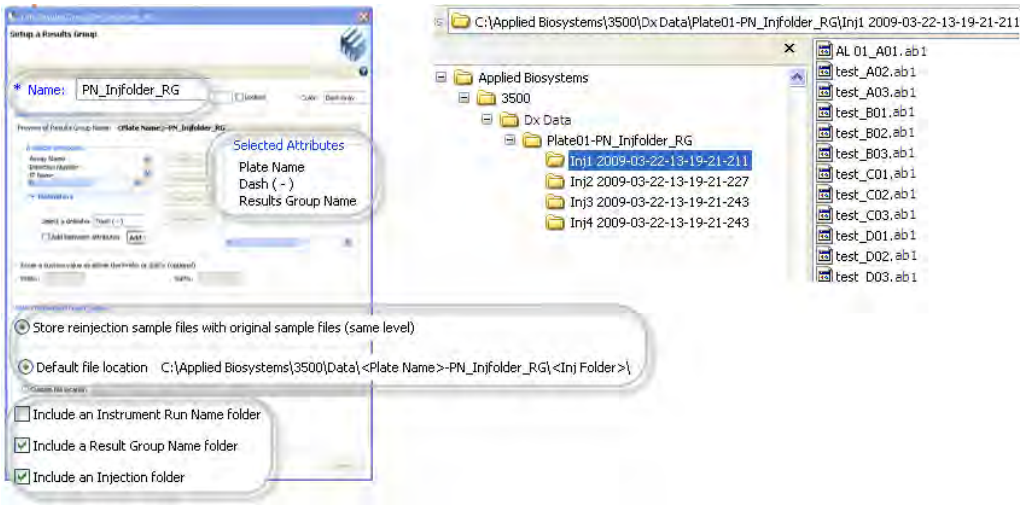


Figure 12 PN_Injfolder_RG results group

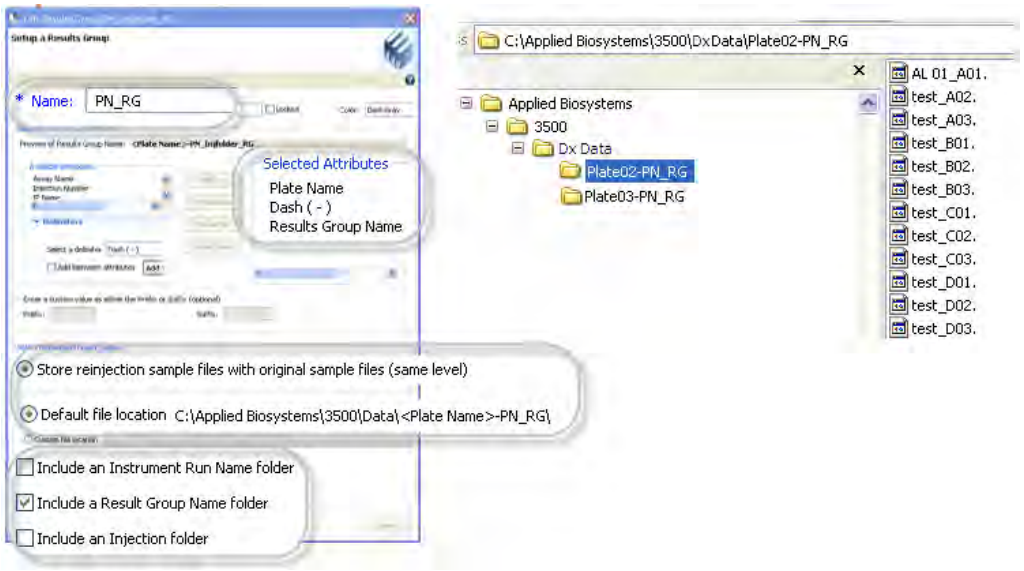


Figure 13 PN_RG results group

Results Group example 2: store re-injections in separate folders

Figure 14 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 17).

Figure 14 Results group example

Figure 15 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 17).

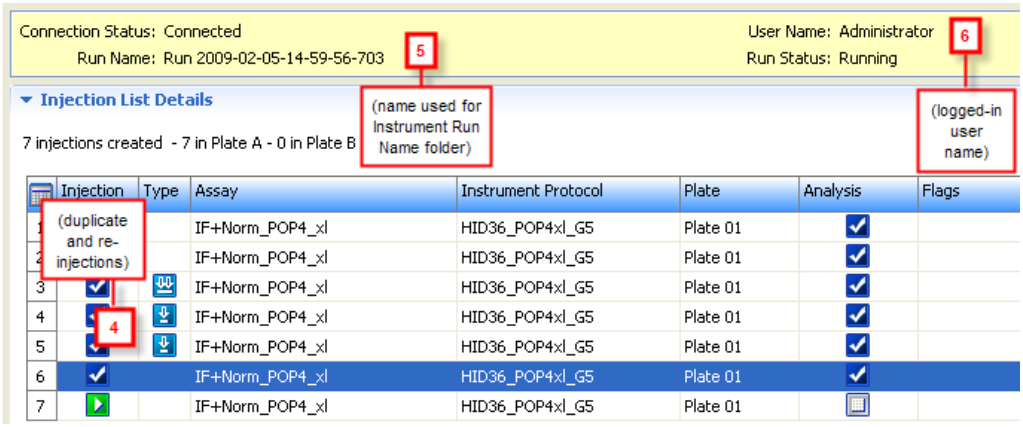


Figure 15 Injection list example

Figure 16 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 17).

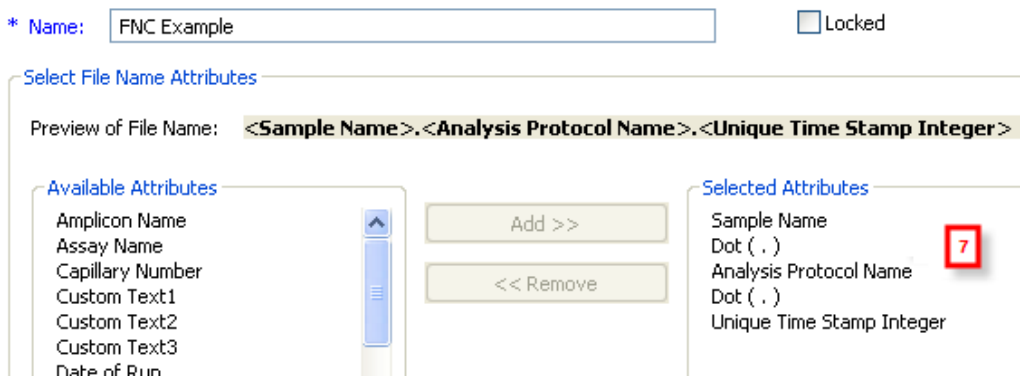


Figure 16 File name convention example

Figure 17 shows the folders and files generated by the results group, file name convention, run name, and injections shown in Figure 14, Figure 15, and Figure 16.

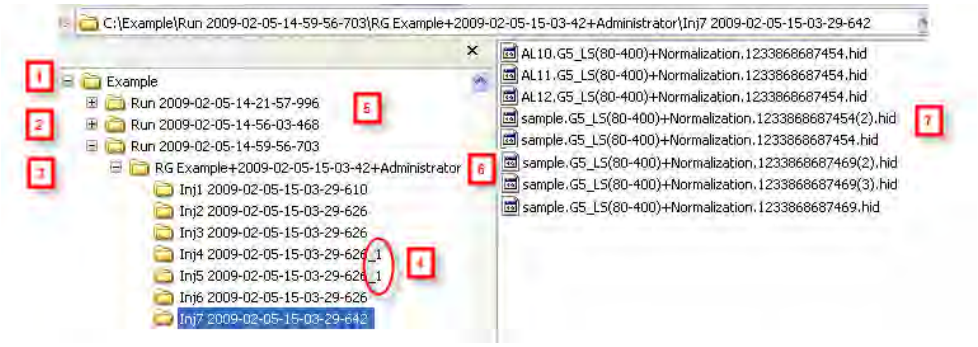


Figure 17 Folder hierarchy and file naming example

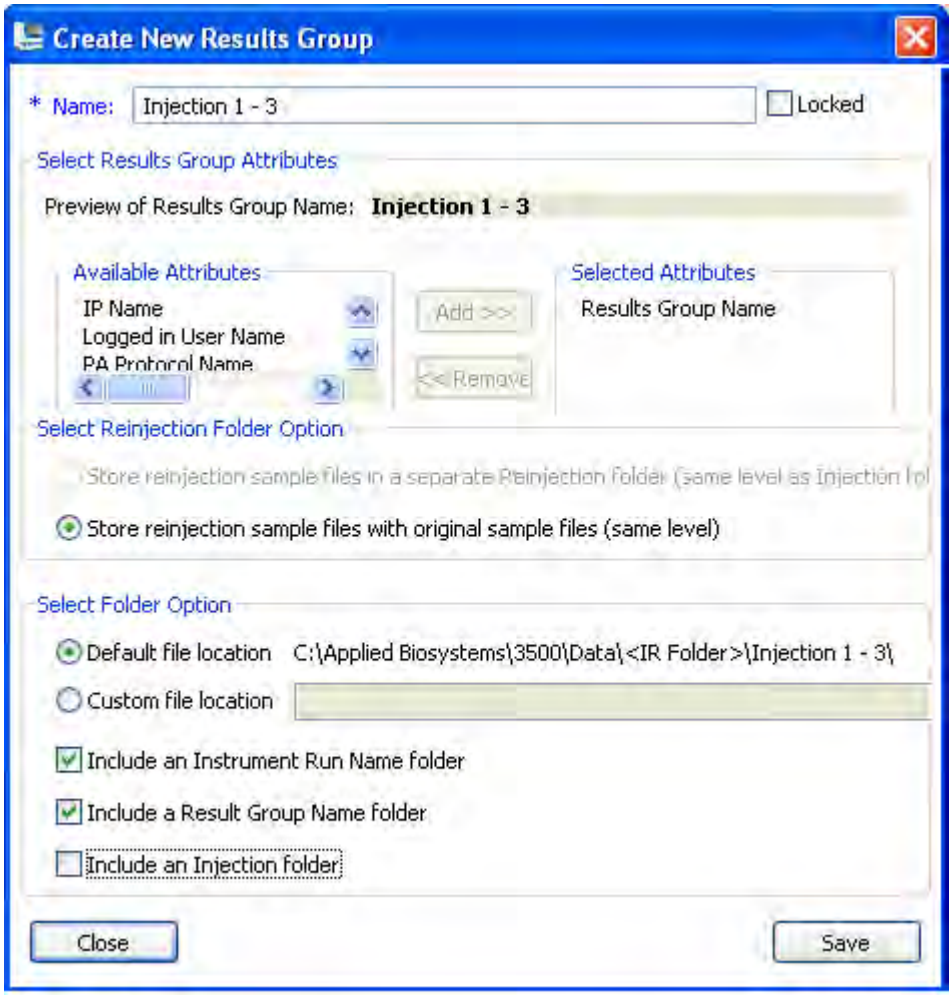
1	File location from results group ◉ Custom file location C:\Example
2	Instrument Run Name folder from results group ☑ Include an Instrument Run Name folder
3	Results group Name folder from results group ☑ Include a Result Group Name folder
4	Injection folder from results group ☑ Include an Injection folder Duplicate injections indicated with `_n` where `n` is the number of duplicates.
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 **RG Example+<Start Instrument Run Date/Time Stamp>+<Logged in User Name**
7	File name syntax from file name convention **<Sample Name>.<Analysis Protocol Name>.<Unique Time Stamp Integer>**

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 155).

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.



Instrument protocol library

Instrument protocol overview

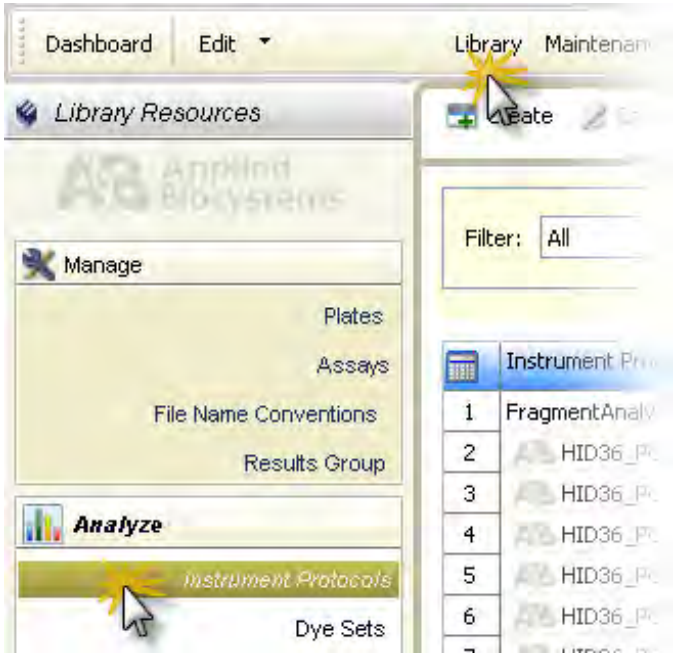
An instrument protocol contains the parameters that control the instrument during data acquisition. An instrument protocol is a required element of an assay for all applications.

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 207.

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**.

3. In the Create New Instrument Protocol dialog box (Figure 18), select an application type: Sequencing, Fragment, or HID. The run module selection list is filtered based on the application you select.

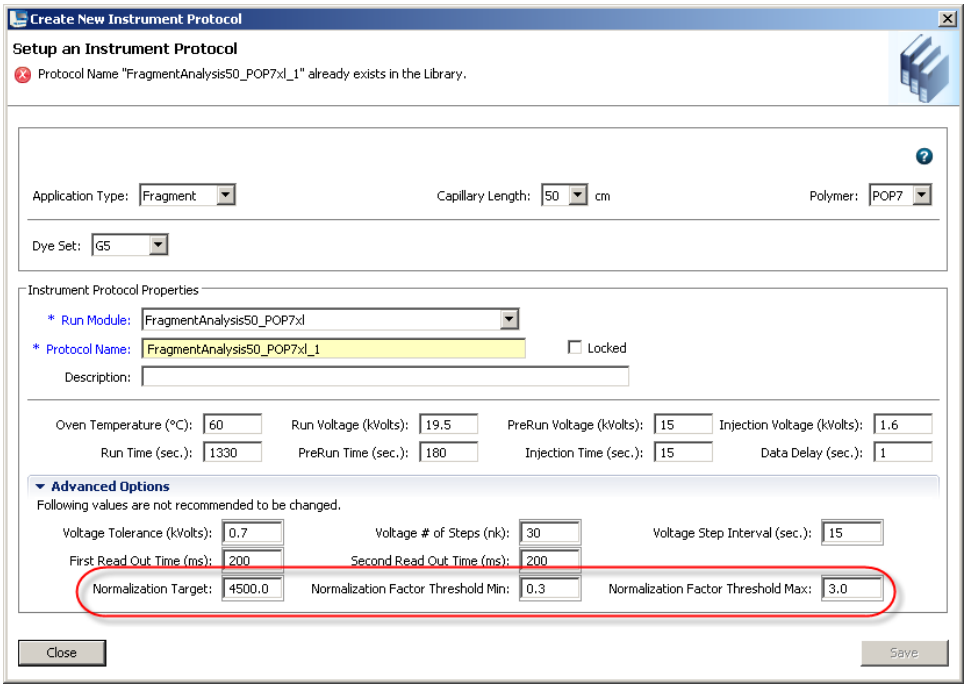


Figure 18 Create New Instrument Protocol

Note: Normalization parameters circled in red are displayed for fragment analysis and HID applications only.

4. Specify settings (“Instrument protocol settings“ on page 166).

5. 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	• **Sequencing** • **Fragment analysis** • HID
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.

Setting	Description
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 8, "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.
Advanced options - Do not change unless advised otherwise by Life Technologies support personnel	
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.
Fragment and HID protocols only: Normalization parameters - Leave at default settings (for information on how these parameters are used, see "Review normalized data" on page 98).	
Normalization Target	The expected average RFU for the subset of peaks in the GS600 LIZ® v2 size standard used for normalization. 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. **IMPORTANT!** 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).

Setting	Description
Normalization Factor Thresholds	The passing range for Normalization Factor (default range is 0.3 to 3.0). **IMPORTANT!** Increasing the factor threshold above 3.0 may cause amplification of noise. 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).
Normalization Factor	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.

Dye sets library

Dye set overview

A dye set defines the following for an instrument protocol:

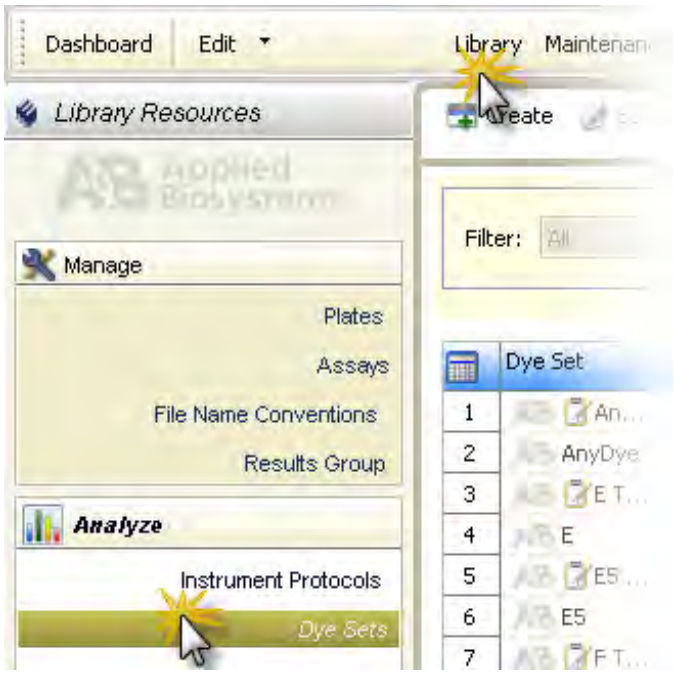
- Dye color(s)
- Order of the dye peaks in the standard
- Spectral analysis parameters

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 207.

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**.

3. In the Create New Dye Set dialog box (Figure 19), specify settings (“Dye set settings“ on page 170).

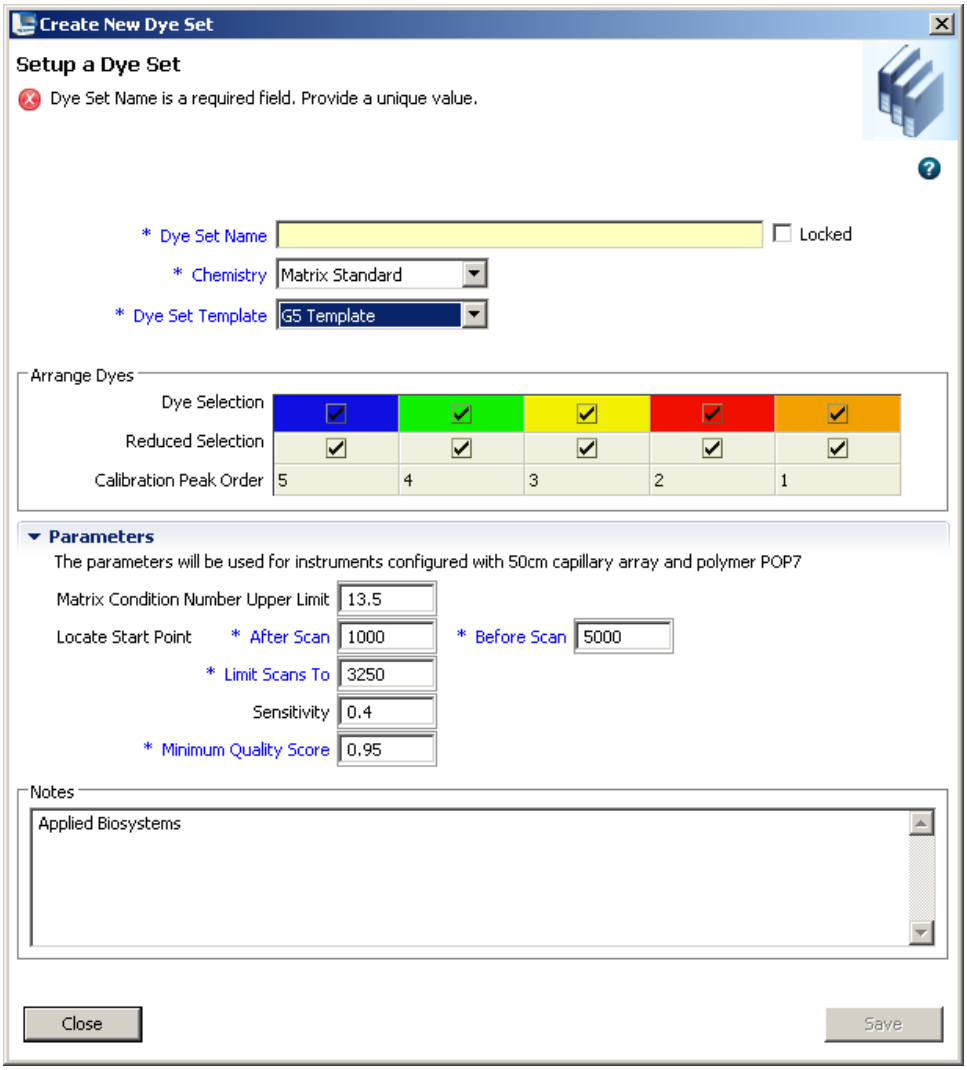


Figure 19 Create New Dye Set

4. Click **Save**.

Dye set settings

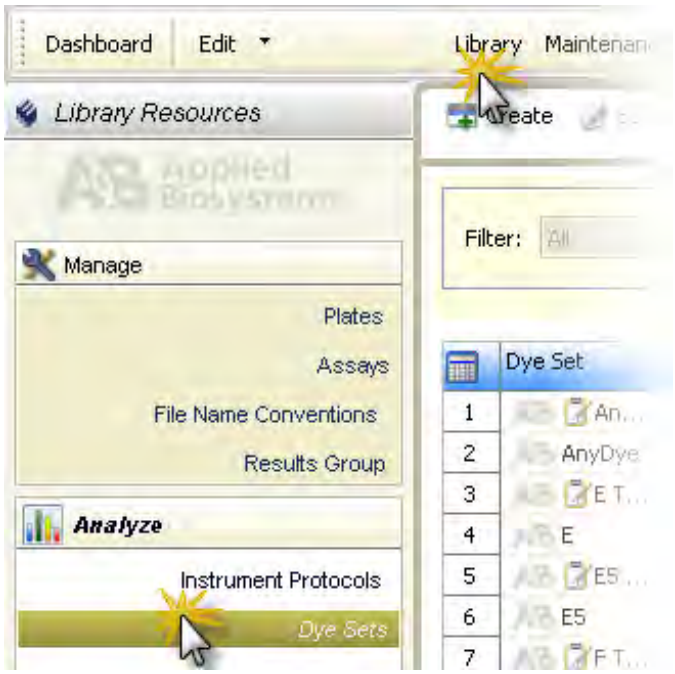
Setting	Description
Dye Set Name	Name of the dye set. Names must be unique.
Locked	When enabled, allows the entry to be unlocked and modified only by the user who created it, the administrator, or another user with unlock permissions. Useful when your system includes the SAE module (described in Chapter 8, “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

Setting	Description
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 171.
Arrange Dyes	Displays the dyes and the peak order for the dye set template selected. Editable only for AnyDye template: • **Dye Selection** — Specifies the dyes to use for calibration • **Reduced Selection** — Specifies the dyes used in the samples. 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.

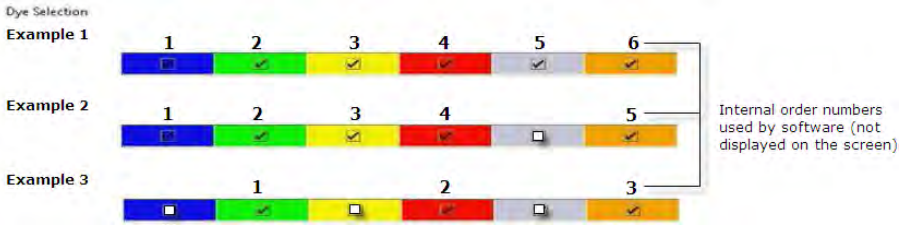


2. Click **Create**.
3. Enter a dye set name.
4. Select a chemistry and the **AnyDye** dye set template.

5. 5. Select the dye colors to use and set the calibration peak order:
   a. Select the dye colors to use.

      The dye colors you select sets the order number of the dye used internally by the software. Note that when you deselect a dye, the order number of the dye used internally by the software changes.

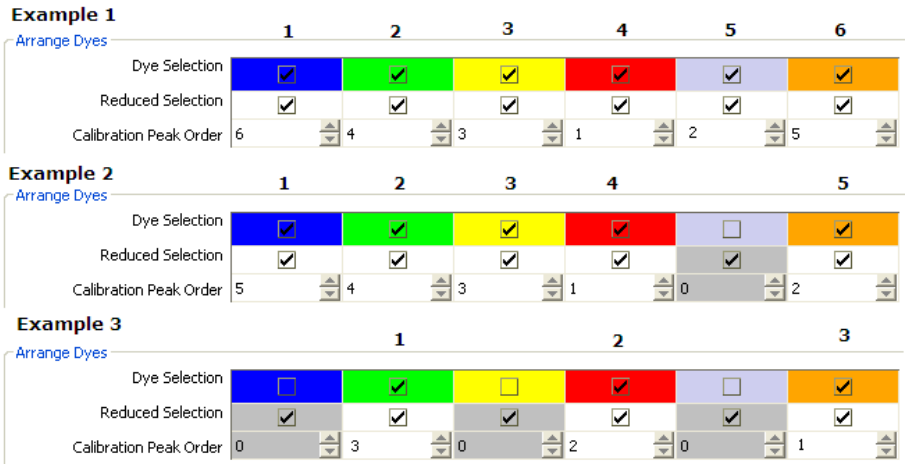
      - **Example 1** — With all dyes selected, internal order number is Blue (1), Green (2), Yellow (3), Red (4), Purple (5), Orange (6).
      - **Example 2** — With the Purple dye deselected, internal order number is Blue (1), Green (2), Yellow (3), Red (4), Orange (5) - the internal order number of Orange changes to 5.
      - **Example 3** — With the Blue, Yellow, and Purple dyes deselected, internal order number is Green (1), Red (2), Orange (3) - the internal order number of Green changes to 1, Red changes to 2, and Orange changes to 3.



b. Specify the order of the peaks in the calibration standard you are using. Use the internal order number of the dye based on the dyes selected.

IMPORTANT! The Calibration Peak Order fields do not correspond to the dye colors displayed above the Calibration Peak Order fields.

- **Example 1** — If the order of the peaks in the calibration standard you are using is Orange, Red, Yellow, Blue, Green, Purple, specify for Calibration Peak Order: 6 (Orange), 4 (Red), 3 (Yellow), 1 (Blue), 2 (Green), 5 (Purple).
- **Example 2** — If the order of the peaks in the calibration standard you are using is Orange, Red, Yellow, Blue, Green, specify for Calibration Peak Order: 5 (Orange), 4 (Red), 3 (Yellow), 1 (Blue), 2 (Green).
- **Example 3** — If the order of the peaks in the calibration standard you are using is Orange, Red, Green, specify for Calibration Peak Order: 3 (Orange), 2 (Red), 1 (Green).



6. Expand the Parameters section, then specify remaining settings.

7. 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 207.

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.

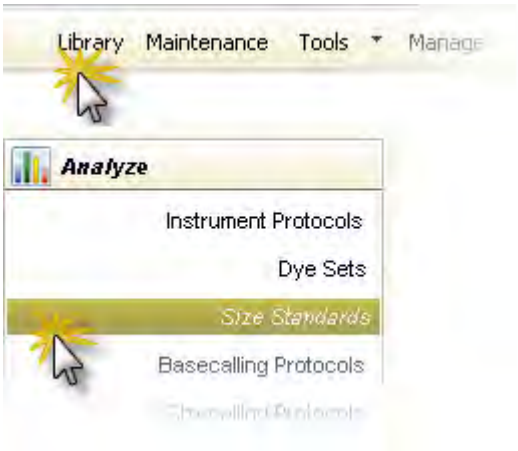
IMPORTANT! Normalization is not applied to samples with failing sizing quality. Select a size standard definition file appropriate for your application that accurately sizes samples. For example, if your application includes small fragments that may be obscured by primer peaks, or large fragments that 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 98.

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 20), 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 (described in Chapter Chapter 8, "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**.

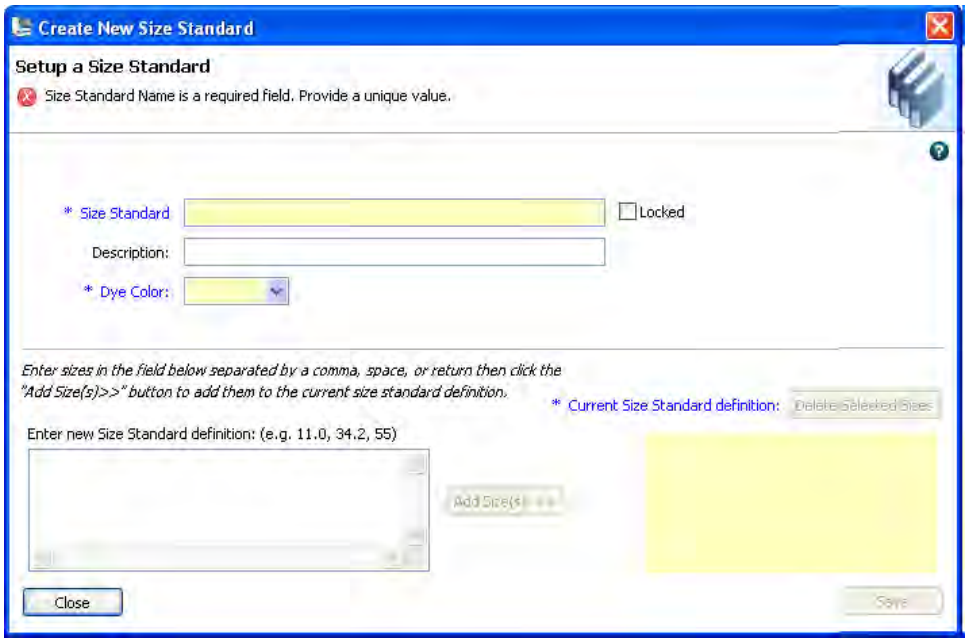


Figure 20 Create New Size Standard

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:

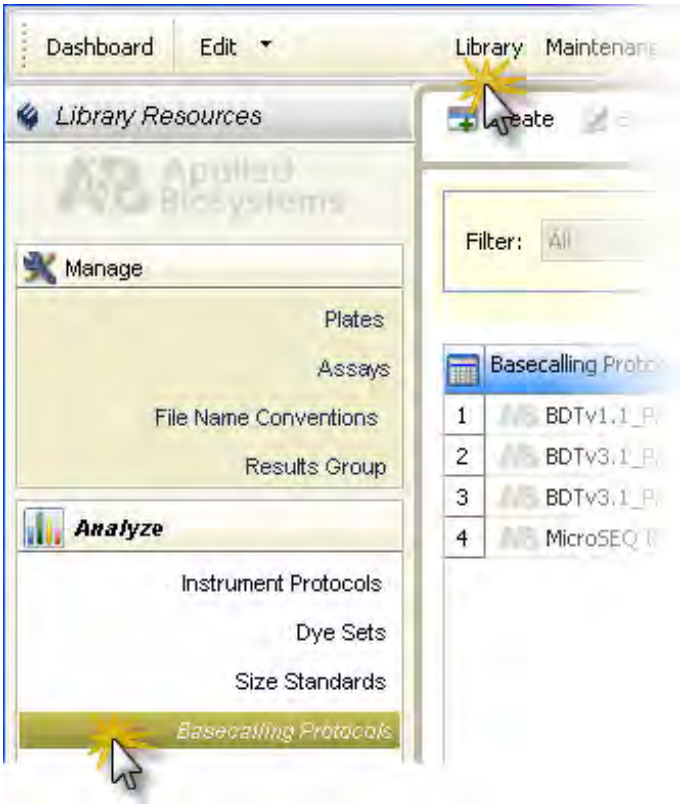
- Analysis settings
- Ranges for the sequencing quality flags displayed in View Results

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 207.

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 21), specify settings "Basecalling protocol - Analysis settings" on page 179.

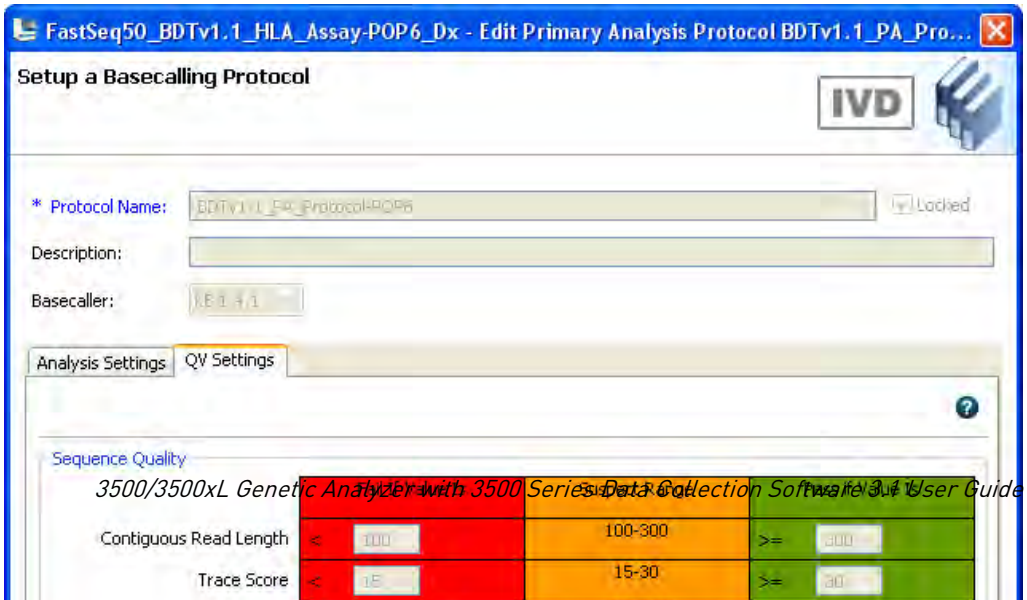
4. Click **QV Settings**. In the QV Settings tab of the Create New Basecalling Protocol dialog box (Figure 22), specify settings (see "Basecalling protocol - QV settings" on page 180).

   QV settings are quality value ranges used in the following screens:

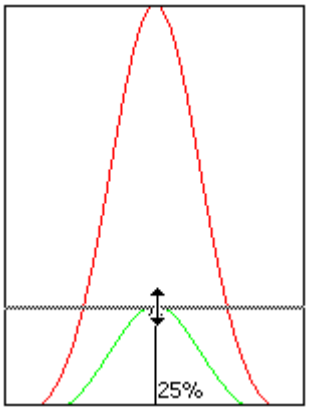
   - **Monitor Run screen** — The state of the QV flag:
     - If all three values are in the pass range, the QV flag in Monitor Run is set to  (green).
     - If any values are in the suspect range, the QV flag in Monitor Run is set to  (yellow).
     - If any values are in the fail range, the QV flag 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.

5. Click **Save**.

Figure 21 Create New Basecalling Protocol - Analysis Settings



Basecalling protocol - Analysis settings

Setting	Description
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 8, "Use Security, Audit, and E-Sig functions (SAE Module)".
Description	Optional text entry.
Basecaller	Basecalling algorithm used to identify bases. **Note:** 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.
Mobility file	Compensates for mobility differences between dyes used to label the DNA.
Quality Threshold	• Basecall Assignment (ambiguous bases): – Do not assign Ns to basecalls – Assign Ns to basecalls with QV<15 - Bases with a QV less than the threshold display N instead of the base letter • Ending base - Last base on which to perform basecalling: • At PCR Stop • After X number of Bases • After X number of Ns in X number of Bases • After X number of Ns **Note:** If you have PCR products with sequences that end while data is still being collected, select the **At PCR Stop** check box.
Mixed bases threshold	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 <= to 25 % 

Setting	Description
Analyzed Data Scaling	Determines scaling of the processed traces. This parameter does not affect the accuracy of the basecalling. • **True Profile** — 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. • **Flat Profile** — 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 (> about 40 bases).
Clear range methods	• **Use clear range minimum and maximum** — Specifies the first and last base in the range to consider, or trims the specified number of bases from the 3′ end. • **Use quality values** — Sets a window with a specified number of allowed low-quality bases by removing bases until there are < X number of bases per Z number of bases with QV < Y. • **Use identification of N cells** — Sets a window with a specified number of allowed ambiguous base calls (Ns) by removing bases until there are < X number of Ns per Y number of bases.

Basecalling protocol - QV settings

Setting	Description
Contiguous Read Length	The longest uninterrupted segment of bases with an average Quality Value (QV) ≥20. In addition to evaluating the QV of a base call, the software considers the QV of adjacent bases within a ±20-bp moving average 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 20, sliding 1 bp at a time, to the 3′ end. The resulting longest contiguous segment is determined as the CRL.
Trace Score	The average basecall quality value (QV) of bases in the clear range sequence of a trace. The *clear range* 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.
QV20+	The total number of bases in the entire trace with quality values ≥20.

Sizecalling protocols library (primary analysis - fragment)

Sizecalling protocol overview

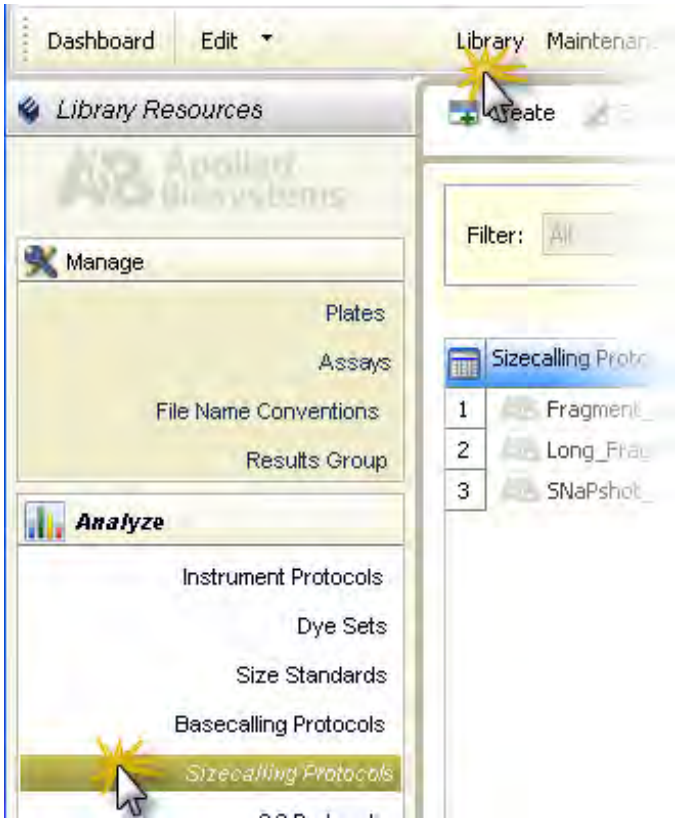
A sizecalling protocol is the required primary analysis protocol for fragment applications.

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 207.

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 23), specify settings (see "Sizecalling protocol - Analysis settings" on page 183).
4. Click **QC Settings**. In the QC Settings tab of the Create New Sizecalling Protocol dialog box (Figure 24), specify settings ("Sizecalling protocol - QC settings" on page 186).

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 3500 Series Data Collection Software 3.1 does not support re-analyzing data with new settings.

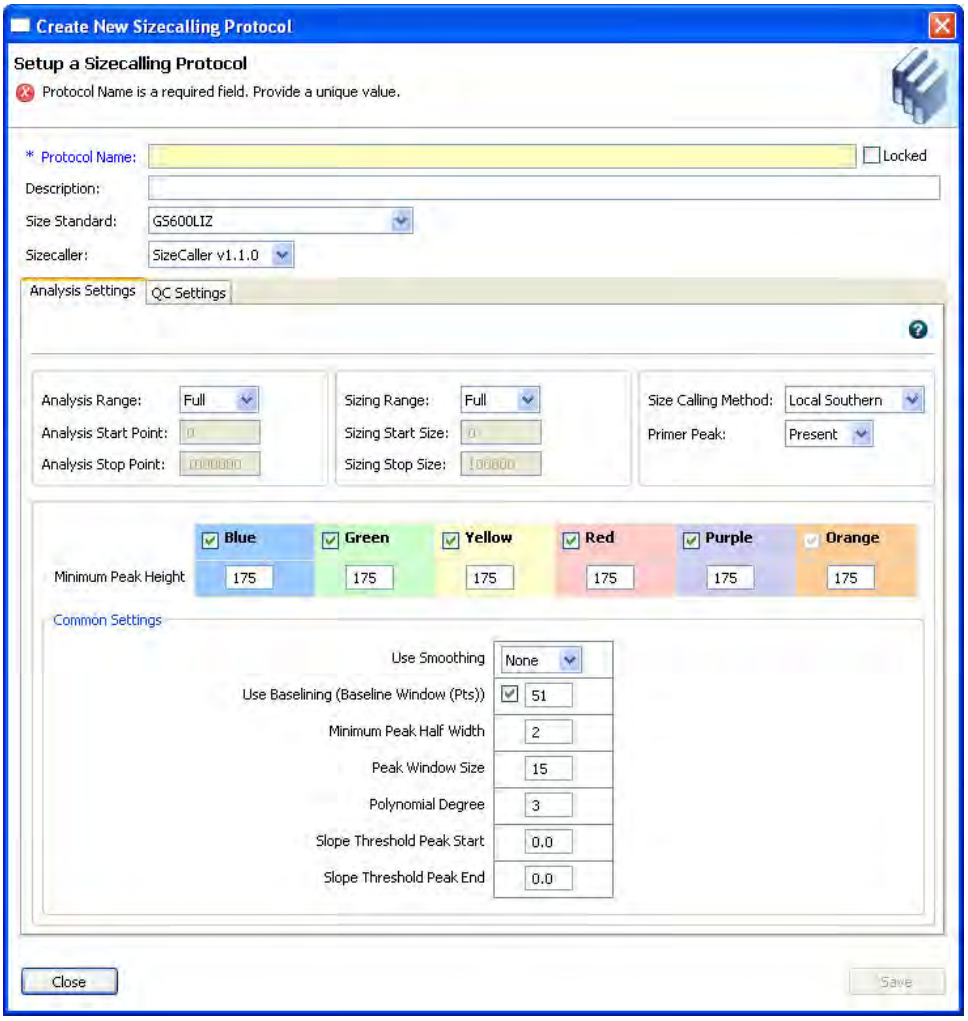


Figure 23 Create New Sizecalling Protocol – Analysis Settings

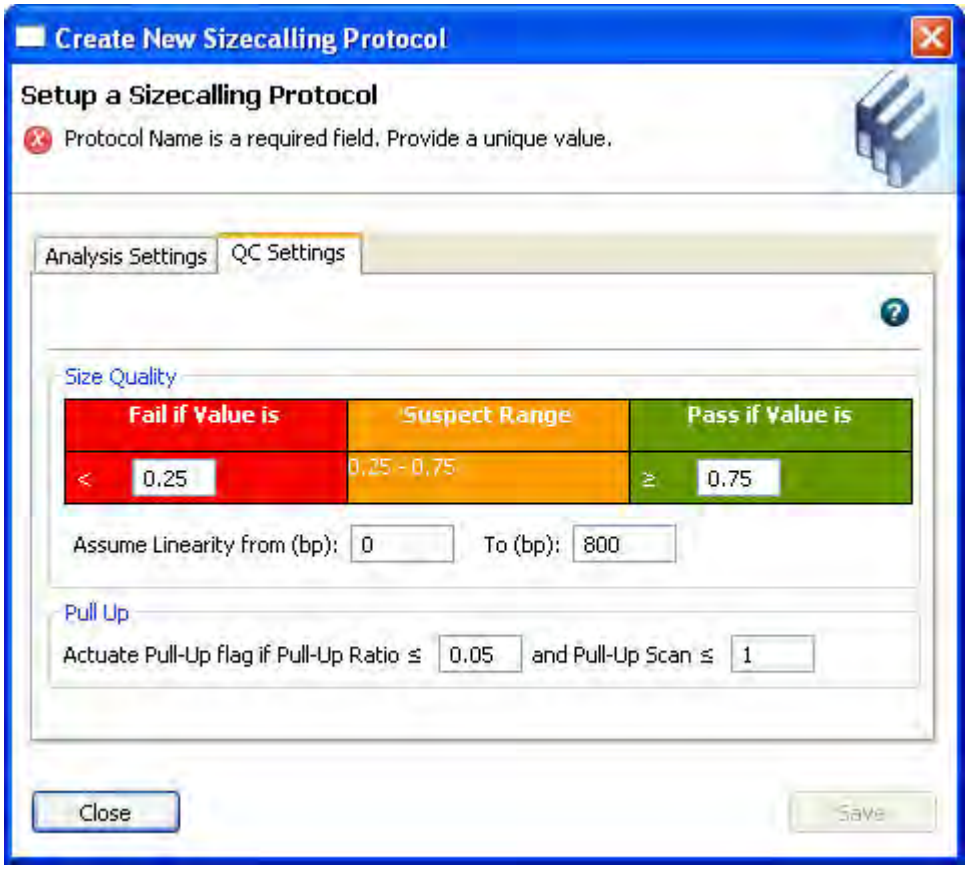


Figure 24 Create New Sizecalling Protocol – QC Settings

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 174).

Setting	Description
Analysis Range	The range (in data points) to analyze: • **Full Range** to analyze the entire scan region as collected by the genetic analysis instrument, including the primer peak. • **Partial Range** to analyze only data points within a specified range. Enter **Start Point** in data points after the primer peak and before the first required size standard peak. Enter a **Stop Point** 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. Data points outside the specified analysis range are ignored. **Note:** Ensure the Analysis Range contains all size standard fragments included in the Sizing Range specified below.
Sizing Range	The size range (in base pairs) appropriate for the kit you are using: • **All Sizes** for the software to analyze fragments of all sizes in the Analysis Range. • **Partial Sizes** for the software to analyze only fragments within a specified range. Enter a **Start Size** and a **Stop Size** appropriate for the size standard used.
Size Calling Method	• **Local Southern** — (default) Determines the fragment sizes using the reciprocal relationship between fragment length and electrophoretic mobility. • **3rd Order Least Squares** — Uses regression analysis to build a best-fit size calling curve. • **2nd Order Least Squares** — Uses regression analysis to build a best-fit size calling curve. • **Cubic Spline Interpolation** — Forces the sizing curve through all the known points of the selected size standard. • **Global Southern Method** — Compensates for standard fragments with anomalous electrophoretic mobility (similar to least squares methods).
Primer Peak	If the primer peaks in your application obscure peaks of interest, select **Present**. Selecting Present instructs the algorithm to ignore primer peaks. Primer peaks are still displayed in the trace. **Note:** 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.
Peak Amplitude Thresholds	Specify the threshold (RFU) for peak detection for each dye color. Peaks below the threshold are not detected. 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. **Note:** Use the same peak amplitude thresholds in secondary analysis software.

Setting	Description
Smoothing	Select an option to smooth the outline of peaks and reduce the number of false peaks detected: • **None** (default) to apply no smoothing. Best if the data display sharp, narrow peaks of interest. • **Light** to provide the best results for typical data. Light smoothing slightly reduces peak height. • **Heavy** for data with very sharp, narrow peaks of interest. Heavy smoothing can significantly reduce peak height.
Baseline Window	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: • 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. • 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.
Min. Peak Half Width	Specify the minimum full peak width at half maximum **Peak Height** required for peak detection. The range is 2 to 99 data points.
Polynomial Degree	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.
Peak Window Size	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: • The maximum value is the number of data points between peaks. • The Peak Window Size setting is limited to odd numbers. To increase peak detection sensitivity: Increase polynomial degree, decrease peak window size. To decrease peak detection sensitivity: Decrease polynomial degree, increase peak window size.

Setting	Description
Slope Thresholds Peak Start and End	• **Peak Start** — 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. • **Peak End** — 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.

Sizecalling protocol - QC settings

Setting	Description
Size Quality	The **Pass Range** and the **Fail Range** for the SQ flag displayed in **View Fragment Results**. 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). For example, with a Pass Range of 0.75 to 1.0 and a Fail Range of 0.0 to 0.25, any result ≥0.75 is , any result <0.25 is , and any result between ≥0.25 to <0.75 is . **How Size Quality is determined** 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).
Assume Linearity	Defines the expected linear range. Useful in large fragment size standards where non-linearity might be expected.
Pull-Up	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: • ≤X% (pull-up ratio) of the major peak *and* • Within ±Y data point (pull-up scan) of the major peak 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.

QC protocols library (primary analysis - HID)

QC protocol overview

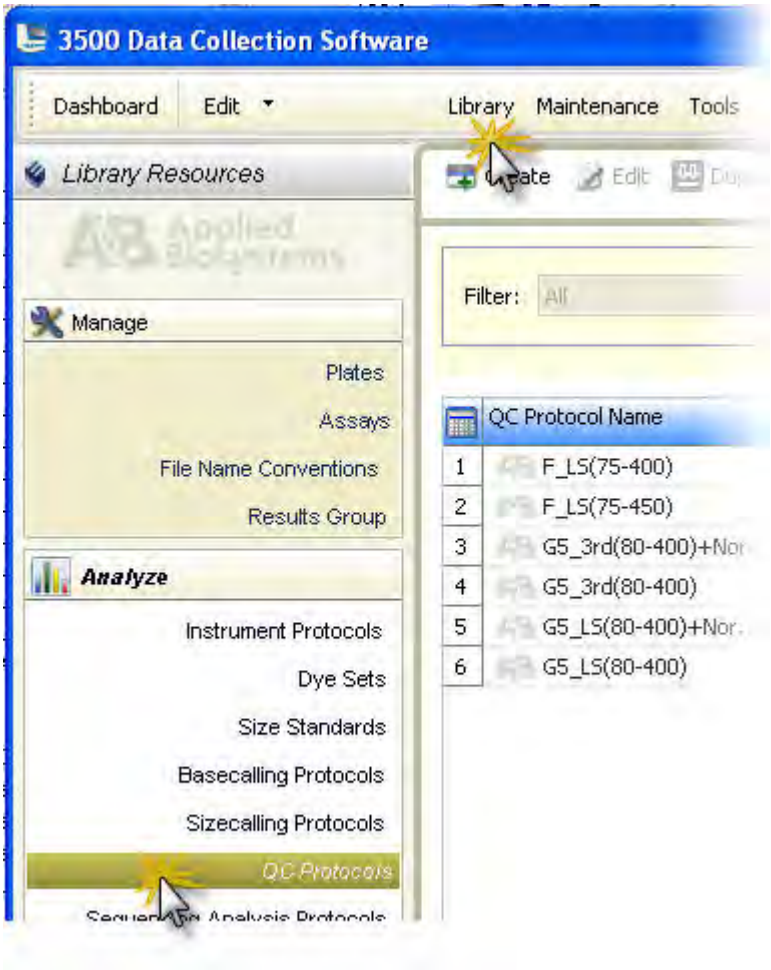
A QC protocol is the required primary analysis protocol for HID applications. A QC protocol defines peak detection, sizing, and quality values.

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 207.

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 25), specify settings ("QC protocol - Analysis settings" on page 189).

4. Click **QC Settings**. In the QC Settings tab of the Create New QC Protocol dialog box (Figure 26), specify settings ("QC protocol - QC settings" on page 192).

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 3500 Series Data Collection Software 3.1 does not support re-analyzing data with new settings.

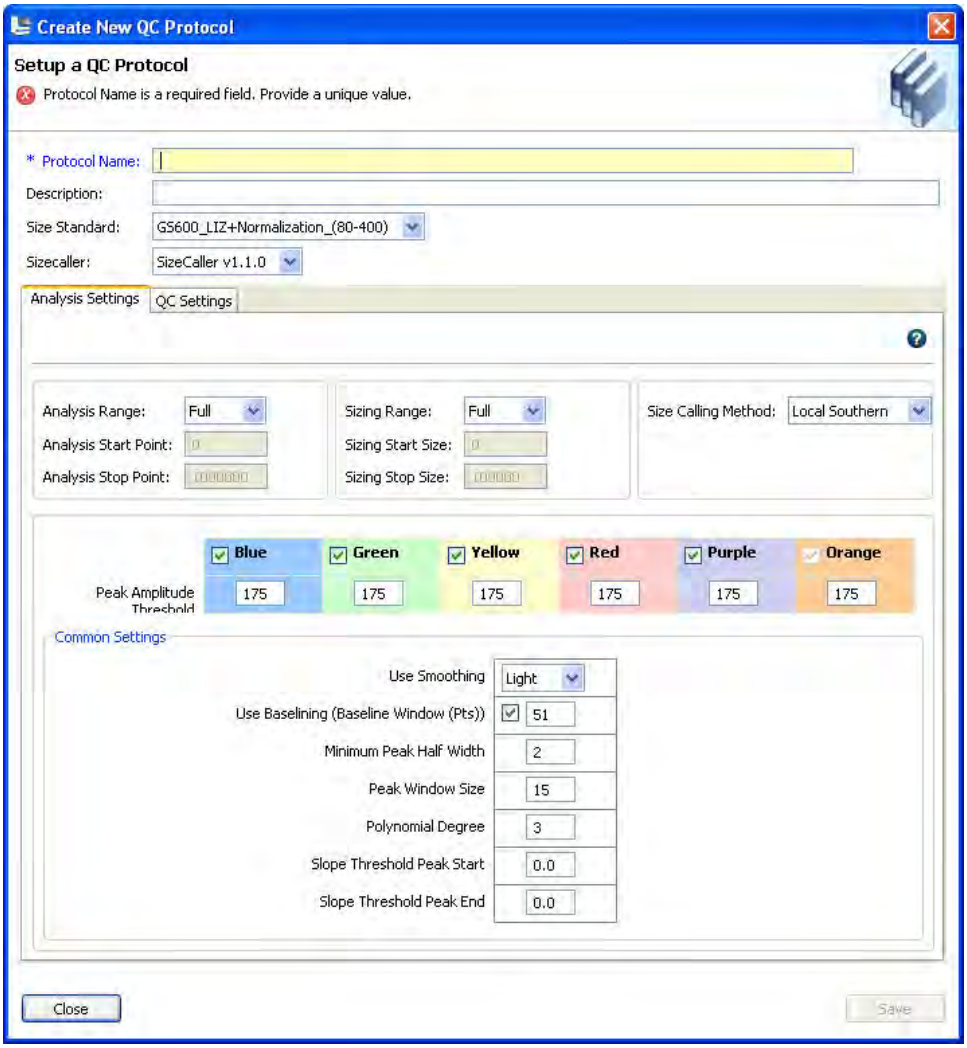


Figure 25 Create New QC Protocol – Analysis Settings

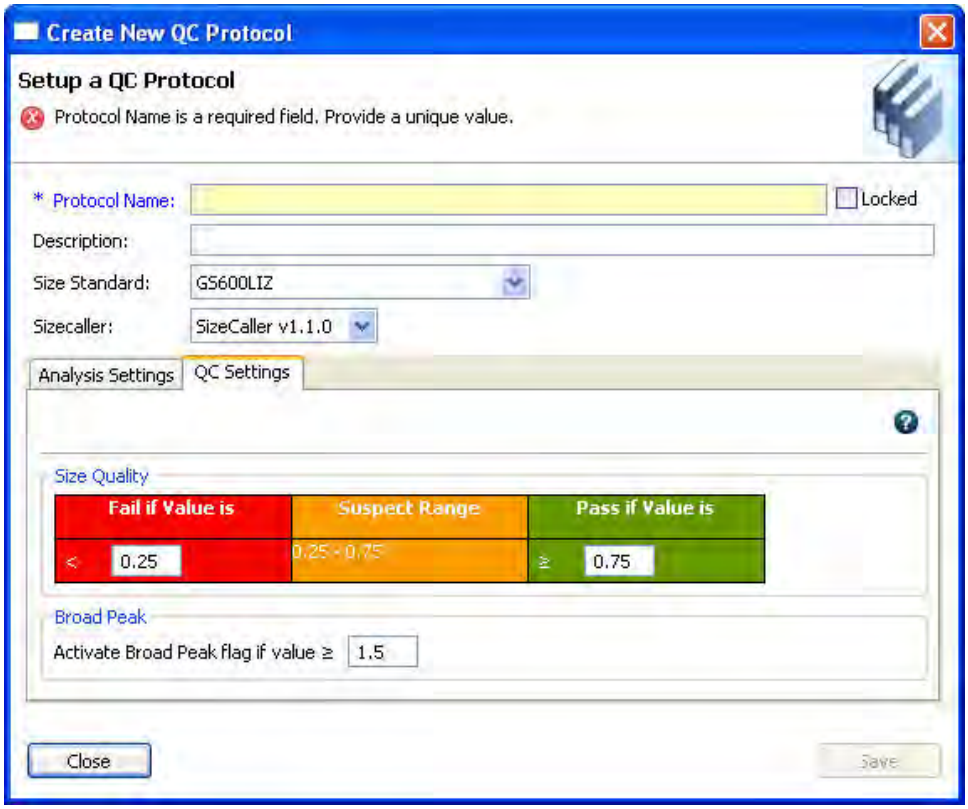


Figure 26 Create New QC Protocol – QC Settings

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 174).
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. **Note:** If you select Partial, ensure that the Analysis Range contains all size standard fragments included in the Sizing Range specified below.
Sizing Range	Select **Partial**, then specify **80** to **400** to limit the fragment sizes evaluated for the size standard. If you specify sizes outside this range, the Sizing Quality may fail.

Setting	Description
Size Calling Method	Select the method to determine the molecular length of unknown fragments appropriate for the AmpFℓSTR® kit you use: • **Local Southern** — (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. • **3rd Order Least Squares** — Uses regression analysis to build a best-fit size calling curve. • **2nd Order Least Squares** — Uses regression analysis to build a best-fit size calling curve. • **Cubic Spline Interpolation** — Forces the sizing curve through all the known points of the selected size standard. • **Global Southern Method** — Compensates for standard fragments with anomalous electrophoretic mobility (similar to least squares methods).
IMPORTANT! 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 3500 Series Data Collection Software 3.1 does not support re-analyzing data with new settings. For more information on peak detection parameters, see the *GeneMapper® ID-X Software Reference Guide*.	
Smoothing	Select an option to smooth the outline of peaks and reduce the number of false peaks detected: • **None** to apply no smoothing. Best if the data display sharp, narrow peaks of interest. • **Light** (default) to provide the best results for typical data. Light smoothing slightly reduces peak height. • **Heavy** for data with very sharp, narrow peaks of interest. Heavy smoothing can significantly reduce peak height.
Baseline Window	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: • 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. • 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.
Peak Amplitude Thresholds	IMPORTANT! Optimize these thresholds during internal HID validation. Specify the threshold (RFU) for peak detection for each dye color. Peaks below the threshold are not detected. 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. **Note:** Use the same peak amplitude thresholds in secondary analysis software.

Setting	Description
Min. Peak Half Width	Specify the smallest half peak width at full height for peak detection. The range is 2 to 99 data points.
Polynomial Degree	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.
Peak Window Size	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: • The maximum value is the number of data points between peaks. • The Peak Window Size setting is limited to odd numbers. To increase peak detection sensitivity: Increase polynomial degree, decrease peak window size. To decrease peak detection sensitivity: Decrease polynomial degree, increase peak window size.
Slope Thresholds Peak Start and End	Not recommended for use with AmpFℓSTR® kit data. • **Peak Start** — 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. • **Peak End** — 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.

QC protocol - QC settings

Setting	Description
Size Quality	Enter the Pass Range and the Fail Range for the SQ flag displayed in View HID Results. 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). For example, with a Pass Range of 0.75 to 1.0 and a Fail Range of 0.0 to 0.25, any result ≥0.75 is , any result <0.25 is , and any result between ≥0.25 to <0.75 is . **How Size Quality is determined** 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). **Weighting** The Broad Peak (BD) threshold specified in the QC Protocol - QC Settings tab affects the SQ. To determine the final SQ value, the software: • Evaluates size standard peak widths in the sample in the dye color specified in the size standard definition. • If the width of any size standard peak in the sizing range exceeds the broad peak threshold, applies a 0.5 weighting factor: • Interim SQ × (1 – 0.5) **Note:** The GeneMapper® *ID-X* Software allows you to set broad peak weighting. For more information, see the *GeneMapper® ID-X Software Reference Guide*.
Broad Peak	Enter the maximum peak width (in base pairs). 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.

8 Use Security, Audit, and E-Sig functions (SAE Module)

Section 8.1 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.

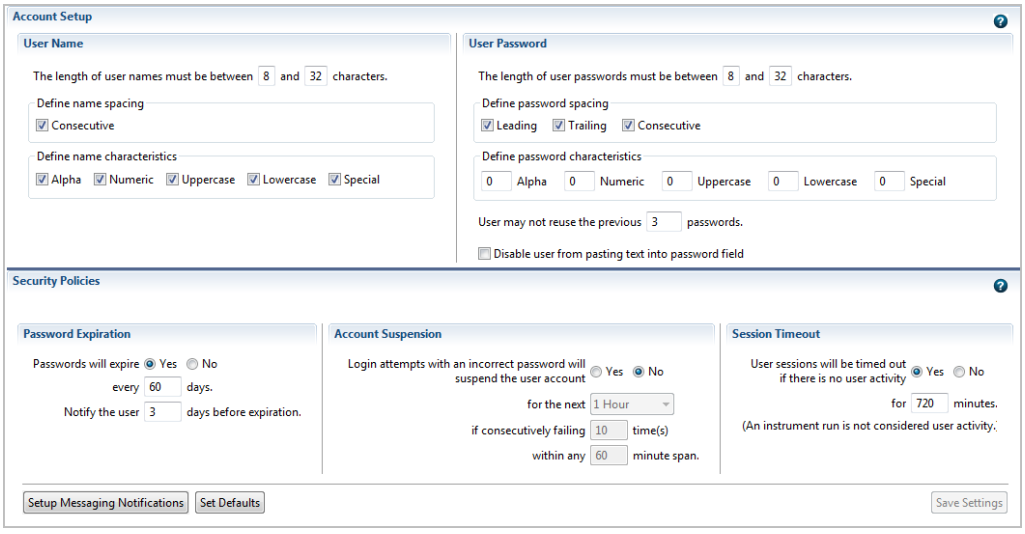
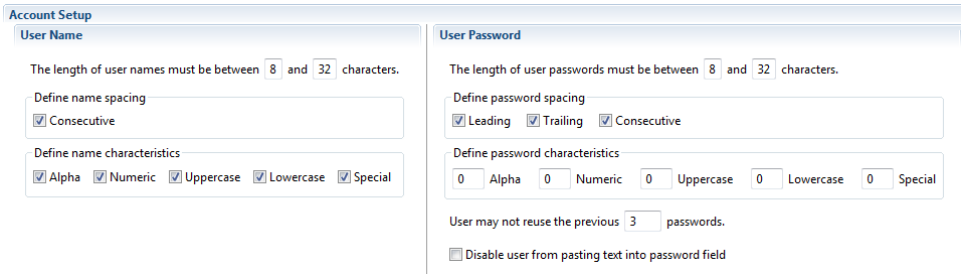


Figure 27 Security screen

Set account setup and security policies

Security policies apply to all user accounts.

1. Under **Account Setup**, specify user name limits.



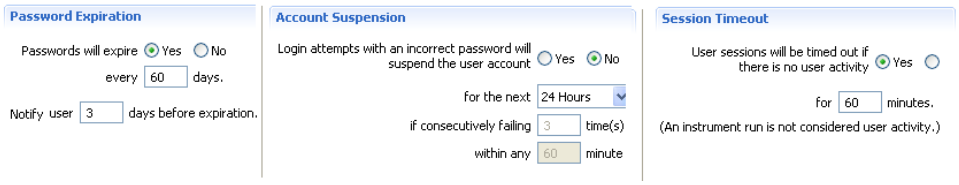
IMPORTANT! The software allows spaces in user names (Define name spacing). Use spaces in user names with caution. For information, see "Spaces in user names" on page 196.

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.



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 197.

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

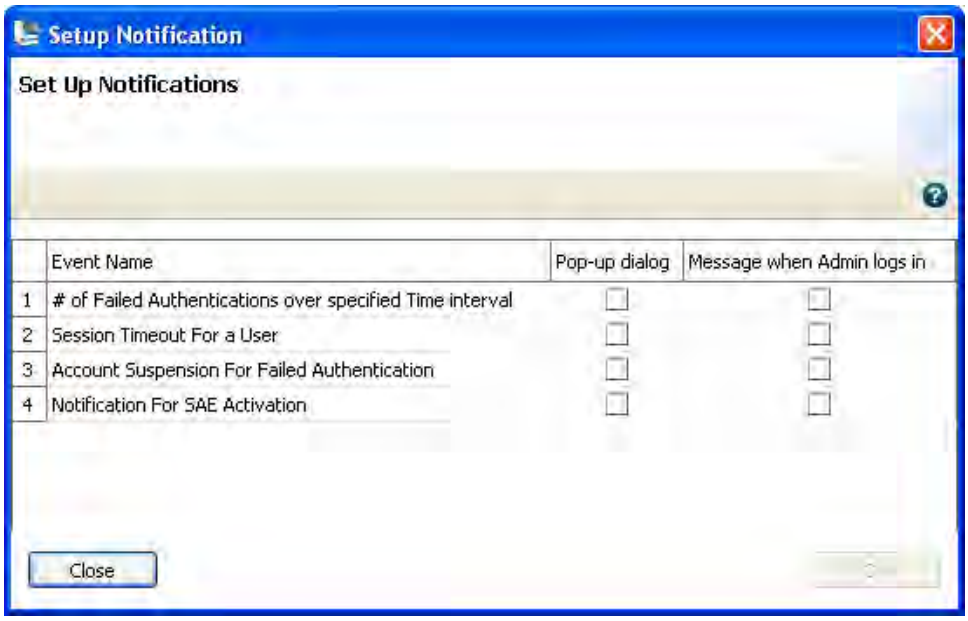
If you allow spaces in user names, be aware of the following issues:

- 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 27), 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**.

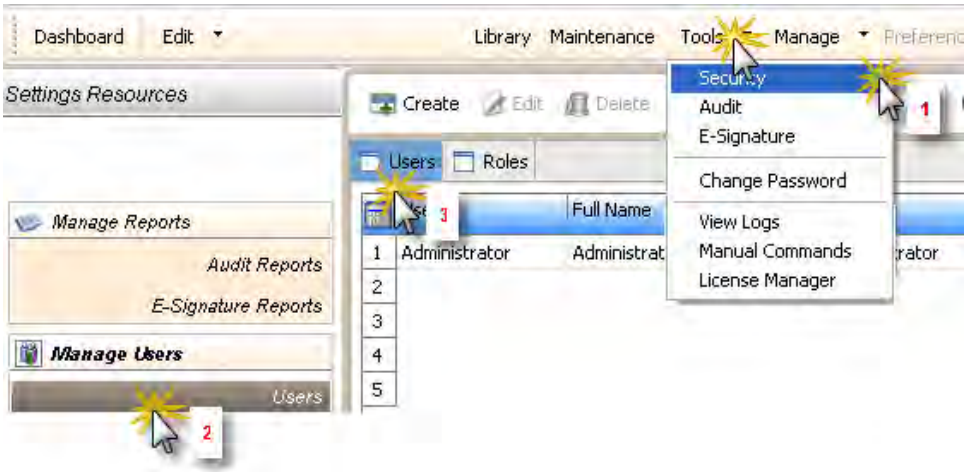
Manage user accounts

Create or edit a user account

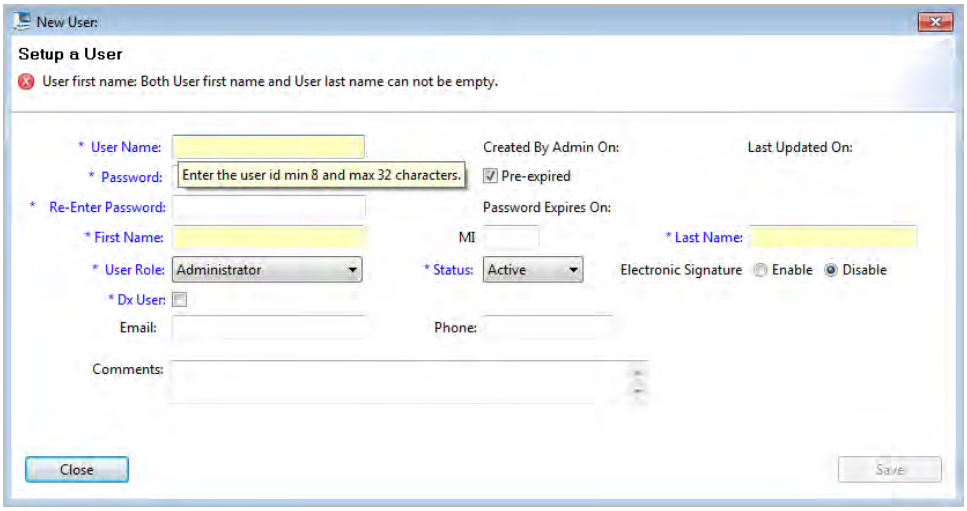
The software includes a default Administrator user account with permissions (defined by the account user role) to perform all functions in the software.

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 200) 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.

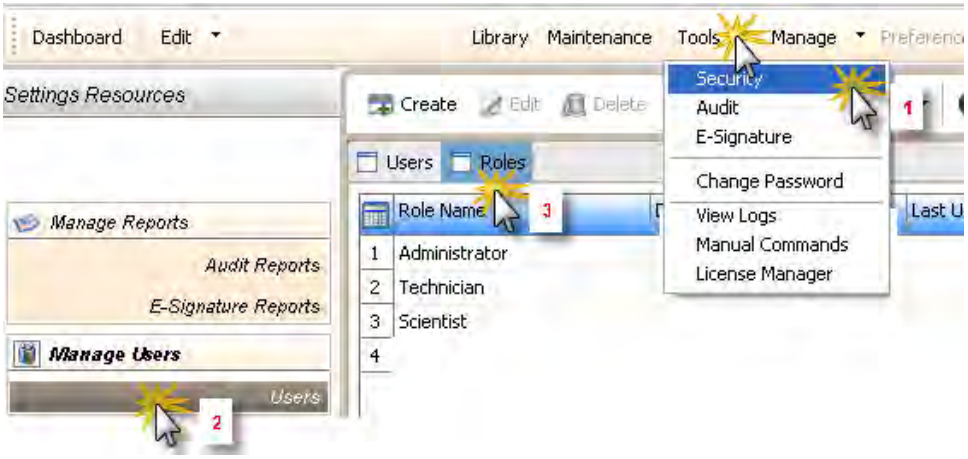
Three default user roles are included in the software. You can modify two of them, and can create your own roles with customized settings as needed:

- 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	• Start plate run • Edit default instrument run name • Manage injection list • Duplicate injection • Re-inject
Primary Analysis	• Edit sample (names) • Export sequencing results
• Assay • File name convention • Results group • Instrument protocol • PA protocol • Size standard • Dye sets	• Create • Edit • Delete • Import • Export
Plates and templates	• Edit • Delete • Import • Export
Locking/Unlocking	• Assays • File name convention • Results group • Instrument protocols • PA protocols • Size standards • Dye sets

Category	Permissions
Preferences	• Edit system preferences • Export system preferences • Import system preferences • Edit user preferences • Import user preferences • Export user preferences (all)
Calibrations	• Perform spatial calibration • Perform spectral calibration
Install check	Run install standard check
Archiving	• Archive • Purge • Restore
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

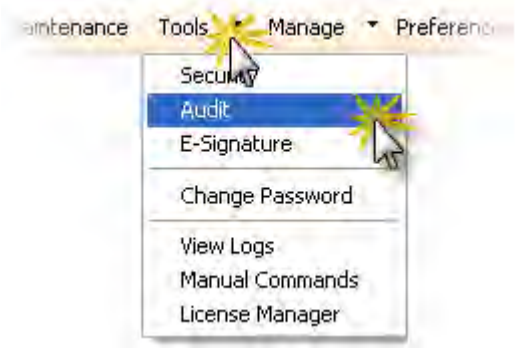
To save the report electronically (.pdf), print the report and select **CutePDF Writer** as the printer.

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.



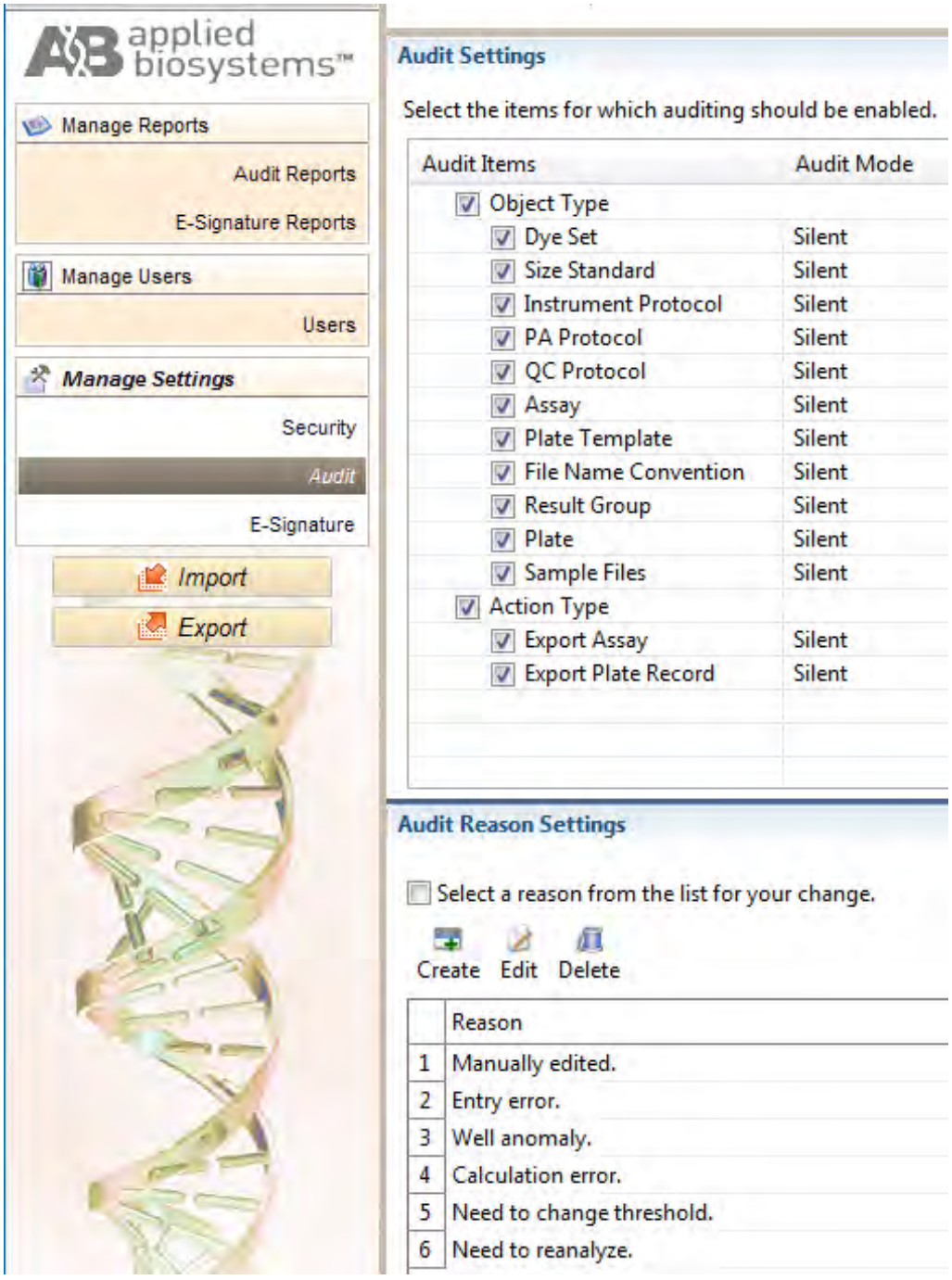


Figure 28 Audit Settings

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 206.

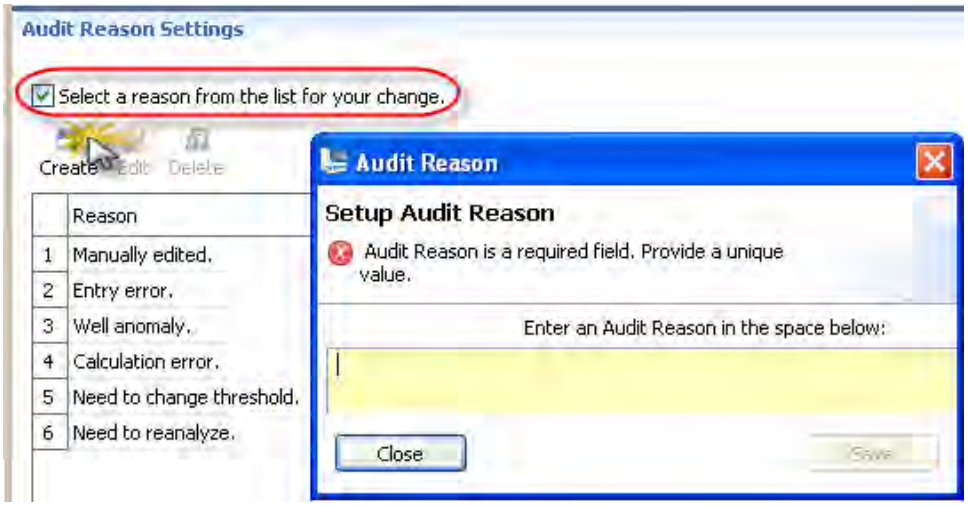
2. Set the Audit Mode for each item you enable for auditing:
   - **Prompt** — The event is audited, a reason prompt is displayed, but the user can cancel and continue without entering a reason.
   - **Required** — The event is audited, a reason prompt is displayed, and the user must specify a reason.
   - **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.

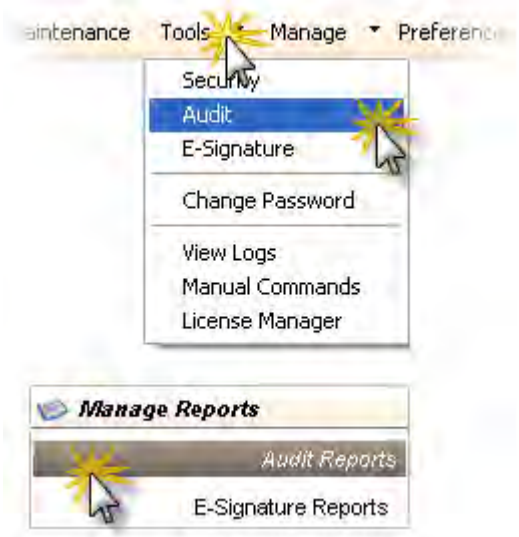


2. As needed, click **Create**, or select a reason, then click **Edit** or **Delete**.

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 144).

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 77.
   - 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
Update	The auditing of updates depends on whether an object is modified or overwritten: • **Modified** — A record is created when an object is modified. • **Updated** — A record is not created when an object is overwritten in the library. 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.

Action	Description
Create	A record is created when you: • Create an item in the library. • Create an item from within another item. • 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). **Note:** An audit record is not created when a sample file is generated. However, an audit record is generated when a sample is renamed.
Delete	The auditing of deletions depends on the item deleted: • **Items in the library** — 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 *delete* a size standard from the library, no audit record for the deletion is listed in the Object Audit Detail History. • **Items within other items** — The deletion of an item from within another item is audited.

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**	• Enable security • Disable security • Modify security policies: – Session timeout settings
Account settings	Update	• Modify user name settings • Modify password settings • Modify security policies: – Password expiration – Account suspension
Audit reason for change	Update	Modify reason for change
	Create	Create reason for change
	Delete	Delete reason for change

Record Type	Action	Corresponds to
Audit settings	Update	• Enable auditing • Disable auditing
Audit type	Update	Modify audit settings
E-Signature function	Update	• Modify the authorities for a "prompt before" function • Modify the Enable state of either a "check after" or "prompt before" function
E-Signature settings	Update	• Enable e-signature • Disable e-signature
E-Signature type	Update	• Modify e-signature settings • Modify the enable state of an E-Signature Type
Role assignment	Create	• Create a new user account • Assign a different user role to an existing user account
	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
User account	Update	• Edit • Suspend
	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

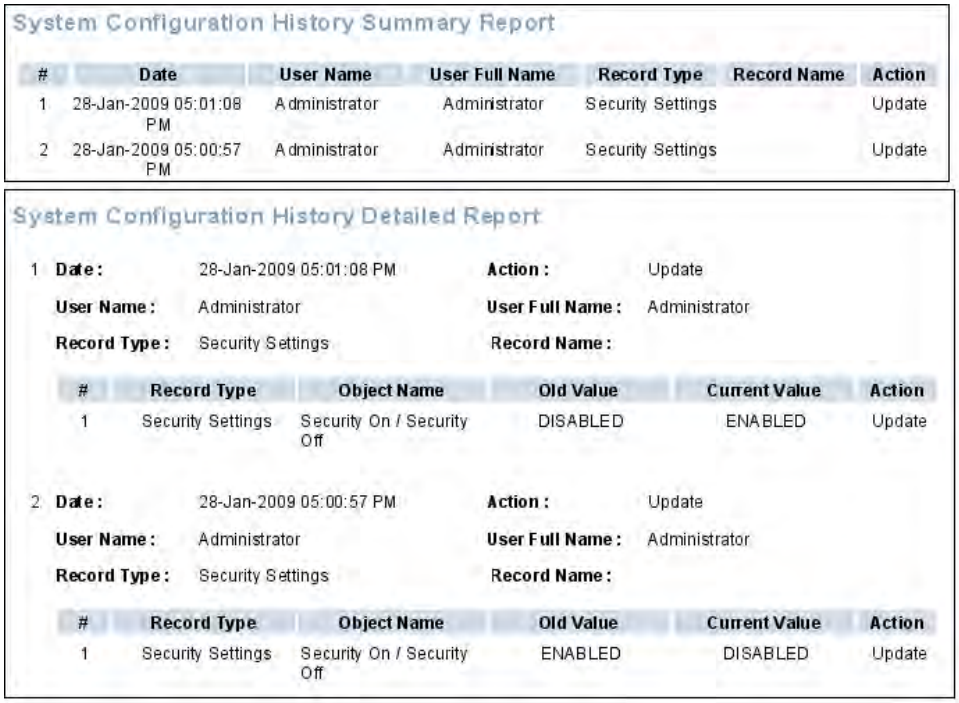
Category	Action
Assay	Assay exported successfully
Log In	• User logged in • Login failed • User logged out
Maintenance Wizards	• Remove Bubbles Wizard started • Change Polymer Type Wizard started • Change Array Wizard started • Replenish Polymer Wizard started • Fill Polymer Wizard started • Water Wash Wizard started • Instrument Shutdown Wizard started
Plate	Plate exported successfully
Run	• Start • Pause • Resume • Stop (Abort injection) • Terminate (injection list)
SAE Configuration	• Export
System Audit Records	• Archive • Purge • Restore
System Action Records	• Archive • Purge • Restore
User Profile	• Export

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 **Date :** 28-Jan-2009 05:01:08 PM **Action :** Update
User Name : Administrator **User Full Name :** Administrator
Record Type : Security Settings **Record Name :**

#	Record Type	Object Name	Old Value	Current Value	Action
1	Security Settings	Security On / Security Off	DISABLED	ENABLED	Update

2 **Date :** 28-Jan-2009 05:00:57 PM **Action :** Update
User Name : Administrator **User Full Name :** Administrator
Record Type : Security Settings **Record Name :**

#	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 **CutePDF Writer** as the 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 3500 Series Data Collection Software 3.1.

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**.

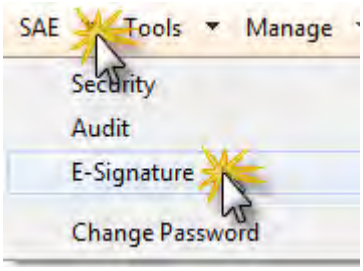
   Note: If you export audit records for samples that are not in their original location (samples have been deleted or moved), an error message is displayed. Return sample data files to their original location, then export again.

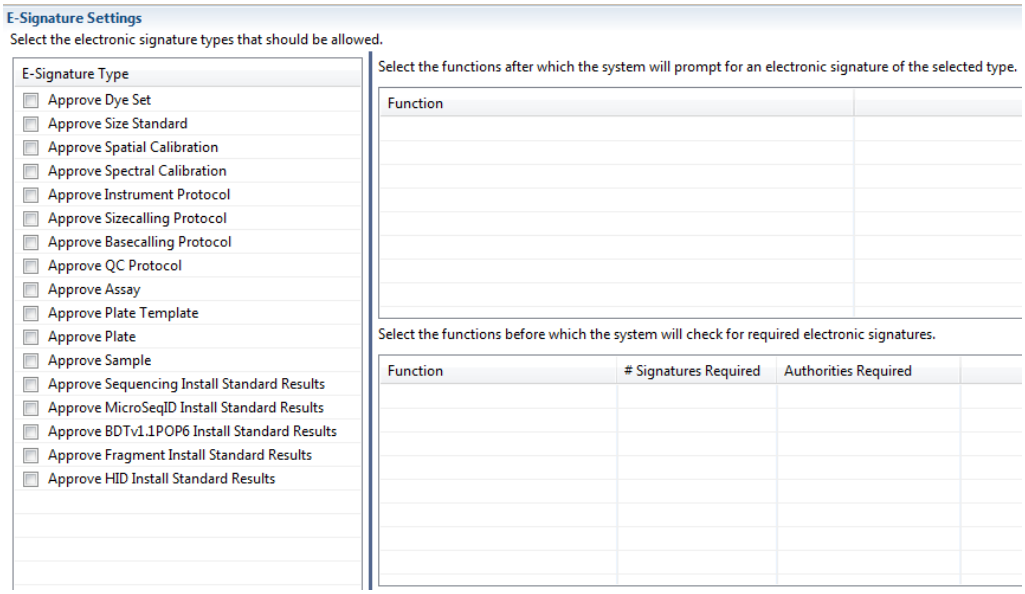
Manage electronic signature (E-sig)

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.



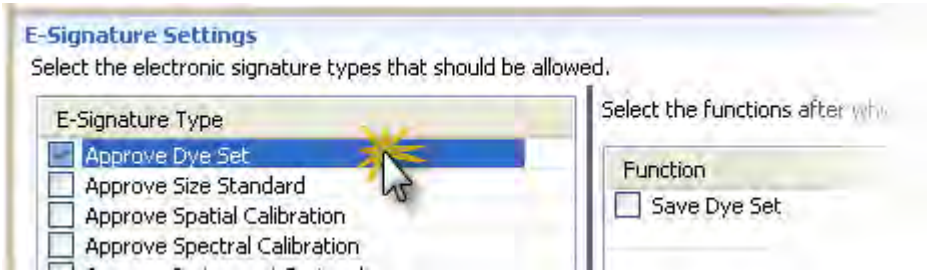


Select the actions that allow signature

IMPORTANT! Do not change e-sig settings during a spectral calibration.

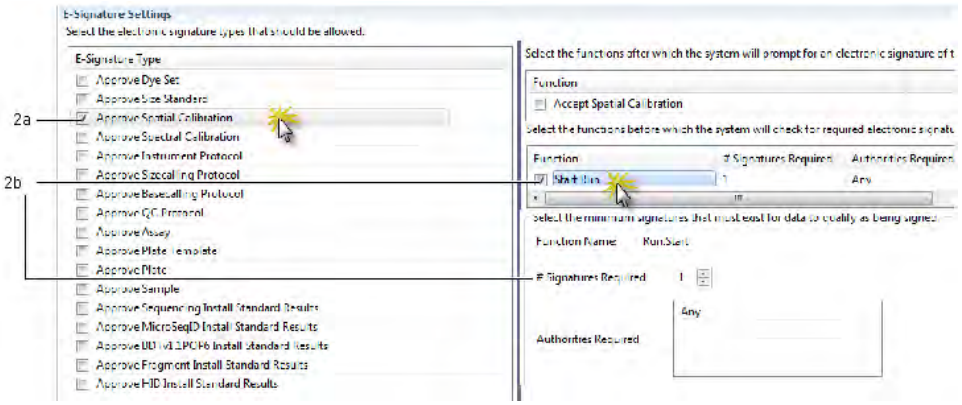
By default, no events require electronic signature. To use e-sig, enable events that require an e-signature.

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
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		

E-Signature type	Function to check before	Signatures and authorities required (defaults if enabled)
Approve BDTv1.1 POP6 Install Standard Results	Start Run	1 signature, any authorities (any user, any user role)
Approve Fragment Install Standard Results		
Approve HID Install Standard Results		

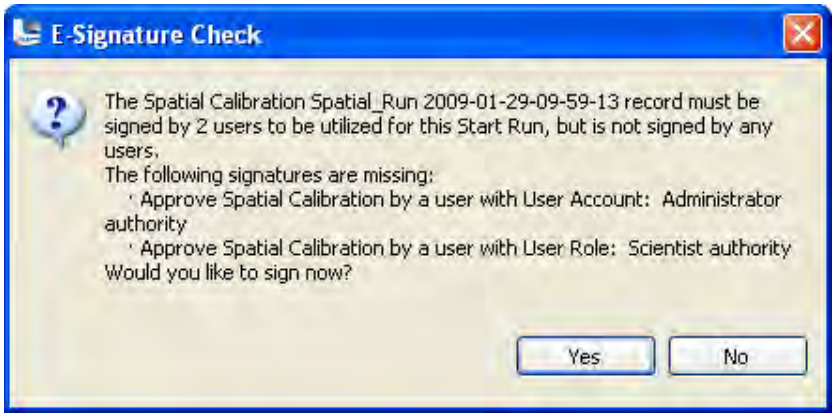
How the software prompts electronic signature before a run

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 77.
   - Customize the table (see "Customize a table" on page 77).

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 217.

   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 **CutePDF Writer** as the 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 3500 Series Data Collection Software 3.1.

1. Display the records of interest as described in "Display e-sig records" on page 217.

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:

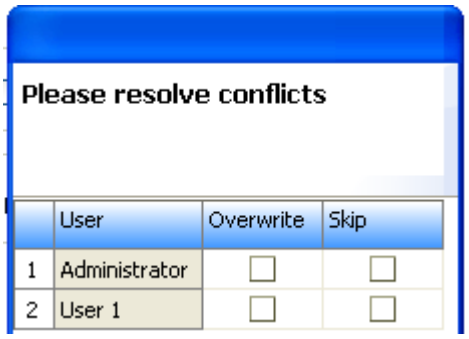
- **User Profiles** — Contains all settings in the following screens:
  - **Edit User** — All user accounts with Active status
  - **User Role** — All user roles and associated permissions (in case a user account specifies a user role that does not exist on the system into which you import the profiles)
- **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.



Section 8.2 Users

Users overview of System Security Audit Trail and E-Signature

The Security, Audit, E-Signature (SAE) module provides the following functionality:

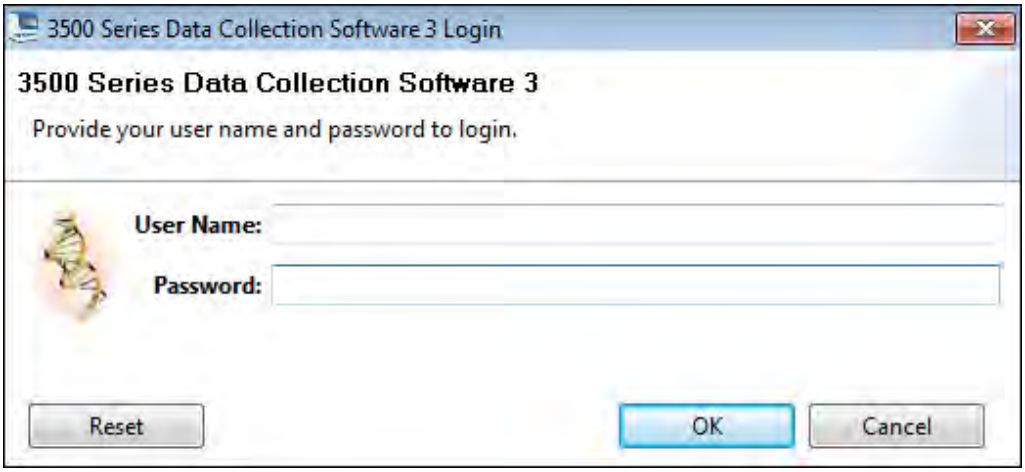
- **System security** — Controls user access to the software.
- **Auditing** — Tracks changes made to library items, actions performed by users, and changes to the SAE settings.
- **Electronic signature (e-sig)** — Requires users to provide a user name and password when performing certain functions.

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

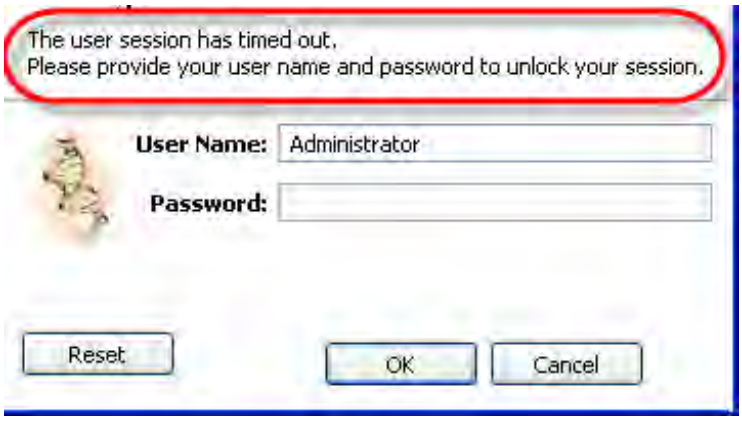
- An administrator can change the account status from **Suspended** to **Active**

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.

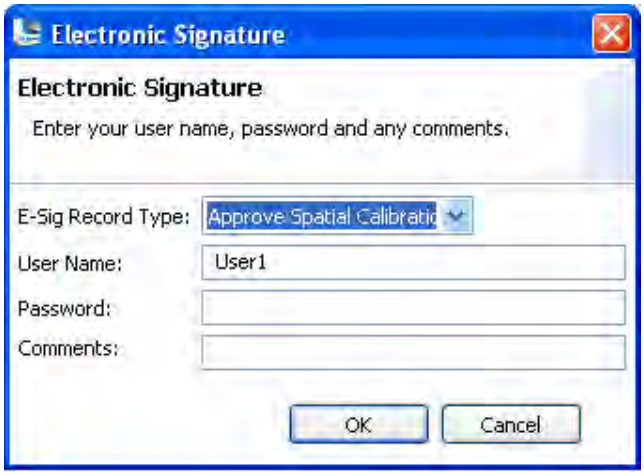


Audit

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

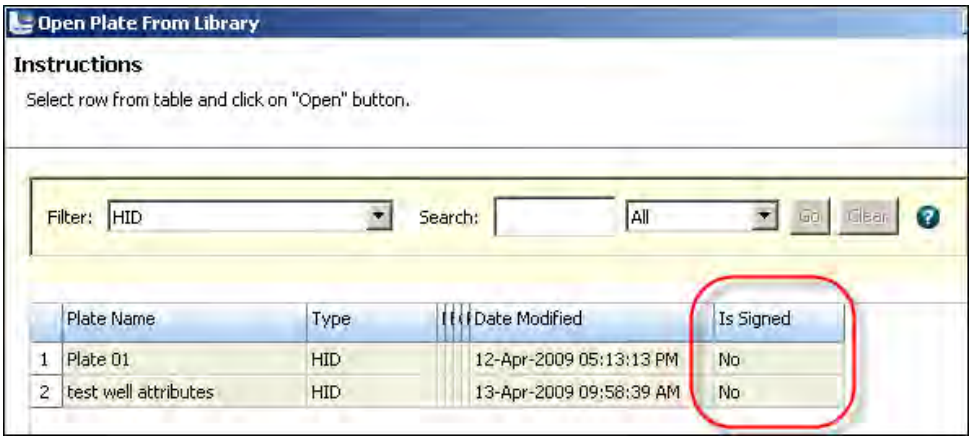
If your system is configured for electronic signature, you may be prompted to provide your user name and password when you perform certain actions in the software.



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 216.
- The **Open Plates** dialog box or the library displays an "**Is signed**" column that reflects the e-sig status of an item.



9 Maintain the Instrument

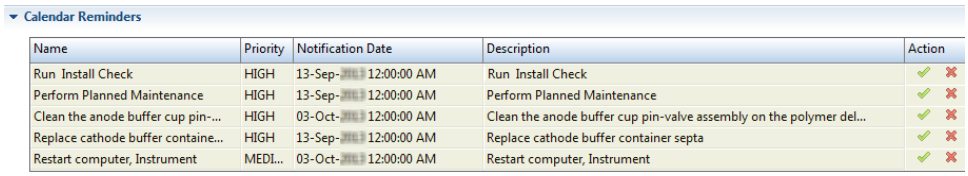
Maintenance schedule

WARNING! This section lists the common tasks required to maintain your Applied Biosystems® 3500/3500xL Genetic Analyzer 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.



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 230.
   - 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 225.

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 **Refresh**, then check consumables on the **Dashboard** - Refer to 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 34
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.		"Install the anode buffer container (ABC)" on page 231 "Install the cathode buffer container (CBC)" on page 232 "Ensure proper installation of CBC septa" on page 37
Ensure that the CBC septa are properly seated on the container.		
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 54
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 56
Ensure the array locking lever on the capillary array is secured.		Figure 29
Check for bubbles in the pump block and channels. Use the **Remove Bubble wizard** to remove bubbles.	Daily or before each run	"Remove bubbles from the polymer pump" on page 239
Check the loading-end header to ensure that the capillary tips are not crushed or damaged.		"Install or change the capillary array" on page 237
Ensure that the pump block is in pushed back position.	Daily	Figure 29

Task	Frequency	For information, see ...
Clean the instrument surfaces of dried residue, spilled buffer, or dirt.	Daily	"Clean the instrument" on page 231
Check for leaks and dried residue around the buffer-pin valve, check valve, and array locking lever. If leaks persist, contact Life Technologies.		"Check calendar reminders" on page 34

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 238
Run the **Wash Pump and Channels wizard**.		"Wash the pump chamber and channels" on page 240
Use a lab wipe to clean the anode buffer container valve pin assembly on the polymer delivery pump.		Figure 29
Restart the computer and instrument.		"Restart the instrument and the computer" on page 253

Monthly instrument maintenance tasks

Task	Frequency	For information, see ...
Run install check.	Monthly or as needed	"Run an install check" on page 123
Flush the pump trap.		"Flush the water trap (pump trap)" on page 240
Empty the oven condensation reservoir.		Figure 29
Replace cathode buffer container septa.		"Install the cathode buffer container (CBC)" on page 232
Clean the autosampler.		"Clean the instrument" on page 231
Clean the drip tray.		
Check disk space.		"Monitor disk space" on page 247
If Security, Audit, and E-sig is enabled, archive and purge audit records.		"Archive and purge" on page 212
Defragment the hard drive.	Monthly, or before fragmentation reaches 10%	"Defragment the computer hard drive" on page 248

Quarterly maintenance tasks

Task	Frequency	For information, see ...
Archive and purge audit records	Every three months	"Archive and purge" on page 212

Annual planned maintenance tasks

Call your Life Technologies 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 231
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 7, "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 230).

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	Mothnly factory repeating tasks in calendar
• Clean the anode buffer cup pin-valve assembly on the polymer delivery pump • Restart instrument and computer	• Replace cathode buffer container septa • Clean drip tray • Clean autosampler • Check disk space • Defragment hard drive • Run install check • Flush pump trap

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.

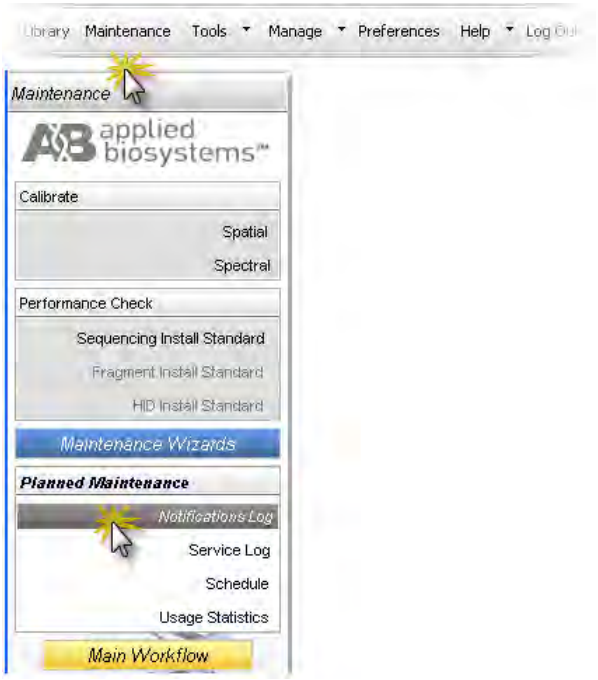
View the Planned Maintenance Report

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 **CutePDF Writer** as the 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 225).

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 77).

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, “Part numbers“.

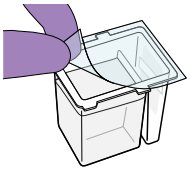
Install the anode buffer container (ABC)

1. Check the expiration date on the label to ensure it is not expired and will not expire during use.
2. Allow the refrigerated ABC to equilibrate to room temperature prior to first use. Do not remove the seal until you have completed step 5.
3. Verify that the seal is intact. Do not use if buffer level is too low or seal has been compromised. A fill tolerance of ±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.

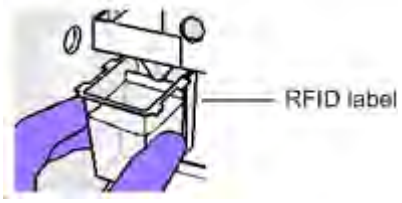
5. Verify that the buffer is at the fill line.

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.

Install the cathode buffer container (CBC)

1. Check the expiration date on the label to ensure it is not expired and will not expire during use.

2. Allow refrigerated CBC to equilibrate to ambient temperature.

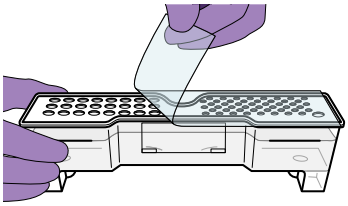
3. Wipe away condensation on the CBC exterior with a lint-free tissue. Condensation can cause arcing and termination of the run.

4. Check that seal is intact. Do not use if buffer level is too low or seal has been compromised. A fill tolerance of ±0.5 mm is acceptable.

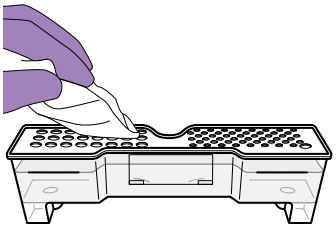
5. Tilt the CBC back and forth gently and carefully to ensure that the buffer is evenly distributed across the top of the baffles. If you do not tilt the CBC back and forth, the buffer sticks to the baffles because of surface tension.

6. Verify that the buffer is at or above the fill line.

7. When ready to install CBC, place the container on a flat surface (such as a lab bench) and peel off the seal.

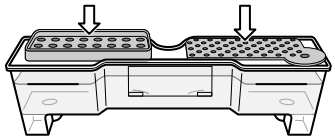


8. Wipe off any buffer on top of the CBC with a lint-free tissue. Ensure that the top of the container is dry. Moisture can cause arcing and termination of a run.



9. Place the appropriate septum on each side of 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 and then push firmly to seat it.
   c. Align the capillary washing septum over the other chamber of the CBC.

d. Push the septum lightly into the holes to start and then push firmly to seat it.

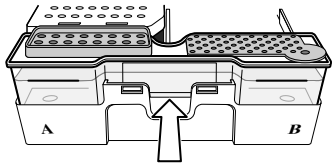


IMPORTANT! Look at the CBC from the side and ensure there is no gap between the container and the lip of the septum.

IMPORTANT! Ensure that the washing septum is securely seated to prevent displacement of the septum during operation.

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, “Part 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 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

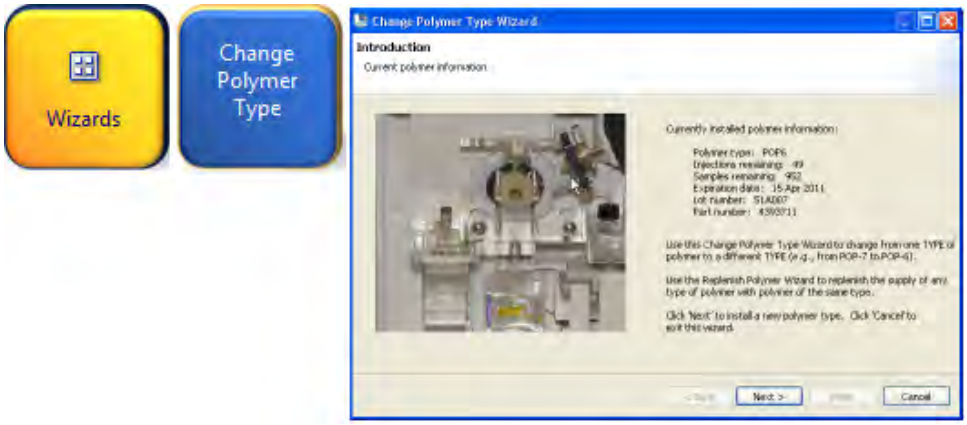
1. Check the expiration date on the label to ensure that the polymer is not expired and will not expire during intended use.

   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 ambient temperature (15–30°C) before use.

3. In the Dashboard, click **Wizards**, then click **Replenish Polymer** (requires 10 to 20 minutes) or **Change Polymer Type** (requires 60 to 70 minutes).

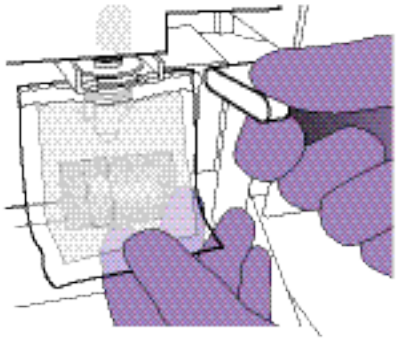
4. Follow the prompts in the Wizard window.



5. When instructed to install the polymer, peel off the seal at the top of the pouch fitment.

   Note: You may notice a tiny droplet of polymer inside the fitment (residual from the pouch filling process). This is **not** expected to cause any performance issues.

6. With the RFID label facing the instrument, slide the pouch fitment 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.

7. In the Dashboard, click **Refresh**, then check the Quick View section for the updated polymer status.

Refer to the instrument user guide for instructions on initiating the runs.

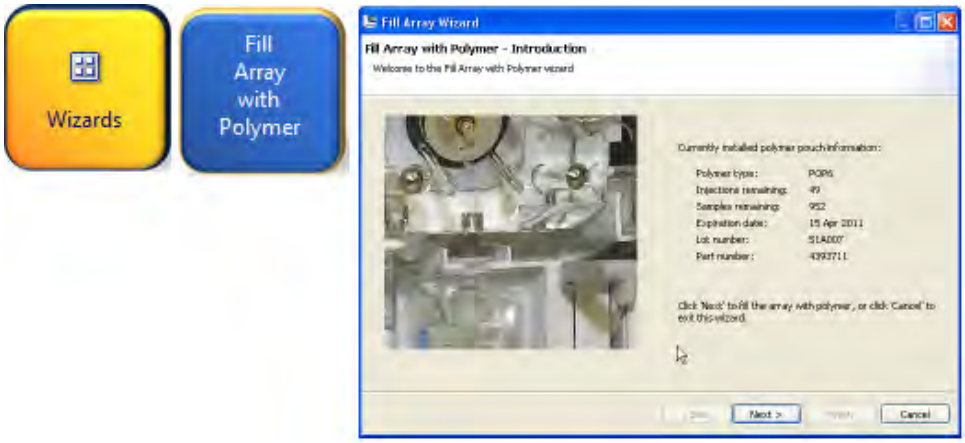
Store partially used polymer

If you remove a polymer pouch for storage (2–8°C), place a pouch cap 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.

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 load-end of the capillary array has 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 to 45 minutes to complete.

1. In the **Dashboard**, click **Wizards**.

2. In the **Maintenance wizards** screen, click **Install Capillary Array**.

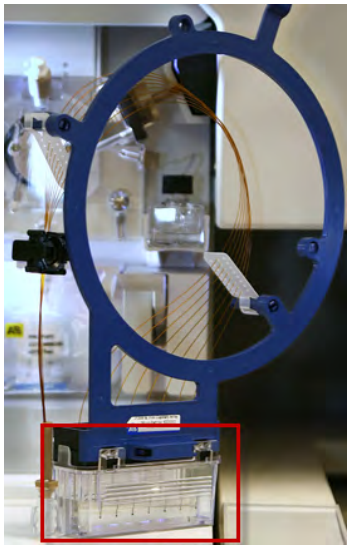
3. Follow the prompts in the Install Capillary Array wizard window.

4. Check the **Quick View** section of the Dashboard for updated status of the capillary array.

Store a capillary array

WARNING! SHARP The load-end of the capillary array has 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 if:

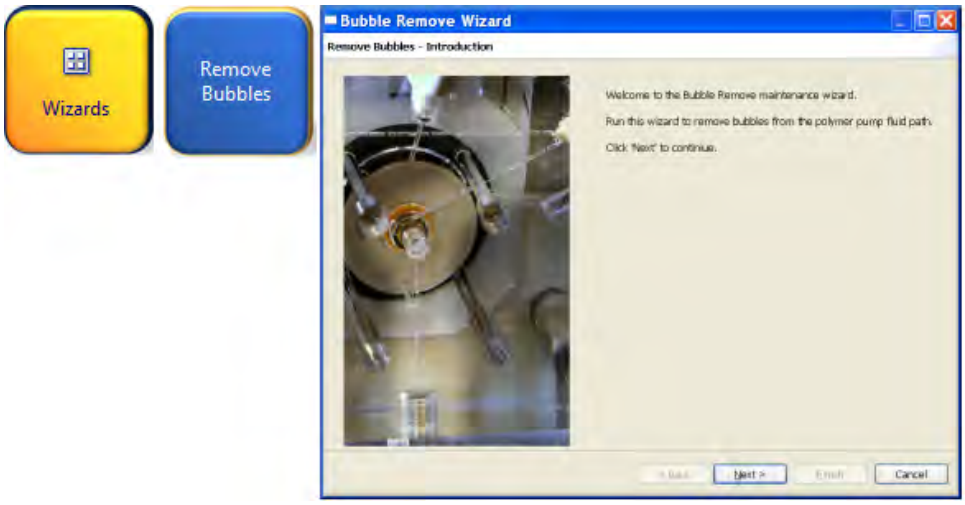
- Polymer dries in the polymer channels of the pump assembly, which can scratch the channels in the pump, and can cause blockage.
- The pump assembly is exposed to organic solvent, which can cause cracking and clouding of the acrylic pump material.
- The pump assembly is exposed to temperatures greater than 40°C, which can damage the pump components.
- There is arcing 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 226 for more information.

Note: The **Bubble Remove wizard** takes 5 to 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.



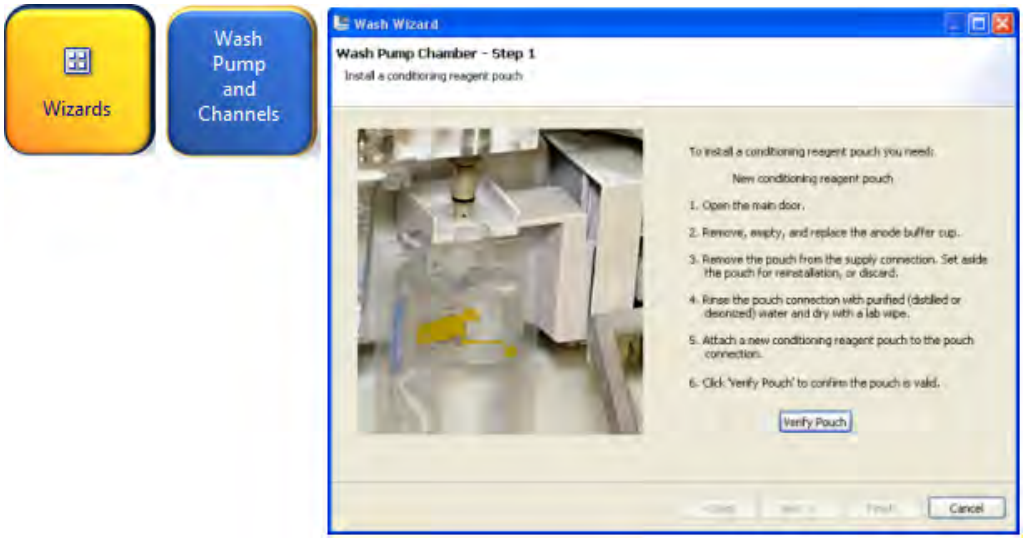
Wash the pump chamber and channels

In the following situations, use the Polymer Delivery Pump Cleaning Kit (Part no. 4359572) in addition to the **Wash Pump 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 Life Technologies.
- 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 Wash 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.

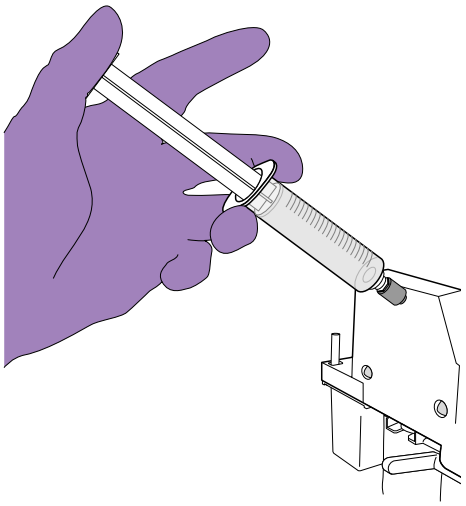
Flush with distilled or deionized water and ensure that the water flows into the overflow container. Dispose of the excess water (inside the overflow container). See “Chemical safety“ on page 309.

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 , Part No. 4359572) 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 µL, 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

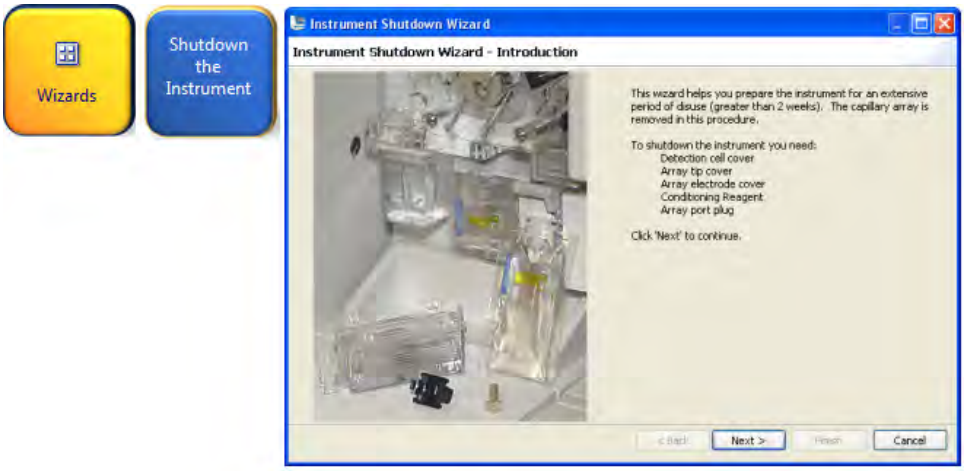
Shutdown the instrument

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	1. Run the Install Capillary wizard and store the capillary array. 2. Clean any spills or residual polymer. 3. Run the Shutdown the Instrument wizard. 4. Unplug the instrument.

Move and level the instrument

IMPORTANT! If you relocate the instrument, we recommend that you have an IQ OQ performed. Contact Life Technologies 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 242.
   - 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)

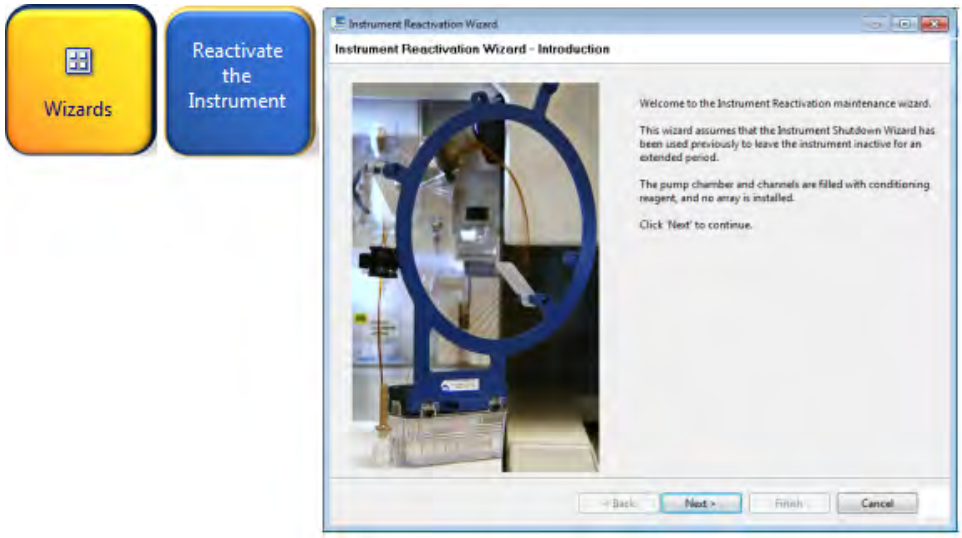
6. Have an IQ OQ performed before using the instrument.

   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 3500/3500xL Genetic Analyzer in good working condition.

Note: In the event of a power disruption, restart the computer (Appendix A, "Troubleshoot").

Back up the datastore during software uninstall

IMPORTANT! Do not uninstall the software unless instructed to do so by Life Technologies.

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.

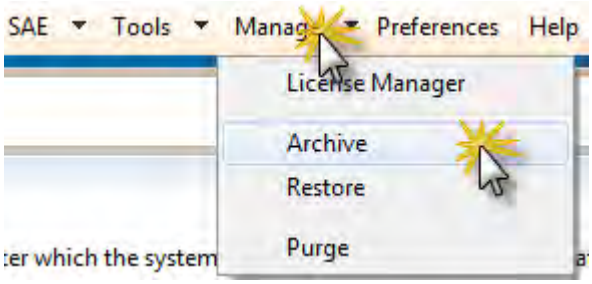
See also "Archive, purge, and restore audit records" on page 212.

Frequency

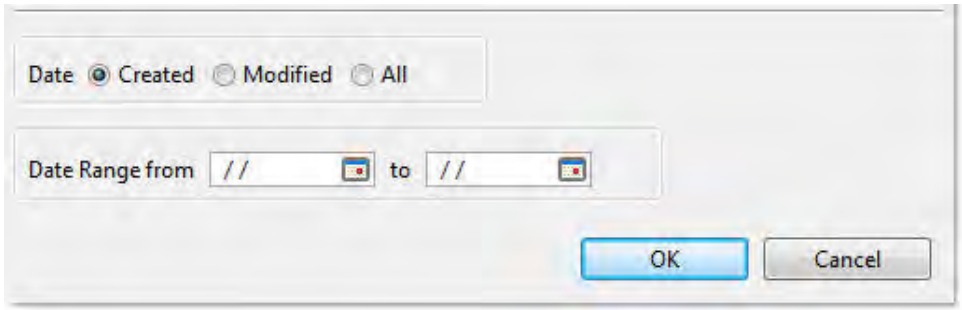
We recommend that you purge the library objects once every three months.

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 212.

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 212.

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.

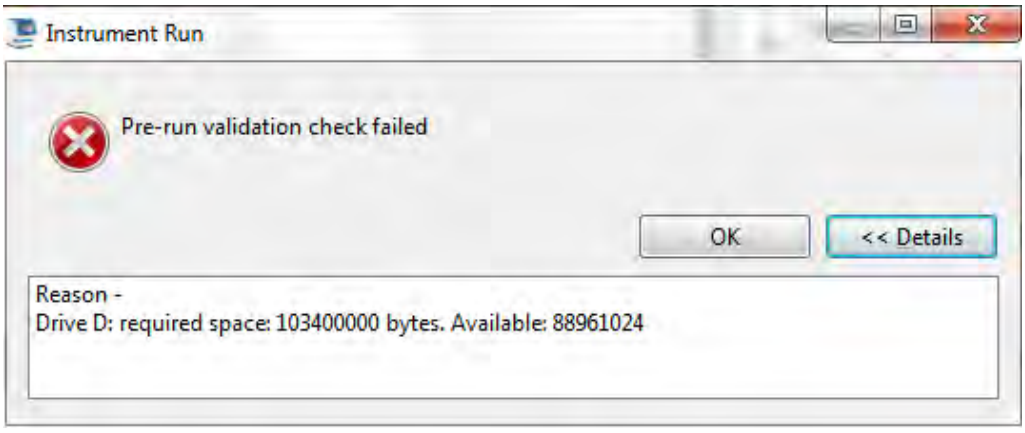
Monitor disk space

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.

Manage software licenses

The 3500 Series Data Collection Software 3.1 requires a license to run.

IMPORTANT! If you replace or add a network card in the computer running the software or relocate the software to a new computer, contact Life Technologies to update your license for the new network card or computer.

Create an email address for license activation and renewal

You must use the same email address to activate and renew software licenses.

Create an email address that is routinely monitored by your team (rather than a single individual). Use this email address to activate and renew software licenses.

Obtain and activate a software license

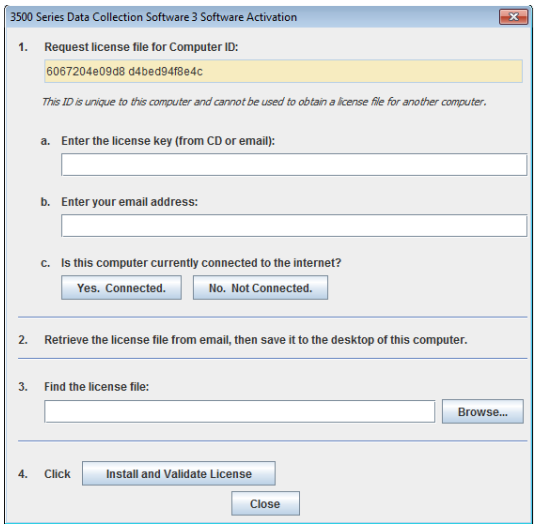
The 3500 Series Data Collection Software 3.1 **Software Activation** dialog box is displayed when you start the software if no license is installed and activated on your computer.

This task is typically performed by the Life Technologies service representative during installation of the instrument.

1. Ensure that all network cards in the computer are enabled.

   IMPORTANT! You can run the 3500 Series Data Collection Software 3 using only the network cards that were enabled when you activate the software license. For example, if you activate the software when your wireless network card is disabled, you will not be able to run the software when the wireless network card is enabled.

2. Display the Software Activation dialog box by starting the 3500 Series Data Collection Software 3 (see "Step two: Start the 3500 Series Data Collection Software 3" on page 33).



3. Obtain the license key. The license key is provided on the 3500 Series Data Collection Software 3 CD case, or in an email from Life Technologies.

4. Request the software license file by performing steps 1a, 1b, and 1c as listed on the activation screen.

   IMPORTANT! Keep a record of the email address used to activate the software license. You must use the same email address to renew the software license when it expires.

5. Obtain the software license file from your email.

6. Make a copy of the software license file and keep in a safe location.

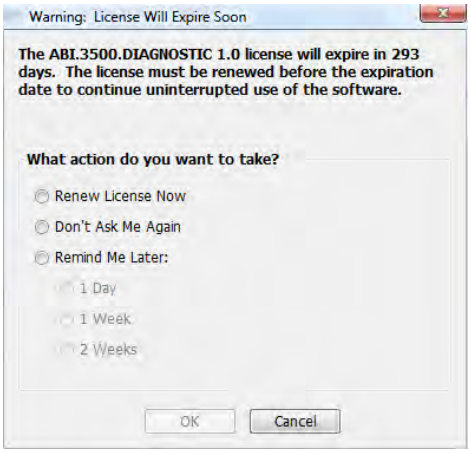
7. Copy the software license file to the desktop of the 3500 Series Data Collection Software 3 computer.

8. If the Software Activation dialog box has closed, start the 3500 Series Data Collection Software 3 to open it (see "Step two: Start the 3500 Series Data Collection Software 3" on page 33).
9. Click **Browse**, then navigate to the software license file saved on your computer.
10. Click **Install** and **Validate License**. A message is displayed when the license is installed and validated.
11. Click **Close**.

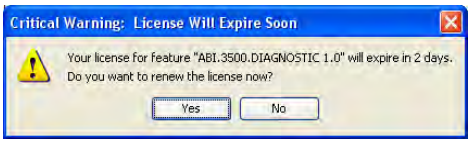
Renew a software license

1. Ensure that all network cards in the computer are enabled.
2. Display the **Software License Renewal** dialog box by doing any of the following:

   - Select **Renew License Now** in the **Warning: License Will Expire Soon** dialog box.

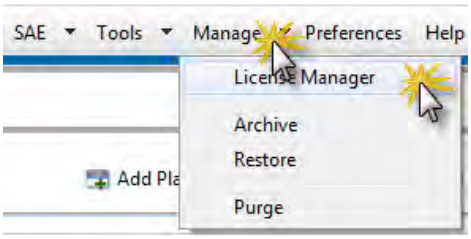


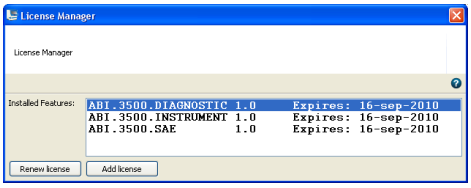
   - Click **Yes** in the **Critical Warning: License Will Expire Soon** dialog box.



   - Click the license, then click **Renew License** in the **License Manager**.

     Note: The **Add License** function is for future use.





3. Enter the email address used to activate the software license.

   IMPORTANT! You must use the same email address to activate and renew the software license. If you do not have the activation email address available, enter any email address, click the licensing link in the Software Renewal dialog box, then click **Contact Support** in the License Renewal web page.

4. Request the renewed software license file by performing step 1c as listed on the renewal screen.

5. Obtain the renewed software license file from your email.

6. Copy the renewed software license file to the desktop of this computer.

7. If the Software renewal dialog box has closed, access it by selecting **Manage ▸ License Manager**.

8. Click **Browse**, then navigate to the renewed software license file saved on your computer.

9. Click **Install and Validate License**. A message is displayed when the license is installed and validated.

10. Click **Close**.

Service Log and Usage Statistics

The Service Log and Usage Statistics functions are for use by Life Technologies service engineers at the time of service.

Troubleshoot

If you encounter any unforeseen and potentially hazardous event while operating the instrument, turn off the power, unplug the instrument, and call your Life Technologies service representative.

IMPORTANT! See "Safety and electromagnetic compatibility (EMC) standards" on page 307 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
- 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

When you are instructed to restart the instrument and the computer:

1. Exit the 3500 Series Data Collection Software 3.1.
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.
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 two: Start the 3500 Series Data Collection Software 3" on page 33.

8. Start the 3500 Series Data Collection Software 3.1.

Instrument components

Figure 29, Figure 30, and Figure 31 are provided below for reference in this section.

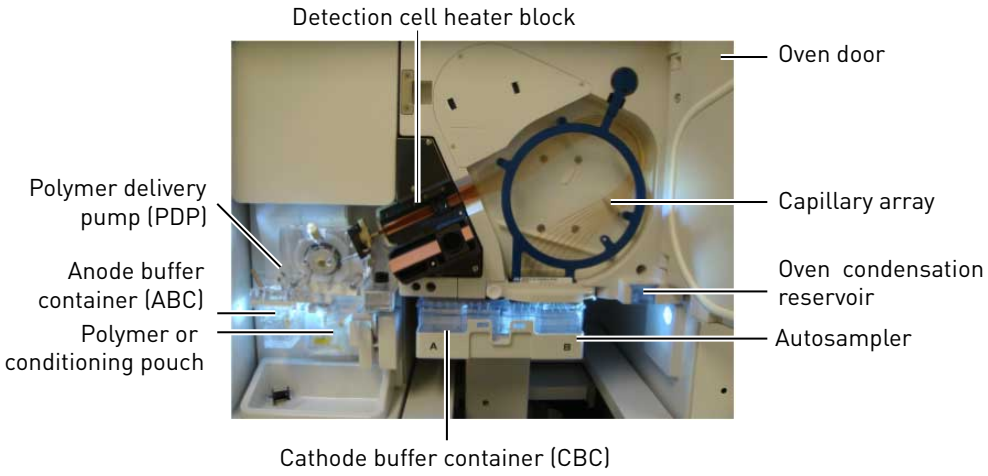


Figure 29 Instrument interior

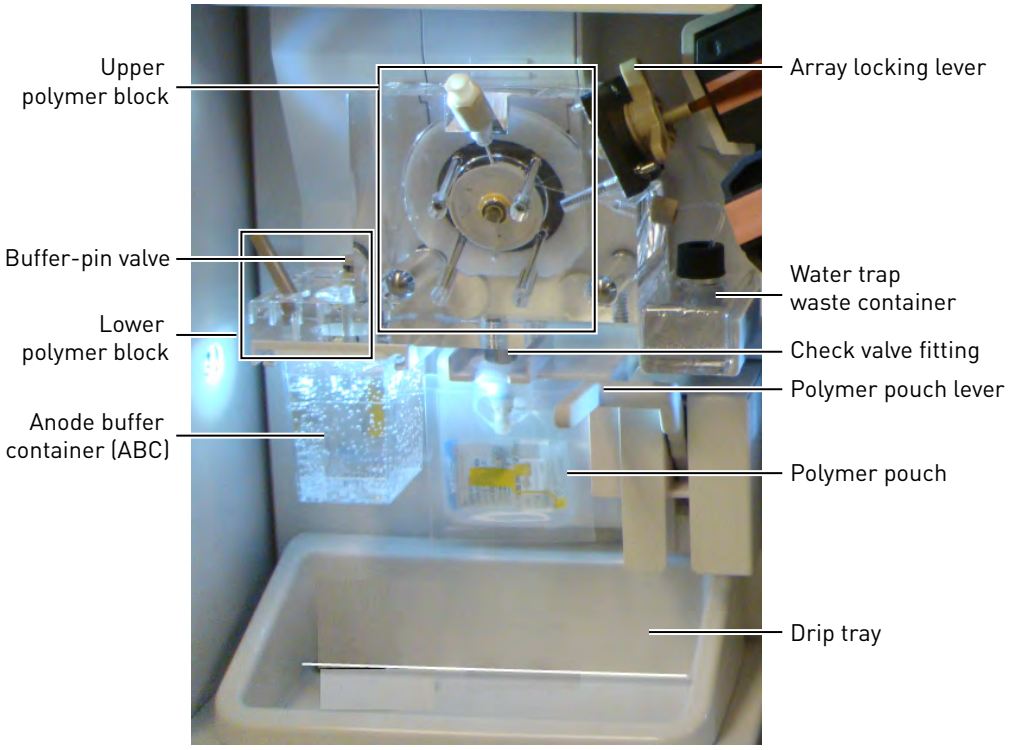


Figure 30 Polymer delivery pump (PDP)

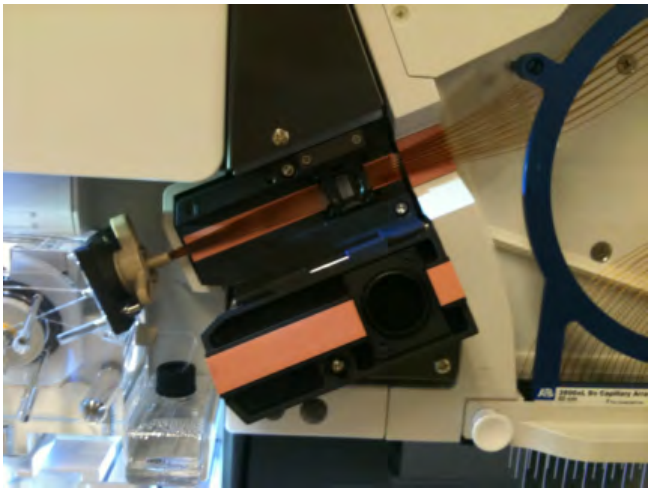
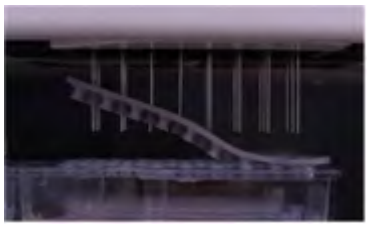


Figure 31 Detection cell

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 253).
Front panel indicator: Amber light (blinking)	Run paused	Resume run.
	Door open	Close the instrument door.
CBC septum is lifted off the container 	Septum was not seated properly when installed.	See "Ensure proper installation of CBC septa" on page 37.
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 54. **IMPORTANT!** If array tips are bent, replace the array.

Symptom	Possible cause	Action
Autosampler does not move the plate to a higher position	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. IMPORTANT! 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 Life Technologies.
	Polymer delivery pump block is not pushed back into position after capillary array change	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 253). After the instrument has restarted, check the lever movement. If the lever does not move up and down freely, contact Life Technologies. If the lever moves up and down freely, push the upper polymer block all the way back against the wall.

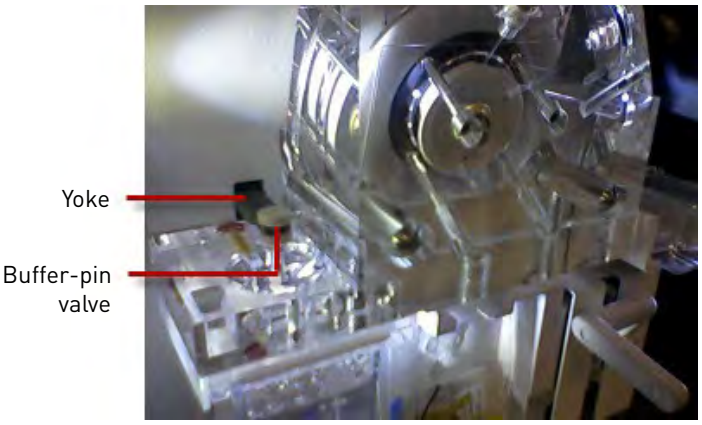
<table>
<tr><th>Symptom</th><th>Possible cause</th><th>Action</th></tr>
<tr><td>Polymer delivery pump (PDP) is extremely noisy and vibrating while running any wizard</td><td colspan="2"> 

Figure 32 Buffer-pin valve lever (yoke)</td></tr>
<tr><td rowspan="2">Polymer is not pumping properly - wizard fails - filling array</td><td>Check Valve is clogged

Crystals present in polymer delivery pump path</td><td>Run the Wash Pump and Channels wizard.

See “Flush the water trap (pump trap)“ on page 240 and “Wash the pump chamber and channels“ on page 240.

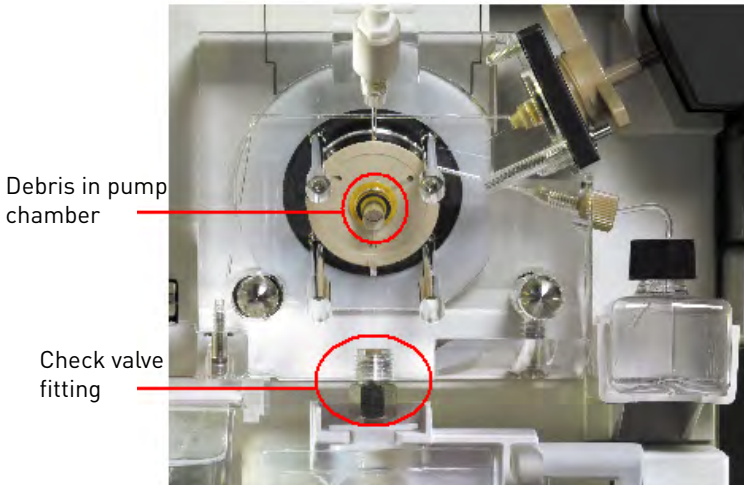
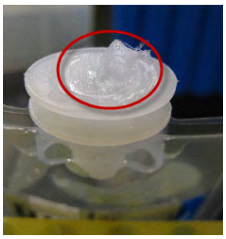
If the problem persists, contact Life Technologies.</td></tr>
<tr><td colspan="2"> 

Figure 33 Pump chamber and valve fitting</td></tr>
</table>

Symptom	Possible cause	Action
Buffer-pin valve does not move	Polymer crystallizations have formed around the buffer-pin valve	If you see any crystals, leaks, and dried residue around the buffer-pin valve, clean the valve and the array locking lever immediately. Add DI water to the buffer solution to dissolve crystals. **Note:** Use the lint-free swabs, included in the PDP Cleaning kit (PN 4461875). If leaks persist, contact Life Technologies.
		Perform maintenance tasks routinely as described in "Maintenance schedule" on page 225. If leaks persist, contact Life Technologies.
	The vent hole behind the buffer-pin valve is clogged	Clean the vent hole behind the buffer-pin valve with DI water.
	The PDP block is not in the correct position	See "Polymer delivery pump (PDP) is extremely noisy and vibrating while running any wizard" . If the problem persists, contact Life Technologies.
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 225.
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 Life Technologies.
Poor signal and resolution after replenishing polymer	The Check Valve is clogged (see Figure 33.	Wash the channels using the Polymer Delivery Pump Cleaning Kit (Part no. 4359572). If the problem persists, contact Life Technologies.
Any of the following visual or audible conditions: • Unstable current • Arc-detect errors • A crackling noise at the beginning of electrophoresis • A blue lightning symbol below the oven • An error message regarding electrical current • Electric discharge	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.	**IMPORTANT!** 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 Life Technologies.
	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.	

Symptom	Possible cause	Action
Any of the following visual or audible conditions: • Unstable current • Arc-detect errors • A crackling noise at the beginning of electrophoresis • A blue lightning symbol below the oven • An error message regarding electrical current • Electric discharge	Condensation inside the oven.	**IMPORTANT!** 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 Life Technologies.
	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 ±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 in "Install the anode buffer container (ABC)" on page 231
When you remove the heat seal from a new pouch, some residual seal remains on top of the pouch. 	The top seal of the pouch has become delaminated and left the polyethylene behind on the pouch cap.	Use a pipette tip to remove the entire seal from the pouch cap before installing on the instrument.

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.	Ensure that the RFID label is not visibly damaged and consumable package is properly installed. Ensure that label is close, and parallel, to the instrument. Reposition or re-install pouch, then click **Refresh** on the Dashboard.
		Restart the instrument and the computer (see "Restart the instrument and the computer" on page 253).

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.	Install a new consumable (if available). If problem persists, contact Life Technologies.
	Malfunctioning RFID label or reader.	Place a used CBC, ABC, pouch, or array on the instrument: • If the instrument can read the RFID label, install a new CBC, ABC, pouch, or array. • If the instrument cannot read the RFID label, contact Life Technologies.

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 253).
"**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 253).
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 29).
"**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 33).	While wearing gloves, use a lint-free cloth and water to wipe the CV Fitting. **Note:** 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 Life Technologies.

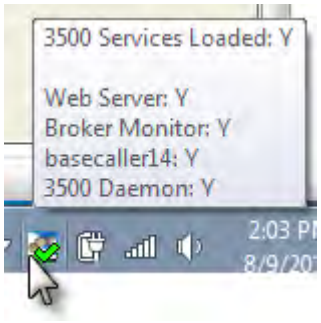
Symptom	Possible cause	Action
"**Leak error**" occurs when capillary arrays are filled with fresh polymer or when replenishing polymer, causing the wizard to fail to complete.	The Yoke is not seated properly on the buffer-pin valve.	Make sure the buffer-pin valve lever (yoke) is seated properly on the buffer-pin valve (see Figure 32). 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 253). After the instrument has restarted, check the lever movement. If the lever does not move up and down freely, contact Life Technologies. If the lever moves up and down freely, push the upper polymer block all the way back against the wall.
• "**Leak detected during polymer delivery**" • "**Leak detected during bubble compression**" The run aborts.	Bubbles in the polymer system.	Run the **Remove Bubbles wizard** to clear bubbles.
	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 (Part no. 4359572) 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 3500 Series Data Collection Software 3.1 notifications.
	Filling the array during install array.	Run **Fill the Array with fresh Polymer** wizard, or run **Change Polymer Type wizard**.
"**Bubble**" error	Bubbles present	Run the **Remove Bubbles wizard**.
"**Java update scheduler**" error message	The Java updater is unable to complete the update.	Close the Java update scheduler. **Note:** The Java update scheduler does not affect the performance of the 3500 Series Data Collection Software 3.1 or the quality and accuracy of the data collected.

Symptom	Possible cause	Action
"**Invalid Contents**" message In **Assign Plate Contents** screen when you use Ctrl+D	The first row you have selected to fill from is empty.	• Enter sample name or select an assay in the first row in you have selected to fill from. • Use the table view to add the assay to the samples.
"**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 253).
"**Instrument is not connected**" message after you start 3500 Series Data Collection Software 3.1.	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 253).
"**Internal buffer data overflow**" message.		

Dashboard troubleshooting

Symptom	Possible Cause	Action
When you click **Refresh** on the **Dashboard**, and consumables information is listed as "**Unknown**."	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 **Refresh**.
After installing new CBC or ABC, the consumables status in the Dashboard is not updated automatically.	Dashboard does not update automatically.	Click **Refresh** 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 253). Contact Life Technologies

Software troubleshooting — general

Symptom	Possible cause	Action
When you start the 3500 Series Data Collection Software 3.1, "**Windows cannot find 3500.exe**" message is displayed.	The Norton Antivirus Sonar Protection feature is enabled on the instrument computer.	• Disable the optional Sonar feature in Norton Antivirus software (contact your IT department for assistance). • Contact Life Technologies.
Status icon is  instead of  . 	One or more of the services are stopped.	Hover the mouse pointer over the status icon. If any item does not display a checkmark, select  ▸ **Programs** ▸ **Applied Biosystems** ▸ **3500** ▸ **Server Monitor**. Right-click the status icon, then select **Services**. If any item does not display a checkmark, click the item to start the service. 
Print dialog box is not displayed when you select or click Print.	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 **OK** 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 **Define Plate Properties screen** ▸ **Open Plate** ▸ **Edit Existing Template**.

Symptom	Possible cause	Action
Specimen name and **Amplicon** 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.	Enter the Specimen name and Amplicon name in the **Sample Name** field in the **Assign Plate Contents** screen, **Customize Sample** information section. To view Specimen Name and Amplicon Name in the Customize Sample Information section, a Sequencing assay must be assigned to a well. **Note:** The Specimen Name and Amplicon Name fields are available in the Plate View only, not the Table View of the Assign Plate Contents screen.
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.	Restart the instrument and the computer (see "Restart the instrument and the computer" on page 253). **Note:** Restart the instrument and the computer as part of weekly maintenance.
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 253).
	Audit records need archiving and purging	See "Archive and purge" on page 212.
Preferences (plate setup, report settings, and sequencing settings) are not retained after data migration from v1.0 to v3 software.	Settings are not migrated.	Manually update settings after migration.
Notification log in Calendar Reminders is not retained after data migration from v1.0 to v3 software.	Settings are not migrated.	Manually update settings after migration.

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.	**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.
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 **Fill Array with Polymer wizard**. 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 24 for storage conditions).

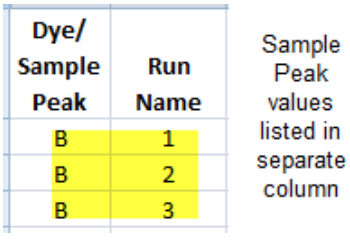
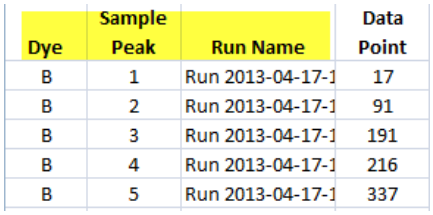
Symptom	Possible cause	Action
Low signal.	Not enough sample: Pipetting error.	Prepare new sample.
	Sample has high salt concentration.	Dilute or desalt samples.
	Insufficient mixing.	Vortex the sample thoroughly, and then centrifuge the tube to condense the sample to the bottom of the tube.
	Weak amplification 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 Life Technologies.
Elevated baseline.	Possible contaminant in the polymer path.	Run the **Wash Pump and Channels wizard**.
	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 **Install Capillary Array wizard**.
	Degraded formamide.	Prepare fresh Hi-Di™ Formamide (see "Hi-Di™ Formamide" on page 24 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 **Fill Array with Polymer wizard** and look for polymer leakage. Check for broken capillaries, run the Install Capillary Array wizard 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 37.

Symptom	Possible cause	Action
No current.	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 **Remove Bubbles wizard**.
Elevated current.	Degraded polymer.	Run the **Replenish Polymer wizard**.
	Arcing in the lower polymer block.	Inspect the lower polymer block for discoloration or damage. Contact Life Technologies.
Fluctuating current.	Bubble in polymer block.	Pause run and inspect for bubbles hidden in the tubing connectors. Run the **Remove Bubbles wizard**.
	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 37.
	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 24 for storage conditions) for sample preparation.
	Leak in system.	Tighten the connectors and array locking lever.
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 Life Technologies.
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 24 for storage conditions) and immediately place on ice.

Symptom	Possible cause	Action
Electrophoresis current is unstable.	Bubbles in the polymer system.	Run the **Remove Bubbles wizard**.
Electrophoresis failure.	Buffer below fill line.	Ensure that the buffer is filled up to the fill line. "Check buffer fill levels" on page 37 .
	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 ±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 "Install the anode buffer container (ABC)" on page 231.
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

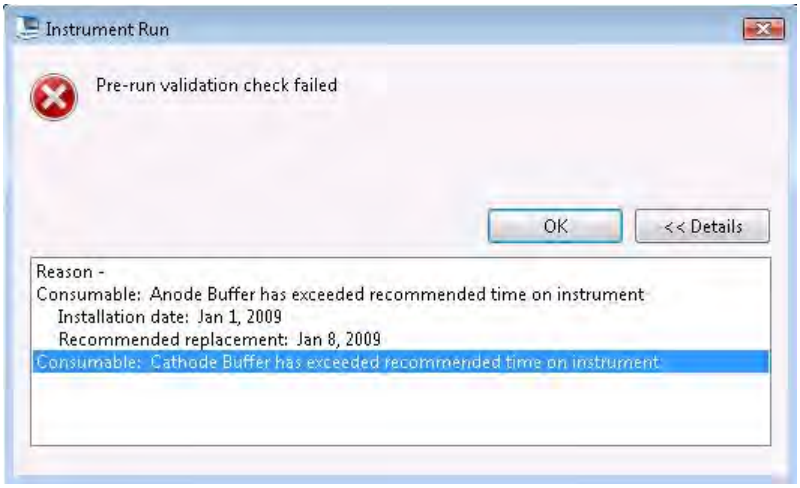
Symptom	Possible Cause	Action
Zoom errors in electropherogram graphical displays (**Monitor Run**, **Review Results**, **Spectral Calibration**, and **Install Check**): • The zoom feature does not re-baseline the sample data view, *or* • The X axis of the sample plot does not stay at the bottom of the screen. It moves up toward the region the user has zoomed in on, making data difficult to review	The zoom feature does not re-baseline the sample data view.	No action.
Samples are not imported when you select multiple folders for import	At least one file is not in the correct format for import, therefore no files are imported.	Select individual folders or files for import instead of multiple folders.

Symptom	Possible Cause	Action
Plate Owner truncated in Annotation tab>Run Configuration	Special characters were included when entering plate information.	Use only alpha-numeric characters for plate information. Special characters in plate information fields may not be correctly displayed in some software screens.
Sample files are not displayed when imported	You imported (.hid) files and you did not click HID Samples.	Click **HID Samples**.
Peaks are not labeled when you access the screen	Labels are not automatically applied.	See "Label peaks" on page 100.
x and y scaling plot settings are not applied when you click **Apply**	Scaling settings are applied only when you click **Zoom**.	Click **Zoom**.
The sizing quality result reported in the 3500 Series Data Collection Software 3.1 differs from the sizing quality result for reported in the GeneMapper® *ID-X* Software	You imported (.fsa) files instead of (.hid) files. The 3500 Series Data Collection Software 3.1 does not consider the presence of broad peaks when determining sizing quality for fragment analysis data, therefore the sizing quality result reported in the 3500 Series Data Collection Software 3.1 will differ from the sizing quality result reported in the GeneMapper® *ID-X* Software, which considers broad peaks in sizing quality.	No action.
Sizing Overlay report displays data for all capillaries including those that fail sizing	Plots displayed in **Sizing Overlay** Plot 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.  Sample Peak values listed in separate column	You changed the order of columns before exporting. **Note:** The exported data is 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
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 **Load Plates for Run** screen from the navigation pane, a plate may not be linked (indicated by the active **Link Plate** button).	Access the Load Plates for Run screen from the navigation pane and click **Link Plate**.
"**No plate in position A**" message.	You physically loaded plate in position B (plate B position) and try to link plate.	Click **Link Plates** 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 56.
		Manually link the plate to position B. See "Link the plate" on page 57.
	You selected Quick Start. **Note:** 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 Life Technologies.
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.
		

Symptom	Possible cause	Action
Link/Unlink Plate error message.	Listed in Details.	Click **Details** to determine the cause of the error. When the plate is successfully loaded, the **Load Plates for Run** screen is displayed.
		
"**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 **Pause After Last Injection** preference is set, and the instrument is paused	Go to **Monitor Run** and resume the run. When the run is complete, Create Injection List and Start Run buttons are active.

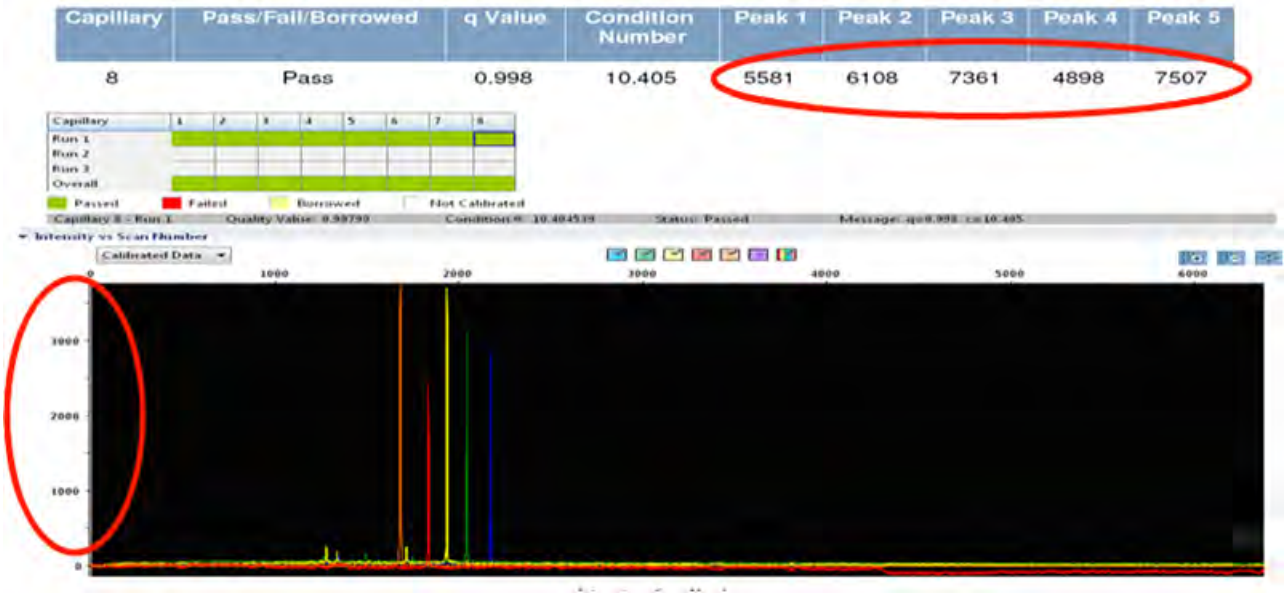
Assign Plate Contents troubleshooting

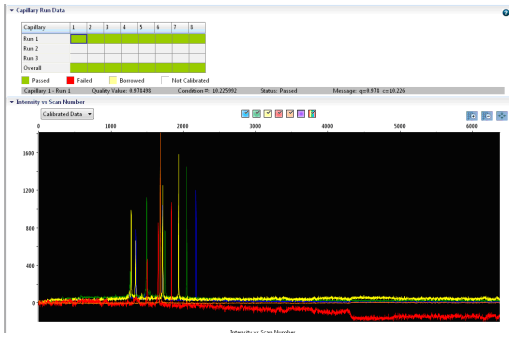
Symptom	Possible Cause	Action
Error message is displayed when you export a newly created plate from the **Assign Plate Contents** screen.	Plate is not saved.	Save the plate, close the plate, open the plate, then export.

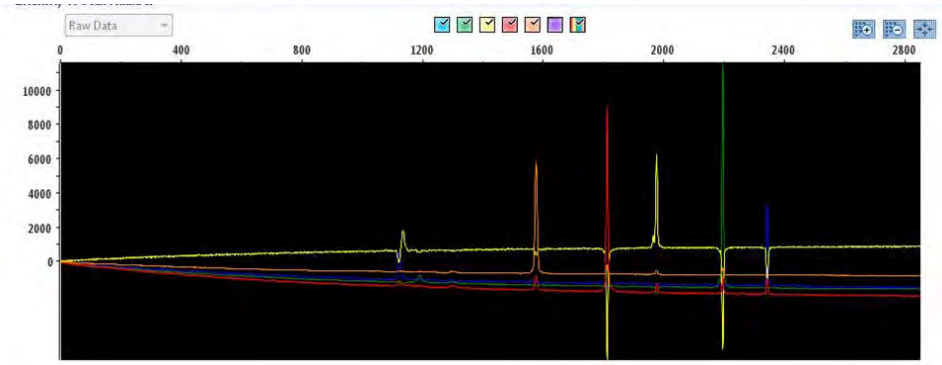
Spatial calibration troubleshooting

Symptom	Possible cause	Action
"**Start**" 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 253).
Unusual peaks or a flat line for the spatial calibration.	Improper installation of the array window in the detection cell (see Figure 31).	Run the **Install a Capillary Array wizard** to uninstall, then re-install the array. If the calibration fails again: • Fill the capillaries with polymer. • Repeat the spatial calibration.
	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 **Install Capillary Array wizard**.
Persistently bad spatial calibration results.	Bad capillary array.	Replace the capillary array using the **Install Capillary Array wizard**, then repeat the calibration. If the problem persists, contact Life Technologies.
"**Spatial Calibration Error**" 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 253).
	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 253).

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 24 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 Life Technologies.
	The capillary tips may be hitting the bottom of the wells. Autosampler not correctly aligned.	Contact Life Technologies.
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.
		

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. **IMPORTANT!** 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 *before* you click **Reject Results.** To generate a report, click **View Summary Report** or **View Detail Report**. To save the report electronically, select **CutePDF** as the printer.
Extra peaks or spikes in the raw data or "**Bad dye order detected**" error message.	Bubbles in the polymer system.	Run the **Remove Bubbles wizard**.
	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.
		
Spectral calibration fails, or "**No spectral files found**" message is displayed.	Blocked capillary	Run the **Fill Array with Polymer wizard** to clear blockage.
	Insufficient filling of array.	Check for broken capillaries. Run the Fill Array with Polymer wizard.
	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.

Symptom	Possible cause	Action
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.
		
AnyDye Set Spectral Calibration fails.	Problem with spectral calibration	See "Perform a spectral calibration" on page 113.
	AnyDye dye set is not set up correctly.	See "Create a new dye set using the AnyDye template" on page 171.

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 24 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 Life Technologies.
	The capillary tips may be hitting the bottom of the wells. Autosampler not correctly aligned.	Contact Life Technologies.
The Sequencing install check fails: Failed capillaries	Blocked capillary	Run the **Fill Array with Polymer wizard**. Install a new capillary array.

Symptom	Possible cause	Action
• One or more (for 8-capillary). • Three or more (for 24-capillary). Accept button is not active, **Reject** button is active.	Insufficient filling of array.	Check for broken capillaries. Run the **Fill Array with Polymer wizard**.
	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 **Remove Bubbles wizard**.
	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 Life Technologies representative.
	The capillary tips may be hitting the bottom of the wells. Autosampler not correctly aligned.	Call your Life Technologies. 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.

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 **Bubble Remove wizard** 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 **Refresh** in the Dashboard. If consumables status does not refresh, restart the instrument and the computer (see "Restart the instrument and the computer" on page 253).
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. Restart the instrument and the computer (see "Restart the instrument and the computer" on page 253).
Estimated Time Remaining in **Monitor Run** 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.
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.

Symptom	Possible Cause	Action
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.	• If the expected read length of the amplicon is <300, adjust the Contiguous Read Length Pass value. • If the expected read length of the amplicon ≥300, review the sample quality throughout the entire trace.
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 **Tools ▸ Manual Commands**, 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.	Refer to the Dashboard for consumables RFID tag information.

Troubleshooting procedures

Run Troubleshooting Utility.bat

If instructed to do so by a Life Technologies 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 Life Technologies representative.

View the log files

Use a text editor (such as Wordpad) to view the 3500 Series Data Collection Software 3-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 **Planned Maintenance ▸ Usage Statistics**.
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.

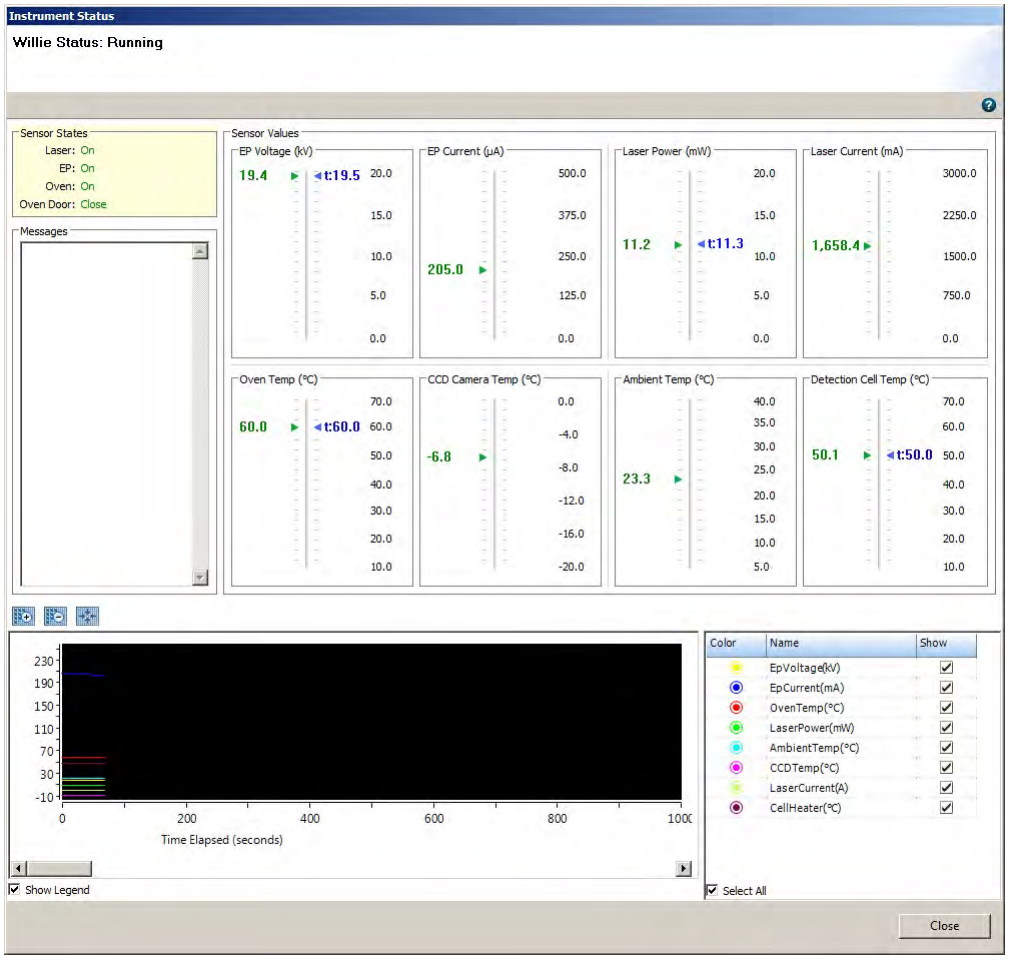


Figure 34 Instrument sensor details

Run status of the instrument is displayed while a run is in progress.

Review error message details

Error messages in the 3500 Series Data Collection Software 3.1 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.

   Note: The Reset button is accessible through a small hole to the left of the Tray button.

B

Run modules and dye sets

Run modules

Table 5 Sequencing analysis run modules

Run module type	Run module name	Configuration		23 hours Throughput[1]			Performance
		Cap. length (cm)	Polymer type	Run time (min)	3500 (8-cap.)	3500xL (24-cap.)	Contig. Read Length (CRL)[2]
Short read sequencing	ShortReadSeq50_POP7 ShortReadSeq50_POP7xl	50	POP-7™	≤30	≥368	≥1104	≥300
Short read sequencing BigDye XTerminator®	BDxShortReadSeq50_POP7 BDxShortReadSeq50_POP7xl	50	POP-7™	≤30	≥368	≥1104	≥300
Rapid sequencing	RapidSeq50_POP6 RapidSeq50_POP6xl	50	POP-6™	≤65	≥168	≥504	≥450
	RapidSeq50_POP7 RapidSeq50_POP7xl	50	POP-7™	≤40	≥280	≥840	≥500
Rapid sequencing	RapidSeq36_POP4 RapidSeq36_POP4xl	36	POP-4®	≤45	≥240	≥720	≥400
	RapidSeq36_POP6 RapidSeq36_POP6xl	36	POP-6™	≤65	≥168	≥504	≥600
	RapidSeq36_POP7 RapidSeq36_POP7xl	36	POP-7™	≤30	≥368	≥1104	≥600
Rapid sequencing BigDye XTerminator®	BDxRapidSeq50_POP6 BDxRapidSeq50_POP6xl	50	POP-6™	≤65	≥168	≥504	≥450
	BDxRapidSeq50_POP7 BDxRapidSeq50_POP7xl	50	POP-7™	≤40	≥280	≥840	≥500
Rapid sequencing BigDye XTerminator®	BDxRapidSeq36_POP4 BDxRapidSeq36_POP4xl	36	POP-4®	≤45	≥240	≥720	≥400

Run module type	Run module name	Configuration		23 hours Throughput[1]			Performance
		Cap. length (cm)	Polymer type	Run time (min)	3500 (8-cap.)	3500xL (24-cap.)	Contig. Read Length (CRL)[2]
Rapid sequencing BigDye XTerminator®	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
Microbial sequencing	MicroSeq50_POP6 MicroSeq50_POP6xl	50	POP-6™	≤135	≥80	≥240	≥600
	MicroSeq50_POP7 MicroSeq50_POP7xl	50	POP-7™	≤125	≥88	≥264	≥850

[1] 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).

[2] 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[1]			Performance			
		Cap. length (cm)	Pol. type	Run time (min)	3500 (8-cap.)	3500xL (24-cap.)	Range[2]	Sizing Precision[3]		
								50bp-400bp	401bp-600bp	601bp-1200bp
Frag. analysis	FragmentAnalysis50_POP7 FragmentAnalysis50_POP7xl	50	POP-7™	≤40	≥280	≥840	≤40 to ≥520	<0.15	<0.30	NA[4]
	FragmentAnalysis50_POP6 FragmentAnalysis50_POP6xl	50	POP-6™	≤100	≥112	≥336	≤20 to ≥550	<0.15	<0.30	NA[4]
	FragmentAnalysis36_POP4 FragmentAnalysis36_POP4xl	36	POP-4®	≤35	≥312	≥936	≤60 to ≥400	<0.15	NA[4]	NA[4]
	FragmentAnalysis36_POP7 FragmentAnalysis36_POP7xl	36	POP-7™	≤30	≥368	≥1104	≤60 to ≥500	<0.15	NA[4]	NA[4]
Frag. analysis	FragAnalysis36_POP6 FragAnalysis36_POP6xl	36	POP-6™	≤60	≥184	≥552	≤60 to ≥400	<0.15	<0.30	NA[4]
Long frag. analysis	LongFragAnalysis50_POP7 LongFragAnalysis50_POP7xl	50	POP-7™	≤125	≥88	≥360	≤40 to ≥700	<0.15	<0.30	<0.45

Run module type	Run module name	Configuration		23 hours throughput[1]			Performance			
		Cap. length (cm)	Pol. type	Run time (min)	3500 (8-cap.)	3500xL (24-cap.)	Range[2]	Sizing Precision[3]		
								50bp-400bp	401bp-600bp	601bp-1200bp
HID	HID36_POP4 HID36_POP4xl	36	POP-4®	≤35	≥312	≥936	≤60 to ≥400	<0.15	NA[4]	NA[4]
SNaPshot®	SNaPshot50_POP7 SNaPshot50_POP7xl	50	POP-7™	≤30	≥376	≥1104	≤40 to ≥120	<0.50	NA[4]	NA[4]

[1] 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).

[2] 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.

[3] 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.

[4] 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
Z (BigDye® Direct)	DNA PCR Amplification/Clean-up/Cycle Sequencing kit

Fragment analysis dye sets for all applications

Table 8 Fragment analysis dye sets

Dye Set	Application
E5	SNaPshot® kit
G5	DNA sizing for 5-dye chemistry
J6	DNA sizing for 6-dye chemistry
F	DNA sizing for 4-dye chemistry
Any dye	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: • COfiler® • Profiler Plus® • Profiler Plus®/*ID* • SGM Plus® • Other 4-dye kits	F
5-dye: • Identifiler® • Identifiler® Direct • Identifiler® Plus • MiniFiler™ • NGM™ • NGM SElect™ • NGM SElect™ Express • SEfiler Plus™ • Sinofiler™ • Yfiler® • Yfiler® Direct • Other 5-dye kits	G5
6-dye: • GlobalFiler® • GlobalFiler® Express	J6

C

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.)[1]
Width	61 cm (24 in.) (closed door) 122 cm (48 in.) (open door)	158 cm (62 in.)[2]
Height	72 cm (28.3 in.)	31 cm (12 in.)
Weight	≈82 kg (180 lbs)	

[1] At the rear of the instrument to ensure adequate airflow and cooling

[2] For the instrument, computer, and computer monitor.

Table 11 Computer dimensions and weight

Parameter	Computer	Monitor	Keyboard
Depth	44.5 cm (17.52 in.)	19.3 cm (7.6 in.)	44.7 cm (17.5 in.)
Width	18.7 cm (7.36 in.)	44.7 cm (17.5 in.)	15.25 cm (6 in.)
Height	41 cm (16.1 in.)	36.6 cm (14.4 in.)	5 cm (2 in.)
Weight	10.9 kg (24 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	• Long-life, single-line 505 nm, solid-state laser excitation source • Laser Output power 20mW • Beam divergence 1.4 mrad
LED	• Emitting color Natural White • Luminous Intensity 250 Cd
Electrophoresis Voltage	Up to 20 kV
Oven Temperature	Active temperature control from 18°C to 70°C

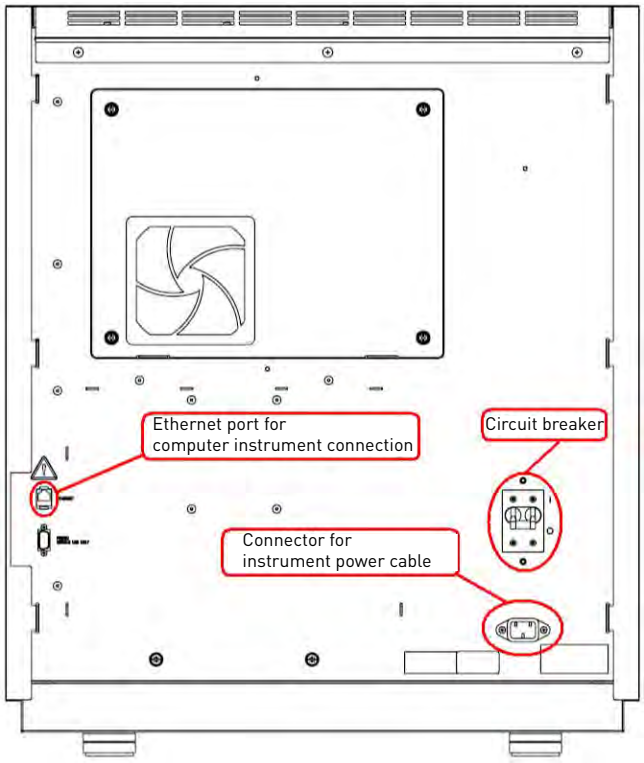
Component	Specification
Minimum Computer Requirements	• Hardware: – OptiPlex™ XE, E8400, 3 GHZ Processor *or* – OptiPlex™OptiPlex™ XE2, with Intel™Core I7-47705, 3.1 GHz Processor • Operating system: Windows® 7 SP1 • Installed RAM: 16 GB • Hard drive: 500 GB SATA 3.0 Gb/s and 8 MB Data Burst Cache

Environmental requirements

Table 13 Environmental requirements

Condition	Requirement
Installation site	Indoor use only
Altitude	Safety tested up to 2000 m (6562 ft)
Electrical ratings	Power cord with ground pin required • Instrument - AC 100-240 V ±10%, 50/60 Hz, 3.1 A, power rated 320 VA • Maximum current - 15 A • Maximum power dissipation - 417 VA, 371 W (approximately, not including computer and monitor)
	• Computer - AC 100-240 V ±10%, 50/60 Hz , 2.1 A, power rated 125 VA
	• Monitor - AC 100-240 V ±10%, 50/60 Hz , 1.5 A, power rated 65 VA
Mains AC line voltage tolerances	Up to ±10 percent of nominal voltage
Transient category	Installation categories II
Pollution degree	2
Operating conditions	15 to 30°C (59 to 86°F) (Room temperature should not fluctuate ±2°C during an instrument run) 20 to 80% relative humidity, noncondensing
Transport and storage conditions	– 30 to +60°C (– 22 to +140°F) Minimum 20% relative humidity, maximum 85% (non-condensing)

Power and communication connections



D Part 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: • 8-strip PCR tubes, standard- or optical-grade polypropylene, 0.1 mL • 8-strip full-height PCR tubes, standard- or optical-grade polypropylene, 0.2 mL
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	Part Number
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	4410229
Retainer and base (Fast), 96-well RUO	4409530
Retainer and base (Standard), 384-well, RUO	4410235
Septa, 8-strip RUO	4410701
Septa, 96-well RUO	4412614
Septa, 96-well	4410700
Septa, 384-well RUO	4412520

Instrument consumables

Name	Part Number
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)[1]	4393710
Polymer, POP-4® (384)[1]	4393715
Polymer, POP-4® (96)	A26070
Hi-Di™ Formamide Four 5-mL bottles	4440753

[1] Validated for HID applications.

Sequencing analysis reagents and consumables

Name	Part Number
BigDye® Terminator (BDT) v1.1 Sequencing Standards, 3500/3500xL	4404314
BigDye® Terminator (BDT) v3.1 Sequencing Standards, 3500/3500xL	4404312
BigDye® Terminator (BDT) v3.1 Matrix Standards Kit, 3500/3500xL	4336974
BigDye® Terminator (BDT) v1.1 Matrix Standards Kit, 31xx and 3500	4336824
BigDye® Terminator (BDT) v3.1 Cycle Sequencing Kit, 24 reactions	4337454
BigDye® Terminator (BDT) v3.1 Cycle Sequencing Kit, 100 reactions	4337455
BigDye® Terminator (BDT) v3.1 Cycle Sequencing Kit, 1000 reactions	4337456

Name	Part Number
BigDye® Terminator (BDT) v3.1 Cycle Sequencing Kit, 5000 reactions	4337457
BigDye® Terminator (BDT) v1.1 Cycle Sequencing Kit, 24 reactions	4337449
BigDye® Terminator (BDT) v1.1 Cycle Sequencing Kit, 100 reactions	4337450
BigDye® Terminator (BDT) v1.1 Cycle Sequencing Kit, 5000 reactions	4337451
BigDye® Terminator (BDT) v1.1 Cycle Sequencing Kit, 5000 reactions	4337452
BigDye® Direct Cycle Sequencing Kit, 24 reactions	4458689
BigDye® Direct Cycle Sequencing Kit, 100 reactions	4458687
BigDye® Direct Cycle Sequencing Kit, 1000 reactions	4458688

Fragment and HID analysis reagents

Name	Part Number
DS-02 Matrix Standard Kit (5-Dye) (E5 dye set)	4323014
DS-32 Matrix Standard Kit (4-dye)	4345831
DS-33 Matrix Standard Kit (5-Dye)	4345833
DS-36 Matrix Standard Kit (6-Dye)	4425042
DS-33 GeneScan Installation Standards with GeneScan™ 600 LIZ® Size Standard v2.0 (G5 dye set)	4376911
GeneScan™ 120 LIZ® Size Standard	4322362
GeneScan™ 500 ROX™ Size Standard	401734
GeneScan™ 600 LIZ® Size Standard v2.0	4408399
GeneScan™ 1200 LIZ® Size Standard	4379950
AmpFℓSTR® Identifiler® Allelic Ladder (For HID install check)	Contact Life Technologies

Limitations

The 3500/3500xL Genetic Analyzer 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 78.
- The following settings are not retained after data migration from v1.0 to v3 software. Manually specify the settings after migration.
  - Plate setup, report settings, and sequencing settings preferences
  - Notification log in Calendar Reminders
- 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. We recommend Norton Antivirus, which has been tested and approved for use with the Applied Biosystems® 3500/3500xL Genetic Analyzer with 3500 Series Data Collection Software 3.1.

Instrument and consumables

- Instrument firmware is to be updated only by a Life Technologies representative.
- Before each run, check buffer fill levels.
- In the event of power being disrupted, restart the computer ("Restart the instrument and the computer" on page 253).
- If you observe "Unable to transmit measurement data. Internal data buffer overflow." error, restart the computer ("Restart the instrument and the computer" on page 253).
- If you observe a "Failure to Read from RFID tag" error, see "Troubleshooting" on page 298.

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 "Run a spatial calibration" on page 106. Refer to examples of passing spatial calibration as shown in "Example spatial profiles" on page 108.
- When performing a spectral calibration, select the dye set appropriate for your application as described in "Perform a spectral calibration" on page 113.
- 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 195.
- 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 88.
- For fragment analysis or HID data, review sample quality as described in “Review sample quality“ on page 96 on page 91.
- 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.

F

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 17).

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 8 inches (20 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

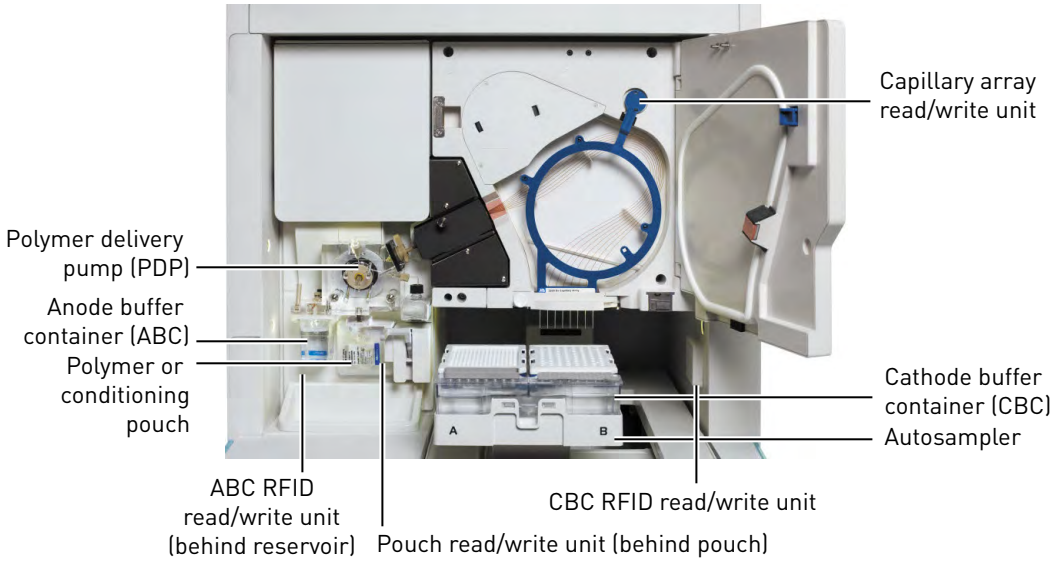


Figure 35 RFID read/write unit locations within instrument interior (shown with door open)

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 3500 Series Data Collection Software 3.1 run.

Specifications

Table 16 RFID read/write unit specifications

Component	Specification
RFID read/write unit	• Ultra-Compact Proximal-Type RFID Reader / Writer • Model ASI4000-98-BS1 • Manufactured by ART Technology Co., Ltd.
RF frequency	13.56 MHz
RF output power	60 mW

Component	Specification
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	• ABC tag: 3 cm • CBC tag: 4 cm • Capillary tag: 3 cm • Polymer tag: 3 cm
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	3 feet
Wireless security	• RFID tag read/write/re-read with checksum • Password access for use of software • Base-64 encoding of data between the instrument and the computer

Troubleshooting

Table 17 RFID troubleshooting

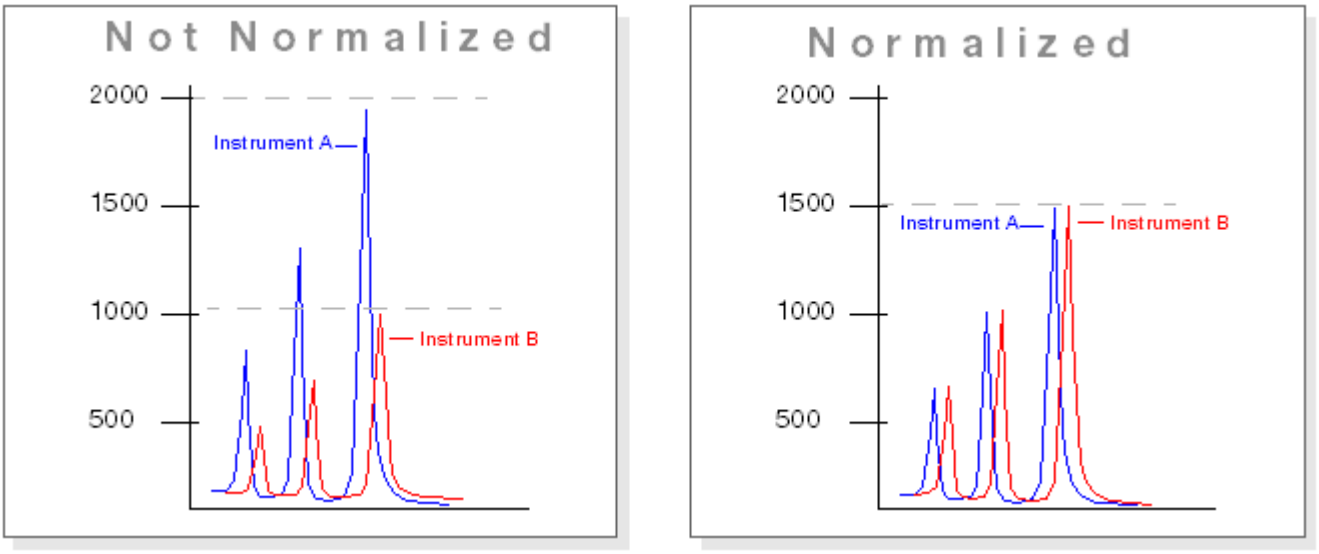
Symptom	Possible cause	Action
Unable to read RFID information. "Failure to Read from RFID tag"	Consumable package is improperly installed or label is defective. Polymer/Conditioning reagent pouch is not positioned properly.	Ensure that the RFID label is not visibly damaged and consumable package is properly installed. Ensure that label is close, and parallel, to the instrument. Reposition or re-install pouch, then click **Refresh** on the Dashboard.
		Restart the instrument and the computer (see "Restart the instrument and the computer" on page 253).
		Install a new consumable (if available). If problem persists, contact Life Technologies.

Symptom	Possible cause	Action
Unable to read RFID information. "Failure to Read from RFID tag"	Malfunctioning RFID label or reader.	Place a used CBC, ABC, pouch, or array on the instrument: • If the instrument can read the RFID label, install a new CBC, ABC, pouch, or array. • If the instrument cannot read the RFID label, contact Life Technologies.

Normalization

Overview of the normalization feature

For fragment analysis applications, the 3500 Series Data Collection Software 3.1 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 3500 Series Data Collection Software 3.1 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, etc). To obtain SDSs, see the "Documentation and Support" section in this document.

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
	Caution, hot surface	Attention, surface chaude

Symbol	English	Français
	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 **CAUTION!** 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. **CAUTION!** 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.
	Indicates conformity with European Union requirements.

Conformity mark	Description
	Indicates conformity with Australian standards for electromagnetic compatibility.

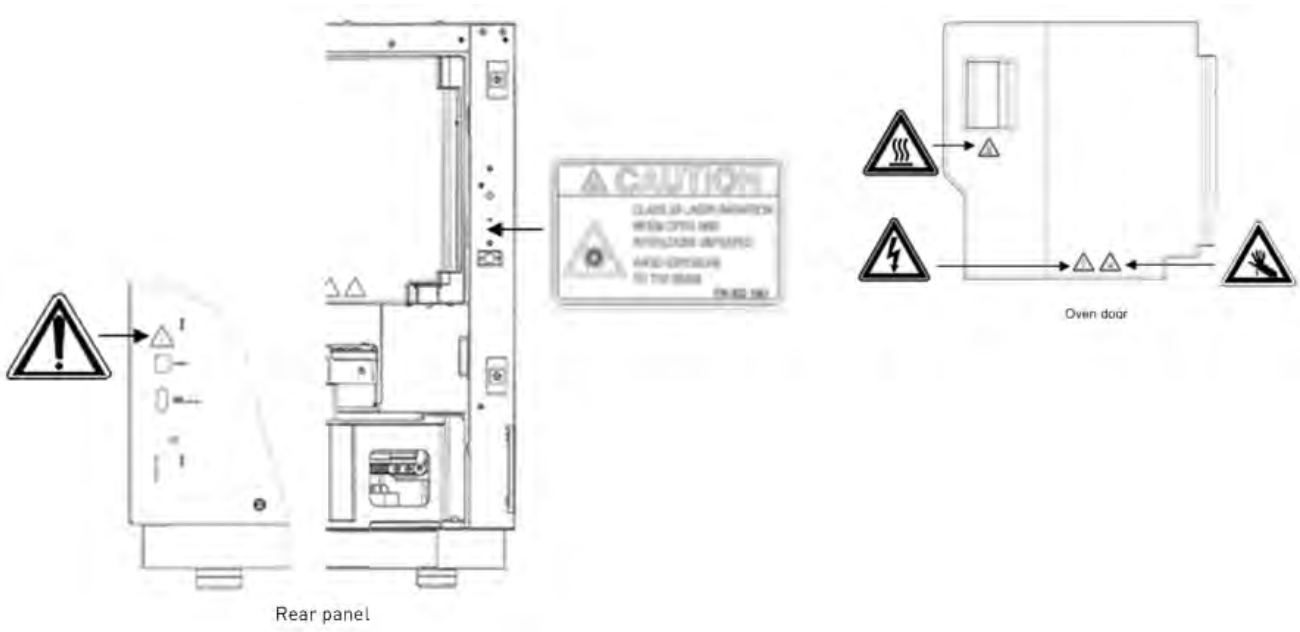
Safety alerts on this instrument

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	French translation
CAUTION! Hazardous chemicals. Read the Safety Data Sheets (SDSs) before handling.	**ATTENTION! Produits chimiques dangereux.** Lire les fiches signalétiques (FS) avant de manipuler les produits.
CAUTION! Hazardous waste. Refer to SDS(s) and local regulations for handling and disposal.	**ATTENTION! Déchets dangereux.** Lire les fiches signalétiques (FS) et la réglementation locale associées à la manipulation et à l'élimination des déchets.
DANGER! Class 3B (III) visible and/or invisible laser radiation present when open and interlocks defeated. Avoid exposure to beam.	**DANGER!** 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
DANGER! Class 3B (III) visible and/or invisible laser radiation present when open and interlocks defeated. Avoid exposure to beam.	**ATTENTION!** 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 

English	French translation	Location on Instrument
		
		

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

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.

WARNING! Power Supply Line Cords. Use properly configured and approved line cords for the power supply in your facility.

WARNING! Disconnecting Power. To fully disconnect power either detach or unplug the power cord, positioning the instrument such that the power cord is 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.

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 Life Technologies 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

Life Technologies 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 standards and requirements for safety and electromagnetic compatibility as noted in the following table:

Safety (compliance)

Reference	Description
EU Directive 2006/95/EC	European Union "Low Voltage Directive"
IEC 61010-1 EN 61010-1 UL 61010-1 CSA C22.2 No. 61010-1	*Safety requirements for electrical equipment for measurement, control, and laboratory use – Part 1: General requirements*
IEC 61010-2-010 EN 61010-2-010	*Safety requirements for electrical equipment for measurement, control and laboratory use – Part 2-010: Particular requirements for laboratory equipment for the heating of materials*
IEC 61010-2-081 EN 61010-2-081	*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*

Reference	Description
IEC 60825-1:2007 EN 60825-1:2007	*Safety of laser products – Part 1: Equipment classification and requirements*
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 2004/108/EC	European Union "EMC Directive"
EN 61326-1	*Electrical Equipment for Measurement, Control and Laboratory Use – EMC Requirements – Part 1: General Requirements*
EN 61326-2-6-20061	*Electrical Equipment for Measurement, Control and Laboratory Use – EMC Requirements – Part 2-6: Particular requirements — In vitro diagnostic (IVD) medical equipment*
FCC Part 15 (47 CFR)	U.S. Standard "Industrial, Scientific, and Medical Equipment"
AS/NZS 2064	*Limits and Methods of Measurement of Electromagnetic Disturbance Characteristics of Industrial, Scientific, and Medical (ISM) Radiofrequency Equipment*
ICES-001, Issue 3	*Industrial, Scientific and Medical (ISM) Radio Frequency Generators*

Environmental design

Reference	Description
Directive 2012/19/EU	European Union "WEEE Directive" – Waste electrical and electronic equipment
Directive 2011/65/EU	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

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, and 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.

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. All work should be conducted in properly equipped facilities using the appropriate safety equipment (for example, physical containment devices). Safety equipment also may 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/biosafety/publications/bmbl5/BMBL.pdf
- World Health Organization, *Laboratory Biosafety Manual*, 3rd Edition, WHO/CDS/CSR/LYO/2004.11; found at:
  www.who.int/csr/resources/publications/biosafety/Biosafety7.pdf

Documentation and support

Related documentation

Document	Publication number	Description
3500/3500xL Genetic Analyzer with Data Collection Software 3 Quick Reference	100026299	Provides abbreviated instructions for using the instrument and software.
3500/3500xL Genetic Analyzer Site Preparation Guide	4401689	Provides information needed to prepare your site for instrument installation.
Polymer Delivery Pump Cleaning Kit Instructions	4414004	Describes how to clean the pump.

Note: For additional documentation, see "Obtaining support" on page 311.

Customer and technical support

Visit **thermofisher.com/support** for the latest in services and support, including:

- Worldwide contact telephone numbers
- Product support
- Order and web support
- Safety Data Sheets (SDSs; also known as MSDSs)

Additional product documentation, including user guides and Certificates of Analysis, are available by contacting Customer Support.

Obtaining support

For service and technical support:

- Call Toll-Free in US: 1.800.831.6844
- Email instrumentservices@lifetech.com

For the latest services and support information for all locations, go to:

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 this product as set forth in the *Applied Biosystems® 3500/3500xL Genetic Analyzer – Instrument Limited Warranty*. If you have any questions, please contact Life Technologies at **thermofisher.com/support**.

Additional instrument symbols

The following table describes symbols that may be displayed on instruments, consumables, or reagents.

Symbol	Description	Symbol	Description
	MANUFACTURER		CONTAINS SUFFICIENT FOR <n> TESTS
	DATE OF MANUFACTURE		USE BY
	BATCH CODE		CATALOG NUMBER
	SERIAL NUMBER		FRAGILE, HANDLE WITH CARE
	LOWER LIMIT OF TEMPERATURE		PROTECT FROM LIGHT
	UPPER AND LOWER LIMITS OF TEMPERATURE		UPPER LIMIT OF TEMPERATURE
	DO NOT REUSE		BIOLOGICAL RISKS
	CAUTION, CONSULT ACCOMPANYING DOCUMENTS		CONSULT INSTRUCTIONS FOR USE
	UPPER AND LOWER LIMITS OF HUMIDITY		OBSERVE PRECAUTIONS FOR HANDLING ELECTROSTATIC SENSITIVE DEVICES

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