SeqStudio™ Genetic Analyzer Instrument and Software

USER GUIDE

for use with:
SeqStudio™ Data Collection Software v1.1.4
SeqStudio™ Genetic Analyzer Cartridge (Cat. No. A33671)
SeqStudio™ Genetic Analyzer Cartridge v2 (Cat. No. A41331)
SeqStudio™ Plate Manager
SeqStudio™ Remote Monitoring App

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Instrument overview

The Applied Biosystems™ SeqStudio™ Genetic Analyzer with SeqStudio™ Data Collection Software is a fluorescent dye-labeled genetic analysis system using capillary electrophoresis technology. It enables both sequencing and fragment analysis applications without the need to switch polymer type or capillary array length.

The instrument uses a self-contained, replaceable cartridge with:

- A 4-capillary array
- A universal polymer capable of performing sequencing and fragment analysis
- A polymer delivery system (PDS)
- Anode buffer

The SeqStudio™ Genetic Analyzer automatically:

- Performs an optical alignment each time a cartridge is inserted.
- Performs an automatic spectral calibration adjustment (auto calibration) for each sample to correct for spectral overlap.

The instrument is compatible with 96-well Standard plates and 8-strip Standard tubes. The SeqStudio™ Genetic Analyzer is a stand-alone instrument. It is run directly from the touchscreen with SeqStudio™ Data Collection Software and does not require a computer. Plate setup can be done directly on the touchscreen, on a computer with SeqStudio™ Plate Manager, or on the Thermo Fisher Cloud. A run can be monitored directly on the instrument touchscreen or remotely on the Thermo Fisher Cloud.
Parts of the instrument

Figure 1  Front of the instrument
1. Front panel indicator—Shows the status of the instrument
2. Touchscreen—User interface
3. Door—Provides access to the cartridge, the cathode buffer, and sample plate or tubes
4. USB port

Figure 2  Interior of the instrument
1. Cartridge rails
2. Cartridge
3. Cathode buffer [located inside the autosampler]
4. Autosampler [contains the plate or tube holder and the cathode buffer]
5. Plate or tube holder
Figure 3  Rear of the instrument

1 RJ45 ethernet port
2 USB port
3 Power receptacle
4 On/Off switch

Instrument status indicator

<table>
<thead>
<tr>
<th>Indicator</th>
<th>Instrument status</th>
</tr>
</thead>
<tbody>
<tr>
<td>All lights off</td>
<td>Powered off or in <strong>Cartridge storage mode</strong>.</td>
</tr>
<tr>
<td>Blue light (blinking)</td>
<td>Starting up.</td>
</tr>
<tr>
<td>Blue light</td>
<td>Ready to start a run or run is in progress.</td>
</tr>
<tr>
<td>Amber light (blinking)</td>
<td>Run is paused, door is open, or error state.</td>
</tr>
</tbody>
</table>

**SeqStudio™ Genetic Analyzer consumables**

<table>
<thead>
<tr>
<th>Description</th>
<th>Cat. No.</th>
<th>Amount</th>
<th>Storage</th>
</tr>
</thead>
<tbody>
<tr>
<td>SeqStudio™ Genetic Analyzer Cartridge</td>
<td>A33671</td>
<td>1 cartridge with an optical cover and a SeqStudio™ Integrated Capillary Protector attached for shipment and storage.</td>
<td>See Table 1 on page 17</td>
</tr>
<tr>
<td>SeqStudio™ Genetic Analyzer Cartridge v2</td>
<td>A41331</td>
<td>1 cartridge with an optical cover and a SeqStudio™ Integrated Capillary Protector attached for shipment and storage.</td>
<td>See Table 2 on page 18</td>
</tr>
<tr>
<td>SeqStudio™ Genetic Analyzer Cathode Buffer Container</td>
<td>A33401</td>
<td>1 package of 4</td>
<td>See page 149</td>
</tr>
<tr>
<td>SeqStudio™ Integrated Capillary Protector</td>
<td>A31923</td>
<td>1 (single-use) for future storage</td>
<td>See page 148</td>
</tr>
</tbody>
</table>
The SeqStudio™ Genetic Analyzer uses a 4-capillary, self-contained, replaceable cartridge. The following cartridges are available:

<table>
<thead>
<tr>
<th>Cartridge</th>
<th>No. of injections</th>
<th>No. of samples</th>
<th>Storage</th>
</tr>
</thead>
<tbody>
<tr>
<td>SeqStudio™ Genetic Analyzer Cartridge [Cat. No. A33671]</td>
<td>125 injections</td>
<td>500 samples</td>
<td>See Table 1 on page 17</td>
</tr>
<tr>
<td>SeqStudio™ Genetic Analyzer Cartridge v2 [Cat. No. A41331]</td>
<td>250 injections</td>
<td>1,000 samples</td>
<td>See Table 2 on page 18</td>
</tr>
</tbody>
</table>

Each cartridge:

- Contains a capillary array, a polymer delivery system, polymer, and anode buffer. See Figure 4 and Figure 5.
- Is shipped with an optical cover and an Integrated Capillary Protector. See Figure 6.
- Has a radio frequency identification (RFID) tag, which is used by the instrument to track remaining usage and expiration.

Figure 4  Parts of the cartridge

1. Universal polymer—Supplies polymer to the polymer delivery pump.
2. Polymer delivery system—Pumps polymer into the capillary array.
3. Anode buffer reservoir—Genetic Analysis running buffer to support electrophoresis.
4. Optical detection window
5. Cartridge track—To insert the cartridge into the instrument.
6. Capillary array (cathode end)—Tips of the four capillaries that enable electrophoretic separation of fluorescent-labeled DNA fragments.
Figure 5  Parts of the polymer delivery system
1 Universal polymer
2 Polymer valve
3 Syringe
4 Capillary fitting (anode end)
5 Buffer valve
6 Anode buffer reservoir

Figure 6  Cartridge with optical cover and Integrated Capillary Protector
1 Optical cover
2 Optical cover hand hold (for removing the optical cover)
3 Integrated Capillary Protector
4 Cartridge hand hold

IMPORTANT! Remove the Integrated Capillary Protector before installing the cartridge into the instrument. Installing the cartridge with the ICP in place can damage the capillary array.
## Cartridge storage

**Table 1** Storage information for the SeqStudio™ Genetic Analyzer Cartridge (Cat. No. A33671)

<table>
<thead>
<tr>
<th>Condition</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Shipping</strong></td>
<td>Shipped at 2–8°C. Store upright at 2–8°C upon receipt. Save the white storage box and optical cover for off-instrument cartridge storage.</td>
</tr>
</tbody>
</table>
| **On-instrument storage** | For routine use, can be used and stored on the instrument for up to 4 months. If you store the cartridge on-instrument:  
  - The instrument must be powered on.  
  - A Cathode Buffer Container must also be installed.  
  The instrument keeps the components under the following conditions when it is powered on and in **Cartridge storage mode**:  
    - **Optical detection window**—Covered  
    - **Capillary array electrodes**—Submerged in cathode buffer (buffer must be above the fill line in the Cathode Buffer Container)  
    - **Polymer**—Chilled  
    - **Anode buffer**—Ambient temperature  

  **IMPORTANT!** The instrument does not maintain the correct temperature conditions for the cartridge when it is powered off. Avoid cartridge exposure to ambient temperature. |
| **Off-instrument storage** | For intermittent use, can be stored off-instrument until the expiry date on the label or up to 4 months after first use. Store upright at 2–8°C, with an integrated capillary protector (ICP) and optical cover installed (see “Store the cartridge” on page 146).  

  **Note:** After you remove the cartridge from the instrument, install an ICP within a few minutes. Avoid cartridge exposure to ambient temperature. |
| **Reuse**            | Can be removed from an instrument then inserted again on the same instrument or a different instrument, if it was stored properly at 2–8°C and has not expired or exceeded 125 injections. Information about the cartridge installation and usage is retained in the cartridge history ([Settings > Cartridge > Instrument–cartridge history](#)). |
Table 2  Storage information for the SeqStudio™ Genetic Analyzer Cartridge v2 (Cat. No. A41331)

<table>
<thead>
<tr>
<th>Condition</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Shipping</td>
<td>Shipped at 2–8°C. Store upright at 2–8°C upon receipt. Save the white storage box and optical cover for off-instrument cartridge storage.</td>
</tr>
</tbody>
</table>
| On-instrument storage| For routine use, can be used and stored on the instrument for up to 6 months. If you store the cartridge on-instrument:  
• The instrument must be powered on.  
• A Cathode Buffer Container must also be installed.  
The instrument keeps the components under the following conditions when it is powered on and in **Cartridge storage mode**:  
• **Optical detection window**—Covered  
• **Capillary array electrodes**—Submerged in cathode buffer (buffer must be above the fill line in the Cathode Buffer Container)  
• **Polymer**—Chilled  
• **Anode buffer**—Ambient temperature  
**IMPORTANT!** The instrument does not maintain the correct temperature conditions for the cartridge when it is powered off. Avoid cartridge exposure to ambient temperature. |
| Off-instrument storage| For intermittent use, can be stored off-instrument until the expiry date on the label or up to 6 months after first use. Store upright at 2–8°C, with an integrated capillary protector (ICP) and optical cover installed (see “Store the cartridge” on page 146).  
**Note:** After you remove the cartridge from the instrument, install an ICP within a few minutes. Avoid cartridge exposure to ambient temperature. |
| Reuse                | Can be removed from an instrument then inserted again on the same instrument or a different instrument, if it was stored properly at 2–8°C and has not expired or exceeded 250 injections.  
Information about the cartridge installation and usage is retained in the cartridge history ([Settings > Cartridge > Instrument–cartridge history](#)) |
SeqStudio™ Genetic Analyzer Cathode Buffer Container

The SeqStudio™ Genetic Analyzer Cathode Buffer Container (CBC) contains running buffer for capillary electrophoresis. The container has two compartments. The rear compartment provides the cathode buffer for electrophoresis. The front compartment is for capillary wash and waste.

The CBC requires a Reservoir Septa.

See “Assemble the SeqStudio™ Genetic Analyzer Cathode Buffer Container (CBC)” on page 149.

Figure 7  SeqStudio™ Genetic Analyzer Cathode Buffer Container with Reservoir Septa

1. Reservoir Septa
2. Notch (inserted towards the rear right in the autosampler)
3. Fill line (replace the CBC when the buffer is at the fill line)
4. Cathode buffer compartment
5. Waste and wash compartment

Figure 8  Autosampler

1. Location of plate or tubes
2. Release button
3. Location of Cathode Buffer Container
4. Location to position the Cathode Buffer Container notch

Radio frequency identification

The cartridge and cathode buffer have radio–frequency identification (RFID) tags. The instrument reads and tracks:

- Expiry date (shelf life)
- Remaining injections (usage)
- Serial number (cartridge only)
- Lot number (cathode buffer only)
### Table 3  RFID tag read/write events and consumables status updates

<table>
<thead>
<tr>
<th>Component</th>
<th>RFID read</th>
<th>RFID write</th>
<th>Consumables status update</th>
</tr>
</thead>
<tbody>
<tr>
<td>SeqStudio™ Genetic Analyzer Cartridge</td>
<td>When a cartridge inserted. The first time a new cartridge is loaded into an instrument, the manufacturer expiry date is listed for <strong>Expiration time</strong> in the <strong>Consumable status</strong> screen.</td>
<td>• The <strong>Expiration time</strong> is reset from the manufacturer expiry date to 4 months from the current date of installation. • After the cartridge has been loaded and before it is ejected, its cartridge history record is updated to include its usage on this instrument. • During each injection, injection count and remaining polymer volume are updated.</td>
<td>Every 8 hours and/or before each run(^\dagger): • When a cartridge is within 2 weeks of expiry date. • When the number of injections is approaching the limit of 125 injections.</td>
</tr>
<tr>
<td>SeqStudio™ Genetic Analyzer Cartridge v2</td>
<td></td>
<td>• The <strong>Expiration time</strong> is reset from the manufacturer expiry date to 6 months from the current date of installation. • After the cartridge has been loaded and before it is ejected, its cartridge history record is updated to include its usage on this instrument. • During each injection, injection count and remaining polymer volume are updated.</td>
<td>Every 8 hours and/or before each run(^\dagger): • When a cartridge is within 2 weeks of expiry date. • When the number of injections is approaching the limit of 250 injections.</td>
</tr>
<tr>
<td>Cathode buffer</td>
<td>• When the autosampler initializes. • When a plate is retracted.</td>
<td>• The first time a new CBC is loaded on an instrument, the installation date is recorded on the CBC. • After each injection, the injection count is updated.</td>
<td>Every 8 hours and/or before each run(^\dagger): • When the CBC is within 2 days of expiry date. • When the number of injections is approaching the limit of 125 injections.</td>
</tr>
</tbody>
</table>

\(^\dagger\) If either limit is met, an email notification is also sent to any Cloud users who are linked to this instrument

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**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.

**Software features**

The instrument can be operated directly from the touchscreen using the SeqStudio™ Data Collection Software. The touch screen allows scrolling and zooming by pinch.

Plates can be set up and saved on a computer using the SeqStudio™ Plate Manager running on a desktop or on the Thermo Fisher Cloud. These plate setups can be saved to and accessed from the instrument from:

- A network drive
- A USB drive
- The Thermo Fisher Cloud

You can monitor runs directly from the instrument or from the SeqStudio™ Remote Monitoring App.

<table>
<thead>
<tr>
<th>Feature</th>
<th>SeqStudio™ Data Collection Software</th>
<th>SeqStudio™ Plate Manager (desktop)</th>
<th>SeqStudio™ Plate Manager (Cloud)</th>
<th>Remote Monitoring App</th>
</tr>
</thead>
<tbody>
<tr>
<td>Plate setup</td>
<td>✓</td>
<td>✓</td>
<td>✓</td>
<td>—</td>
</tr>
<tr>
<td>Create a new plate setup</td>
<td>✓</td>
<td>✓</td>
<td>✓</td>
<td>—</td>
</tr>
<tr>
<td>Enter plate properties</td>
<td>✓</td>
<td>✓</td>
<td>✓</td>
<td>—</td>
</tr>
<tr>
<td>Set up plate wells</td>
<td>✓</td>
<td>✓</td>
<td>✓</td>
<td>—</td>
</tr>
<tr>
<td>Advanced options for plate setup</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Edit sample properties</td>
<td>✓</td>
<td>✓</td>
<td>✓</td>
<td>—</td>
</tr>
<tr>
<td>Edit plate setup</td>
<td>✓</td>
<td>✓</td>
<td>✓</td>
<td>—</td>
</tr>
<tr>
<td>Manage size standards</td>
<td>✓</td>
<td>✓</td>
<td>✓</td>
<td>—</td>
</tr>
<tr>
<td>Feature</td>
<td>SeqStudio™ Data Collection Software</td>
<td>SeqStudio™ Plate Manager (desktop)</td>
<td>SeqStudio™ Plate Manager (Cloud)</td>
<td>Remote Monitoring App</td>
</tr>
<tr>
<td>------------------------------------------------------------------------</td>
<td>-------------------------------------</td>
<td>-----------------------------------</td>
<td>---------------------------------</td>
<td>-----------------------</td>
</tr>
<tr>
<td>Manage run modules (including edit a run module)</td>
<td>✓</td>
<td>✓</td>
<td>✓</td>
<td>—</td>
</tr>
<tr>
<td><strong>Advanced options for plate properties</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Adjust fragment analysis parameters</td>
<td>✓</td>
<td>✓</td>
<td>✓</td>
<td>—</td>
</tr>
<tr>
<td>Adjust sequence parameters</td>
<td>✓</td>
<td>✓</td>
<td>✓</td>
<td>—</td>
</tr>
<tr>
<td>Adjust the file naming format</td>
<td>✓</td>
<td>✓</td>
<td>✓</td>
<td>—</td>
</tr>
<tr>
<td>Select injection options</td>
<td>✓</td>
<td>✓</td>
<td>✓</td>
<td>—</td>
</tr>
<tr>
<td>Create custom dye set</td>
<td>✓</td>
<td>—</td>
<td>—</td>
<td>—</td>
</tr>
<tr>
<td>(to import, open a plate setup containing a custom dye set)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>Edit during a run or after a run is complete</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Monitor run</td>
<td>✓</td>
<td>—</td>
<td>—</td>
<td>✓</td>
</tr>
<tr>
<td>Pause or cancel a run</td>
<td>✓</td>
<td>—</td>
<td>—</td>
<td>✓</td>
</tr>
<tr>
<td>Edit injection parameters and re-inject samples</td>
<td>✓</td>
<td>—</td>
<td>—</td>
<td>✓</td>
</tr>
<tr>
<td><strong>View results</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>View run result details</td>
<td>✓</td>
<td>—</td>
<td>—</td>
<td>✓</td>
</tr>
<tr>
<td>View PUP score</td>
<td>✓</td>
<td>—</td>
<td>—</td>
<td>✓</td>
</tr>
<tr>
<td>View trace score (sequence analysis only)</td>
<td>✓</td>
<td>—</td>
<td>—</td>
<td>✓</td>
</tr>
<tr>
<td>View size quality (fragment analysis only)</td>
<td>✓</td>
<td>—</td>
<td>—</td>
<td>✓</td>
</tr>
<tr>
<td>Feature</td>
<td>SeqStudio™ Data Collection Software</td>
<td>SeqStudio™ Plate Manager (desktop)</td>
<td>SeqStudio™ Plate Manager (Cloud)</td>
<td>Remote Monitoring App</td>
</tr>
<tr>
<td>---------------------------------------------</td>
<td>-------------------------------------</td>
<td>-----------------------------------</td>
<td>---------------------------------</td>
<td>-----------------------</td>
</tr>
<tr>
<td>View Contiguous Read Length</td>
<td>✓</td>
<td>—</td>
<td>—</td>
<td>✓</td>
</tr>
<tr>
<td>(sequence analysis only)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>View and export results</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>View real-time results</td>
<td>✓</td>
<td>—</td>
<td>—</td>
<td>✓</td>
</tr>
<tr>
<td>Adjust the graphical view</td>
<td>✓</td>
<td>—</td>
<td>—</td>
<td>✓</td>
</tr>
<tr>
<td>Auto export or manually export data files to the Thermo Fisher Cloud, a network drive, or a USB</td>
<td>✓</td>
<td>—</td>
<td>—</td>
<td>—</td>
</tr>
<tr>
<td>Export a results report</td>
<td>✓</td>
<td>—</td>
<td>—</td>
<td>✓</td>
</tr>
</tbody>
</table>

**SeqStudio™ Plate Manager overview**

The SeqStudio™ Plate Manager is a stand-alone software. It allows you to set up and save plates that you can open and run on the instrument.

The SeqStudio™ Plate Manager is available:

- On the Thermo Fisher Cloud as an app, with access to the SeqStudio™ Remote Monitoring App
- At [thermofisher.com](http://thermofisher.com), for download and installation on a computer
- On a USB, for installation on a computer

Install the Plate Manager by following the instructions in the install wizard.
The following browsers are recommended to use the Plate Manager app on Thermo Fisher Cloud or a desktop computer:

- Mozilla™ Firefox™ Version 32.0.3+
- Google™ Chrome™ Version 38.02+
- Apple™ Safari™ Version 7+
- Microsoft™ Edge 10+ (Windows™ 10)
- Microsoft™ Internet Explorer™ 11 (Windows™ 7)

The use of other browsers or other versions can result in reduced functionality and improper display of information.
SeqStudio™ Remote Monitoring App overview

The Remote Monitoring App allows you to monitor the status of instrument runs from a remote location.

The Remote Monitoring App is available:

- On the Thermo Fisher Cloud as an app, with direct access from the Plate Manager or the InstrumentConnect.
- At thermofisher.com, for download and installation on a mobile device.

![Remote Monitoring App on Cloud](image)

Figure 10 Remote Monitoring App on Cloud
## Network connection options

The SeqStudio™ Genetic Analyzer can be connected to a network or computer in the following configurations:

<table>
<thead>
<tr>
<th>Direct connection</th>
<th>Local area network (LAN) connection</th>
<th>Thermo Fisher Cloud connection</th>
</tr>
</thead>
<tbody>
<tr>
<td>Wired</td>
<td>Wired or wireless</td>
<td>Wired or wireless</td>
</tr>
</tbody>
</table>

## Experiment types

### Sequencing

Sequencing is the determination of the base-pair sequence of a DNA fragment by the formation of extension products of various lengths amplified through PCR.

Fragment analysis

Fragment analysis is the determination of the size of fragments. It uses the size standard in each sample to create a standard curve for each sample. It then determines the relative size of each dye-labeled fragment in the sample by comparing fragments with the standard curve for that specific sample.

For more information, see DNA Fragment Analysis by Capillary Electrophoresis User Guide (Pub. No. 4474504).

<table>
<thead>
<tr>
<th>Intensity (RFU)</th>
<th>Size (bp)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>60 80 100 120 140 160 180 200 220 240 260 280 300</td>
</tr>
</tbody>
</table>

Data output

SeqStudio™ Data Collection Software generates an electropherogram (intensity plot) for each dye that is based on the migration of DNA fragments through the capillaries during a run.

The format of the sample data files is determined by the type of experiment that is specified at the time of plate setup.

- Sequencing experiments use basecalling (the algorithms and settings required to determine the fragment base sequences) and generate an AB1 file.
- Fragment analysis experiments use sizecalling (the algorithms and settings required to determine the fragment sizes) and generate an FSA file.

The AB1 and FSA file formats can be analyzed by secondary analysis software.
Secondary analysis software

Secondary analysis software is available for desktop computers and on the Thermo Fisher Cloud.

Visit [thermofisher.com/cloud](http://thermofisher.com/cloud) for the latest available secondary analysis applications.

**Note:** Data from the SeqStudio™ Genetic Analyzer may be labeled as "3200" in secondary analysis software.

### Thermo Fisher Cloud secondary analysis apps

<table>
<thead>
<tr>
<th>Analysis</th>
<th>App</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sequencing</td>
<td>Quality Check (QC) module</td>
<td>• Automatically checks sequence trace quality.</td>
</tr>
<tr>
<td></td>
<td></td>
<td>• Provides a results summary that is based on quality parameter settings.</td>
</tr>
<tr>
<td></td>
<td></td>
<td>• Auto-flags lower-quality traces for further inspection.</td>
</tr>
<tr>
<td>Variant Analysis (VA) module</td>
<td><img src="image" alt="VA" /></td>
<td>• Finds variants in samples that are sequenced on Applied Biosystems™ genetic analyzers.</td>
</tr>
<tr>
<td></td>
<td></td>
<td>• Reports variants at genomic coordinates.</td>
</tr>
<tr>
<td></td>
<td></td>
<td>• Allows export of variant calls in standard Variant Call Format.</td>
</tr>
<tr>
<td>Next-generation Confirmation (NGC) module</td>
<td><img src="image" alt="NGC" /></td>
<td>• Confirms next-generation sequencing (NGS) variants using CE technology.</td>
</tr>
<tr>
<td></td>
<td></td>
<td>• Allows visualization of the variants that are detected by both NGS and CE platforms.</td>
</tr>
<tr>
<td></td>
<td></td>
<td>• Allows export of confirmed variants in standard Variant Call Format.</td>
</tr>
<tr>
<td>Fragment analysis</td>
<td>Sizing Analysis Module Peak Scanner™ Software</td>
<td><img src="image" alt="PS" /></td>
</tr>
<tr>
<td></td>
<td></td>
<td>Performs peak sizing.</td>
</tr>
</tbody>
</table>
Desktop secondary analysis software

**IMPORTANT!** Older versions of the desktop secondary analysis software cannot analyze data files generated by the SeqStudio™ Genetic Analyzer. Contact Support for information on obtaining the latest versions of software.

<table>
<thead>
<tr>
<th>Analysis</th>
<th>Software</th>
<th>Minimum version required</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sequencing</td>
<td>Sequencing Analysis Software</td>
<td>6.2</td>
</tr>
<tr>
<td></td>
<td>SeqScape™ Software</td>
<td>3.2</td>
</tr>
<tr>
<td></td>
<td>Variant Reporter™ Software</td>
<td>2.2</td>
</tr>
<tr>
<td></td>
<td>Minor Variant Finder Software</td>
<td>1.2</td>
</tr>
<tr>
<td>Fragment analysis</td>
<td>GeneMapper™ Software</td>
<td>5.1</td>
</tr>
</tbody>
</table>
Workflow: Cloud or desktop

**Get started**
- Prepare the instrument (page 38)
- Prepare the samples (page 36)

**Create a plate setup on the Cloud or desktop**
- Access the Plate Manager on the Cloud (page 55)
- Access the Plate Manager on the desktop (page 55)
- Create or open a plate setup PSM file (page 55)
- Enter plate properties (page 55)
- Assign wells: Sample and run information (page 57)

**Start and monitor a run**
- *On the instrument:* Load the plate or the tube assembly (page 76)
- Select a plate setup and start a run (page 77)
- Monitor a run from the Thermo Fisher Cloud (page 79)
- Monitor a run from a mobile device (page 87)
- Monitor a run from the instrument (page 89)

**View and analyze results**
- View results in the Remote Monitoring App on the Cloud (page 83)
- View results on the instrument (page 95)
- Export results from the instrument (sample data files and QC reports) (page 104)
- Analyze data in a secondary analysis software application
# Workflow: instrument

## Get started
- Prepare the instrument  
  (page 38)
- Prepare the samples  
  (page 36)

## Create a plate setup on the instrument
- Create or import a plate setup  
  (page 66)
- Enter plate properties  
  (page 67)
- Assign wells: run module, size standard, and dye set  
  (page 68)
- Assign wells: sample name, sample type, and custom fields  
  (page 70)

## Start and monitor a run
- *On the instrument:* Load the plate or the tube assembly  
  (page 76)
- Select a plate setup and start a run  
  (page 77)
- Monitor a run from the instrument  
  (page 89)

## View and analyze results
- View results on the instrument  
  (page 95)
- Export results from the instrument (sample data files and QC reports)  
  (page 104)
- Analyze data in a secondary analysis software application
Prepare the samples and the instrument

- Precautions for use ................................................... 32
- Power on the instrument .............................................. 33
- Sign in .............................................................. 33
- Sign in with the Guest instrument profile ....................... 34
- Sign out ............................................................. 34
- Parts of the home screen ............................................... 35
- Prepare the samples .................................................. 36
- Prepare the instrument ................................................ 38

Precautions for use

⚠ CAUTION! PHYSICAL INJURY HAZARD. Do not remove the instrument cover. There are no components inside the instrument that you can safely service yourself. If you suspect a problem, contact technical support.

⚠ CAUTION! Moving parts.

⚠ CAUTION! FIRE HAZARD. For continued protection against the risk of fire, replace fuses only with listed and certified fuses of the same type and rating as those currently in the instrument.

⚠ CAUTION! Hot surface.

⚠ CAUTION! Piercing hazard.

⚠ CAUTION! Potential biohazard.

⚠ CAUTION! Risk of electrical shock.
Power on the instrument

**IMPORTANT!** Do not power on the instrument until it has been installed and set up by a Thermo Scientific™ representative.

Press the On/Off switch on the rear panel.

**IMPORTANT!** The instrument does not maintain the correct temperature conditions for the cartridge when it is powered off. Avoid cartridge exposure to ambient temperature.

1. **On/Off switch**

Sign in

1. If the another user is signed in, touch ☐️ in the home screen, then touch **Sign out**.

2. In the **Sign in** screen, touch **Sign In**, then select your instrument profile and enter your PIN.

**Note:** If the instrument is left unattended for 120 minutes, the instrument profile is signed out.
Sign in with the Guest instrument profile

In the home screen:

1. In the **Sign In** screen, touch **Sign In**.
2. Touch **Guest**.

Sign out

In the home screen:

1. Touch 🔄.
2. Touch **Sign out**.
   
   **Note:** If a run is in progress, **Lock the instrument** is displayed instead of **Sign out**.
3. Touch **Yes** to confirm.
Parts of the home screen

1. Eject icon
2. Help
3. Instrument name
4. Status dial—Touch to create a plate setup.
5. Settings—Touch to view previous results (Run History) or configure the instrument.
6. Status of consumables—See “Check the consumables status” on page 38.
7. Current user
8. Connectivity icons

<table>
<thead>
<tr>
<th>Connectivity icon</th>
<th>Status</th>
</tr>
</thead>
<tbody>
<tr>
<td>🔄 or 📱</td>
<td>The instrument is connected to a wired or wireless network.</td>
</tr>
<tr>
<td>📠</td>
<td>The instrument is connected to network drive.</td>
</tr>
<tr>
<td>🌐</td>
<td>The current instrument profile is linked to Cloud.</td>
</tr>
</tbody>
</table>
## Prepare the samples

### Sample preparation guidelines

<table>
<thead>
<tr>
<th>Item</th>
<th>Guidelines</th>
</tr>
</thead>
</table>
| Plates and tubes            | • Use MicroAmp™ Optical 96-Well Reaction Plate or MicroAmp™ Reaction Tubes with a tray and retainer set.  
  **IMPORTANT!** Fast plates are not compatible with the SeqStudio™ Genetic Analyzer. Fast plates will damage the cartridge.  
  • Use the appropriate septa for plates and tubes.  
  • See “Required materials not supplied” on page 198 for more information. |
| **Fragment analysis sample** | **preparation**                                                                                                                                                   |
|                            | • Prepare the samples as recommended by the kit for fragment analysis.  
  • Use a 10–20 µL sample volume.  
  • Ensure that Hi-Di™ Formamide is fresh.  
    - Hi-Di™ Formamide should not undergo more than two freeze-thaw cycles (one to aliquot and one for use).  
    - Use the same day after thawing.  
  • For more information, see *DNA Fragment Analysis by Capillary Electrophoresis User Guide* (Pub. No. 4474504). |
| **Sequence analysis sample** | **preparation**                                                                                                                                                   |
|                            | • Prepare sequencing reactions according to kit instructions, and purify the extension products with ethanol precipitation, spin columns, or the BigDye XTerminator™ Purification Kit.  
  - If ethanol precipitation or spin columns are used, dry the samples in a vacuum centrifuge without heat or at low heat for 10–15 minutes or until dry.  
  **Note:** Do not over dry the samples.  
  - Resuspend in 10–20 µL of Hi-Di™ Formamide.  
  • Use a 65 µL or 130 µL sample volume for samples that are prepared with the BigDye XTerminator™ Purification Kit. See *BigDye XTerminator™ Purification Kit Protocol* (Pub. No. 4374408).  
  **IMPORTANT!** Use the appropriate run modules for samples prepared with BigDye XTerminator™ Purification Kit. See “Run modules, read lengths, size ranges, and run times” on page 123.  
  • Use a 10–20 µL sample volume for samples that are prepared with Hi-Di™ Formamide.  
  • Ensure that Hi-Di™ Formamide is fresh.  
    - Hi-Di™ Formamide should not undergo more than two freeze-thaw cycles (one to aliquot and one for use).  
    - Use the same day after thawing.  
  • Do not resuspend samples in water, which can decrease sample stability.  
  • For more information, see *DNA Sequencing by Capillary Electrophoresis Chemistry Guide Second Edition* (Pub. No. 4305080). |
Plate layout and loading guidelines

- Samples are stable for 16–24 hours on the instrument.
- Load a maximum of 48 samples per plate if you use a long run module (Long Seq, Long Seq BDX, and Long Frag Analysis). The long fragment analysis run modules can take >24 hours to run an entire 96-well plate.
- Add samples to plates in columns. The default injection order is: A1–D1, E1–H1, A2–D2, E2–H2....A12–D12, E12–H12.

1. Injection group 1, wells A1–D1
2. Injection group 2, wells E1–H1
3. Injection group 3, wells A2–D2
4. Injection group 4, wells E2–H2

Prepare the plate

On a clean and level surface:

1. Pipet the sample into the plate.
2. Place a septum onto the plate.
   a. Align the holes of the septa with the wells.
   b. Press gently until the septum is inserted into position in each well.
3. Centrifuge the plate assembly briefly to collect the contents at the bottom of each well.
   Centrifuge the plate assembly again if the contents are not at the bottom of the wells.

Load the plate onto the instrument immediately or keep the plate on ice and protected from light until it is loaded onto the instrument.

Prepare the tubes

On a clean and level surface:

1. Place the tubes in the MicroAmp™ 96-well tray, then place the tray retainer over the tubes.
2. Pipet the sample into the tubes.
3. Place a septum on the tubes.
   a. Align the holes of the septa with the tubes.
   b. Press gently until the septum are inserted into position in each tube.

4. Centrifuge the tube assembly briefly to collect the contents at the bottom of each tube.
   Centrifuge the tube assembly again if the contents are not at the bottom of the tubes.

Load the tube assembly onto the instrument immediately or keep the tubes on ice and protected from light until they are loaded onto the instrument.

Prepare the instrument

Check the consumables status

1. Touch Settings > Consumable status.

2. Ensure that:
   • Sufficient consumables are installed for the run.
   • Installed consumables have not exceeded their expiry date.

<table>
<thead>
<tr>
<th>Display</th>
<th>Cartridge</th>
<th>Cathode buffer</th>
</tr>
</thead>
<tbody>
<tr>
<td>NA</td>
<td>Not installed on the instrument.</td>
<td>Not installed on the instrument.</td>
</tr>
<tr>
<td>White</td>
<td>OK for use.</td>
<td>OK for use.</td>
</tr>
</tbody>
</table>
## Display

<table>
<thead>
<tr>
<th>Cartridge</th>
<th>Cathode buffer</th>
</tr>
</thead>
<tbody>
<tr>
<td>Yellow</td>
<td>OK for use, but:</td>
</tr>
<tr>
<td></td>
<td>• It will exceed the manufacturer’s expiry date within 2 weeks or</td>
</tr>
<tr>
<td></td>
<td>• It will exceed the maximum number of days allowed on the instrument within</td>
</tr>
<tr>
<td></td>
<td>2 weeks(^1)</td>
</tr>
<tr>
<td>Red</td>
<td>Expired because either of the following conditions have occurred:</td>
</tr>
<tr>
<td></td>
<td>• It has exceeded the manufacturer’s expiry date or</td>
</tr>
<tr>
<td></td>
<td>• It has exceeded the maximum number of days allowed on the instrument(^1)</td>
</tr>
</tbody>
</table>

\(^1\) The maximum number of days allowed on the instrument is 120 days for the SeqStudio™ Genetic Analyzer Cartridge (Cat. No. A33671) and 180 days for the SeqStudio™ Genetic Analyzer Cartridge v2 (Cat. No. A41331). For more information, see “Cartridge storage” on page 17.

See “Insert the Cathode Buffer Container” on page 150 if a new Cathode Buffer Container is required.
See “Insert the cartridge” on page 144 if a new cartridge is required.

3. Touch Close, then touch ☐.

### Load the CBC, the sample plate, and the cartridge

The Eject plate command is disabled for a few minutes after you insert a cartridge. If you are loading the CBC, sample plate, and cartridge at the same time, you can save time by loading the CBC and sample plate before you insert the cartridge.

For information on loading the individual components, see:
• “Install cathode buffer” on page 149
• “Load the plate or the tube assembly” on page 76
• “Insert the cartridge” on page 144

In the home screen:
1. Touch ⬅️, touch ➡️ Eject plate, then open the instrument door when prompted.

2. Press the release button on the autosampler to open the lid, then remove the CBC.

3. Check the buffer fill level:
   a. Remove the CBC.
   b. Ensure that the level of buffer is above the fill line.
      If the buffer is at or below the fill line, see “Assemble the SeqStudio™ Genetic Analyzer Cathode Buffer Container (CBC)” on page 149 and “Insert the Cathode Buffer Container” on page 150.
      If the buffer is above the fill line, reinsert the CBC.

4. Place the plate or tube assembly firmly in the autosampler.

5. Close the autosampler lid: Press down on the center of the lid or press down on both sides of the lid with equal pressure until the lid clicks shut.

6. Touch Retract plate, then close the instrument door.
7. Touch Eject cartridge, then open the instrument door when prompted.

8. Hold the cartridge at the hand hold above the capillaries, then pull to remove it from the instrument.

9. Insert a new cartridge (see “Insert the cartridge” on page 144).

10. Close the instrument door.
Use the instrument with the Thermo Fisher Cloud

- Understanding instrument and Cloud interaction .................................. 42
- Thermo Fisher Connect administrators for an instrument .................... 47
- Register and obtain a Thermo Fisher Connect account ....................... 49
- Link the instrument to your Thermo Fisher Cloud account ................. 50
- Change your own Cloud instrument profile PIN ............................. 51
- Set up email notifications from the instrument ............................... 51

Understanding instrument and Cloud interaction

"Connect" versus "link"

The words "connect" and "link" are used interchangeably in the software.

In one location you touch a Connect button, in another location you touch a Link button.

Both actions do the same thing:

- Connect the instrument to the InstrumentConnect on the Thermo Fisher Cloud and
- Link your local instrument profile to your Thermo Fisher Cloud account.

First user who links is assigned administrator role

The first user who links the instrument to the Thermo Fisher Cloud is automatically assigned Cloud administrator role for the instrument (even if the user has a standard local profile).

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

For more information, see “Cloud instrument profile roles and functions” on page 46 and “Thermo Fisher Connect administrators for an instrument” on page 47.
Local versus Cloud instrument profiles

• Local instrument profile—All plates and results are stored on the instrument under a local instrument profile.
• Cloud instrument profile—When you link your local instrument profile to your Cloud account, a Cloud instrument profile is created. With a Cloud instrument profile:
  – You can save results and data files directly to your Cloud account, access plate setups that you create in the SeqStudio™ Plate Manager on the Cloud or desktop, and monitor instrument runs from the Cloud.
  – All plate setups, data files, and results are automatically copied to your Cloud account if the plate setup Save location is set to Cloud.

In this scenario, your local instrument profile name is created manually on the instrument before you link. Your local instrument profile name differs from your Cloud instrument profile name.

If you link when you are signed in to the instrument

In this scenario, your local instrument profile name is created manually on the instrument before you link. Your local instrument profile name differs from your Cloud instrument profile name.

If you link to the Cloud when you are signed in to the instrument:

<table>
<thead>
<tr>
<th>Phase</th>
<th>Steps that occur</th>
</tr>
</thead>
<tbody>
<tr>
<td>Before you link:</td>
<td>• You enter your local instrument profile name in the Sign In screen.</td>
</tr>
<tr>
<td></td>
<td><img src="image" alt="Sign In screen" /></td>
</tr>
<tr>
<td></td>
<td>• Your local instrument profile {UserABC} is displayed in the home screen of the</td>
</tr>
<tr>
<td></td>
<td>instrument.</td>
</tr>
<tr>
<td></td>
<td>• All plates and results that you create are accessible only when you are signed</td>
</tr>
<tr>
<td></td>
<td>in with your local instrument profile.</td>
</tr>
<tr>
<td>When you link:</td>
<td>• You use an option described in &quot;Link the instrument to your Thermo Fisher Cloud</td>
</tr>
<tr>
<td></td>
<td>account&quot; on page 50 to link.</td>
</tr>
<tr>
<td></td>
<td>• If this is the first time you link, a Cloud instrument profile is created using</td>
</tr>
<tr>
<td></td>
<td>the FirstNameLastInitial of the user name from your thermofisher.com account.</td>
</tr>
<tr>
<td></td>
<td>Example: <a href="mailto:User1@thermofisher.com">User1@thermofisher.com</a> First name is User, Last name is Gray. Cloud</td>
</tr>
<tr>
<td></td>
<td>account username is User G.</td>
</tr>
<tr>
<td></td>
<td>• Your local instrument profile {UserABC} is linked to your Cloud account</td>
</tr>
<tr>
<td></td>
<td>(<a href="mailto:User1@thermofisher.com">User1@thermofisher.com</a>).</td>
</tr>
<tr>
<td></td>
<td>• Your Cloud instrument profile {User G.} replaces your local instrument profile.</td>
</tr>
</tbody>
</table>
### Chapter 3 Use the instrument with the Thermo Fisher Cloud

#### Understanding instrument and Cloud interaction

<table>
<thead>
<tr>
<th>Phase</th>
<th>Steps that occur</th>
</tr>
</thead>
</table>
| **After you link:**                           | • Your Cloud instrument profile (User G.) is displayed in the home screen of the instrument.  
• Plates and results from your local instrument profile can be copied to the Cloud (see “Export results from the instrument (sample data files and QC reports)” on page 104).  
• New plates and results are saved under your Cloud instrument profile.  
• Your Cloud instrument profile name (User G. ◄) is available for selection in the Sign In screen. |
| **If your Cloud account is unlinked:**       | • Your local instrument profile (UserABC) is displayed in the home screen of the instrument.  
• Plates and results that were saved under your Cloud instrument profile are accessible under your local instrument profile.  
• New plates and results are saved under local instrument profile and can be copied to the Cloud (see “Export results from the instrument (sample data files and QC reports)” on page 104).  
• Your local instrument profile name (UserABC) is available for selection in the Sign In screen. |

**If you link when you are not signed in to the instrument**

In this scenario, your local instrument profile name is created automatically on the instrument before you link. The same user name is used for your local instrument profile and your Cloud instrument profile. Plates and results are accessible when you sign in with either profile.

If you link to the Cloud when you are not signed in to the instrument:

<table>
<thead>
<tr>
<th>Phase</th>
<th>Steps that occur</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Before you link:</strong></td>
<td>• In the Sign In screen, you touch Get Started ▶ Connect.</td>
</tr>
</tbody>
</table>
### Phase | Steps that occur
--- | ---
**When you link:** | • You use an option described in “Link the instrument to your Thermo Fisher Cloud account” on page 50 to link.  
• If this is the first time you link, a Cloud instrument and a local instrument profile (with standard role) are created with the same name using the FirstNameLastInitial of the user name from your thermofisher.com account. Example: User1@thermofisher.com First name is User, Last name is Gray. Cloud account username is User G.  
• Your local instrument profile (User G.) is linked to your Cloud account (User1@thermofisher.com).  
• Your Cloud instrument profile (User G.) replaces your local instrument profile.  
**After you link:** | • Your Cloud instrument profile (User G.) and ☀️ is displayed in the home screen of the instrument.  
• Plates and results from your local instrument profile can be copied to the Cloud (see “Export results from the instrument (sample data files and QC reports)” on page 104).  
• New plates and results are saved under your Cloud instrument profile.  
• Your Cloud instrument profile name (User G. ☀️) is available for selection in the Sign In screen.  
**If your Cloud account is unlinked:** | • Your local instrument profile (User G.) is displayed in the home screen of the instrument.  
• Plates and results that were saved under your Cloud instrument profile are accessible under your local instrument profile.  
• New plates and results are saved under local instrument profile and can be copied to the Cloud (see “Export results from the instrument (sample data files and QC reports)” on page 104).  
• Your local instrument profile name (User G.) is available for selection in the Sign In screen.

**IMPORTANT!** If you sign in with a local profile, without linking to the cloud, sign out, then link using Get Started » Connect, you can potentially have two local instrument profiles with different names. Plates are results created when you are signed in with one local instrument profile are not accessible when you are signed in with the other local instrument profile.
### Cloud instrument profile roles and functions

<table>
<thead>
<tr>
<th>Instrument profile</th>
<th>Location</th>
<th>Functions allowed</th>
</tr>
</thead>
</table>
| Standard           | Cloud[1] | • Create, save, open, import, and run plate setups  
|                    |          | • Create and modify run settings  
|                    |          | • View and export results |
| Administrator      | Cloud[1] | All the permissions of a local administrator profile, plus the following functions performed in InstrumentConnect:  
|                    |          | • Access the Manage users function on the Cloud to see a list of all instrument profiles that are linked to the instrument.  
|                    |          | • Assign Cloud administrator role to one or more users.  
|                    |          | • Remove a user from an instrument.  
|                    |          | • Disconnect the instrument from InstrumentConnect.  
|                    |          | • Change the instrument name. |

[1] The first user who links their local instrument profile to their Cloud account is assigned a Cloud profile with administrator role.

For more information on using the Thermo Fisher Cloud

In the top left of the screen you are viewing in the Thermo Fisher Cloud, click ☰, then select Help guide.
Thermo Fisher Connect administrators for an instrument

**Cloud administrator functions**

The first user who links the instrument to the Thermo Fisher Cloud is automatically assigned Cloud administrator role for the instrument (even if the user has a standard local profile).

At least one Cloud administrator is required for each instrument.

A Cloud administrator can perform the following tasks from the InstrumentConnect:

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

**Assign instrument administrator role to other users**

A Cloud administrator for an instrument can assign instrument administrator role to other users.

2. Click 🌐 to access InstrumentConnect.
3. Select the instrument.

![Manage users](image)

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

4. To assign the Admin role to a user, click 📋 **Manage users**, then select the Administrator check box for the user.
Any user with a Cloud administrator profile can manage users for an instrument or disconnect an instrument from InstrumentConnect.

<table>
<thead>
<tr>
<th>If a Cloud administrator...</th>
<th>The software...</th>
</tr>
</thead>
<tbody>
<tr>
<td>Assigns Admin role to a user</td>
<td>Allows the user to perform all Cloud administrator functions (see “Cloud administrator functions” on page 47).</td>
</tr>
<tr>
<td>Removes a user</td>
<td>Unlinks the instrument from their Thermo Fisher Cloud account.</td>
</tr>
<tr>
<td>Disconnects the instrument</td>
<td>• Unlinks the instrument from all user Thermo Fisher Cloud accounts.</td>
</tr>
<tr>
<td></td>
<td>• Removes the instrument from InstrumentConnect.</td>
</tr>
</tbody>
</table>

1. Sign in to thermofisher.com/cloud.

2. Click to access InstrumentConnect.

3. Select the instrument.

4. To assign the Admin role to a user or to remove a user, click Manage users, then:

<table>
<thead>
<tr>
<th>To...</th>
<th>Do this...</th>
</tr>
</thead>
<tbody>
<tr>
<td>Assign the Admin role to an additional user</td>
<td>Select the Admin checkbox, then click Close.</td>
</tr>
<tr>
<td>Remove a user</td>
<td>Click , then click Confirm.</td>
</tr>
</tbody>
</table>

Note: The Manage users and other administrator functions are not displayed until you select an instrument.
You cannot disconnect individual users from an instrument.

To disconnect a user, or to unlink the instrument from a Cloud account, you must disconnect the instrument from InstrumentConnect. Doing so unlinks all instrument profiles and removes the instrument from InstrumentConnect.

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

For more information, see “Manage the users and administrators of your instrument” on page 48.

Register and obtain a Thermo Fisher Connect account

2. On the home page, select Sign In ▶ Register.
3. Fill in all information, then click Create account.
Link the instrument to your Thermo Fisher Cloud account

Note: For detailed information on linking the instrument to your Cloud account, see Appendix B, “Link the instrument to your Cloud account—detailed instructions”.

1. If a user is signed in, touch .userName, then touch Sign out.

2. In the Sign In screen, touch Get started ▶ Connect.

3. In the Connect to the Thermo Fisher Cloud screen, touch a connection option.
<table>
<thead>
<tr>
<th>Option</th>
<th>Action</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mobile devices</td>
<td><strong>Note:</strong> Before selecting this option, install and sign in to the InstrumentConnect app on your mobile device.</td>
</tr>
<tr>
<td></td>
<td>In the Connect to the Thermo Fisher Cloud screen:</td>
</tr>
<tr>
<td></td>
<td>1. Touch Mobile devices.</td>
</tr>
<tr>
<td></td>
<td>2. Hold the camera on your mobile device over the QR code that is displayed on the touchscreen.</td>
</tr>
<tr>
<td></td>
<td>3. Click Close.</td>
</tr>
<tr>
<td>PC</td>
<td>In the Connect to the Thermo Fisher Cloud screen, a link code is displayed.</td>
</tr>
<tr>
<td></td>
<td>On a computer:</td>
</tr>
<tr>
<td></td>
<td>1. Access the Thermo Fisher Cloud.</td>
</tr>
<tr>
<td></td>
<td>3. Click Add instrument.</td>
</tr>
<tr>
<td></td>
<td>4. Select SeqStudio.</td>
</tr>
<tr>
<td></td>
<td>5. Enter the link code.</td>
</tr>
<tr>
<td>Instrument</td>
<td>In the Connect to the Thermo Fisher Cloud screen, enter your account information, then click Link account.</td>
</tr>
</tbody>
</table>

### Change your own Cloud instrument profile PIN

1. Sign in to thermofisher.com/cloud.
2. Click 📱 to access InstrumentConnect.
3. Click Update PIN number.

### Set up email notifications from the instrument

When an instrument is linked to your Cloud account, email notifications are automatically sent to your Cloud account email address.

Perform this procedure to disable any of the default notifications.
1. Sign in to the instrument with your Cloud instrument profile and PIN.

2. In the home screen of the instrument, touch **Settings** ➔ **Instrument settings** ➔ **Email notifications**.

   ![Instrument Settings](image1)

   **Note:** If you are signed in with a local instrument profile instead of a Cloud instrument profile, the **Email notifications** button is not displayed on the **Instrument Settings** screen.

3. In the **Email notifications** screen, select or deselect the options for which you want to receive email notifications, then touch **Done**.

   ![Email Notifications](image2)
Create or modify a plate setup from the Plate Manager

- Overview of plate setup settings ........................................ 53
- Set up a plate using default settings (Plate Manager) ............. 55
- Additional plate settings (Plate Manager) .......................... 59

### Overview of plate setup settings

<table>
<thead>
<tr>
<th>Category</th>
<th>Setting</th>
<th>Notes</th>
</tr>
</thead>
</table>
| Plate      | • Plate properties<br>• Plate setup security (Shared or Hidden)<br>• File name convention<br>• Analysis settings | Analysis settings that are saved with the plate setup:<br>  
  • Hidden plates—No analysis settings are saved with the plate setup. The last-used analysis settings for a user are applied to a plate setup when it is opened.<br>  
  • Shared plates—The analysis settings specified for a plate setup when it is created are saved with the plate setup.  
  User-created analysis settings:<br>  
  • Users can name and save analysis settings.<br>  
  • In the instrument software and in the Plate Manager (Cloud), user-created analysis settings are accessible only to the user who saves them.<br>  
  • In the Plate Manager (desktop), user-created analysis settings are accessible to all users. |
<table>
<thead>
<tr>
<th>Category</th>
<th>Setting</th>
<th>Notes</th>
</tr>
</thead>
<tbody>
<tr>
<td>Injection group [a set of 4 wells]</td>
<td>• <em>(Fragment analysis only)</em> Size standard</td>
<td>User-created size standards and dye sets are accessible to all users.</td>
</tr>
<tr>
<td></td>
<td>• Run module</td>
<td>User-created run modules:</td>
</tr>
<tr>
<td></td>
<td>• Application type [mixed plate only]</td>
<td>• Users can name and save run modules.</td>
</tr>
<tr>
<td></td>
<td>• Dye set</td>
<td>• In the instrument software and in the Plate Manager [Cloud], user-created run modules are accessible only to the user who saves them.</td>
</tr>
<tr>
<td></td>
<td></td>
<td>• In the Plate Manager [desktop], user-created run modules are accessible to all users.</td>
</tr>
<tr>
<td>Well</td>
<td>• Sample name</td>
<td><strong>Specimen</strong> and <strong>Amplicon</strong> fields are useful in secondary analysis software applications that organize sample data files based on amplicon and specimen information.</td>
</tr>
<tr>
<td></td>
<td>• <em>(Fragment analysis only)</em> Sample type</td>
<td>• Custom fields are text fields in which you can include additional sample attributes or identifiers. Custom fields can be used by some secondary analysis applications.</td>
</tr>
<tr>
<td></td>
<td>• <em>(Sequencing only)</em> Specimen and amplicon</td>
<td><strong>Specimen</strong> and <strong>Amplicon</strong> fields are useful in secondary analysis software applications that organize sample data files based on amplicon and specimen information.</td>
</tr>
<tr>
<td></td>
<td>• Custom fields 1–5</td>
<td><strong>Specimen</strong> and <strong>Amplicon</strong> fields are useful in secondary analysis software applications that organize sample data files based on amplicon and specimen information.</td>
</tr>
</tbody>
</table>

Chapter 4 Create or modify a plate setup from the Plate Manager
Overview of plate setup settings

*SeqStudio™ Genetic Analyzer Instrument and Software User Guide*
Set up a plate using default settings (Plate Manager)

Access the Plate Manager on the Cloud

1. Sign in to thermofisher.com/cloud.
2. In the My Apps list, select SeqStudio™ Plate Manager.
   If SeqStudio™ Plate Manager is not listed under My Apps, scroll down in the All Apps list.

Access the Plate Manager on the desktop

Select Start ▶ All Programs ▶ Applied Biosystems ▶ Plate Manager ▶ Plate Manager.

Create or open a plate setup PSM file

1. Click to display the home screen.
2. In the Plate setup screen, create or open a plate setup:
   If you are running the Plate Manager on the Thermo Fisher Cloud:

<table>
<thead>
<tr>
<th>Click...</th>
<th>To...</th>
</tr>
</thead>
<tbody>
<tr>
<td>New</td>
<td>Create a new plate setup or to create a plate setup from a template.</td>
</tr>
<tr>
<td>Open from cloud</td>
<td>Open a plate setup that you created in Plate Manager on the Thermo Fisher Cloud.</td>
</tr>
<tr>
<td>Open from local drive</td>
<td>Open a plate setup that you created in Plate Manager on your computer (PSM file) or in another application (CSV file).</td>
</tr>
</tbody>
</table>

   If you are running the Plate Manager on the desktop:

<table>
<thead>
<tr>
<th>Click...</th>
<th>To...</th>
</tr>
</thead>
<tbody>
<tr>
<td>New</td>
<td>Create a new plate setup or to create a plate setup from a template.</td>
</tr>
<tr>
<td>Open</td>
<td>Open a plate setup that you created in Plate Manager (PSM file) or in another application (CSV file).</td>
</tr>
</tbody>
</table>

Enter plate properties

In the Properties tab:
1. (Optional) Edit the Plate name, Barcode, or Owner.

![Plate Properties](image)

2. Select an option in the Plate setup security field.
   - **Hidden**—Prevents other users from using or accessing the plate on the instrument. The last settings specified by the signed-in user are applied when a Hidden plate setup is opened or imported on the instrument.
   - **Shared**—Allows other users to access and edit the plate on the instrument. Analysis settings saved in the plate setup.

3. Select the Application type: Sequencing, Fragment analysis, or Mixed plate (sequencing & fragment).
   A mixed plate allows you to specify fragment analysis and sequence analysis settings on the same plate.

4. (Optional for Sequencing or Mixed plate)
   Select the I am analyzing my data with Sanger variant analysis software checkbox.
   The amplicon and specimen fields are added to the Plate view, and the attributes are automatically added to the default file name conventions (see “Modify the default file name convention” on page 72).
   This feature is useful in secondary analysis software applications that organize files based on amplicon and specimen information (Cloud applications: Variant Analysis (VA) module, Next-generation Confirmation (NGC) module; desktop...

5. Click Next.

In the Plate screen:

1. Click a well to select an injection group, or Shift-click to select multiple injection groups.
   Each set of 4 wells on the plate is referred to as an injection group.
   The default injection order is: A1-D1, E1-H1, A2-D2, E2-H2....A12-D12, E12-H12.

2. If you are creating a mixed plate, select the Application type for the injection group.

3. (Fragment analysis only) Select the sample type for each well: Allelic ladder, Negative control, Positive control, or Sample.

4. (Fragment analysis only) Select a size standard for the injection group.

5. Select a dye set for the injection group.
6. Select a run module for the injection group.
   For more information, see “Run modules, read lengths, size ranges, and run times” on page 123

7. Click Next and proceed to “Save a plate setup in the Plate Manager” on page 58.

After you assign wells to a plate setup:

1. In the **Save the plate setup** dialog box, modify any settings as needed.

2. Click **Save**.
Note: The **Monitor my run button** is available only in the Cloud app.

<table>
<thead>
<tr>
<th>If you are running the Plate Manager on the...</th>
<th>The plate setup is saved as a...</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cloud</td>
<td>Plate setup that you can open from the Cloud and run on the instrument.</td>
</tr>
<tr>
<td>Desktop</td>
<td>PSM file that you can open from a network drive or a USB and run on the instrument.</td>
</tr>
</tbody>
</table>

Proceed to Chapter 6, “Start and monitor a run”.

## Additional plate settings (Plate Manager)

### Specify replicate injections

In the **Plate** screen:

1. Select **Actions ▶ Add injection**.
2. Select an injection group, then select a run module for the replicate injections.

Factory-installed items cannot be edited or deleted. To create a new item from a factory-installed item, copy, edit, then save the new item.

### Edit analysis settings

In the **Plate properties** screen:

1. Click **Setting details**.
2. To create new analysis settings:
   
   a. Select the default analysis settings or user-created analysis settings, then click **Copy**.

   b. Enter a name and edit settings as needed (see “Fragment analysis settings (size calling)” on page 109 or “Sequencing settings (base calling)” on page 112).

   c. As needed, click **Edit** or **Delete** (user-created settings only).

For more information, see “Manage analysis settings” on page 125.

3. Click **Close**.
The file name convention determines how the data files (AB1 or FSA) associated with a plate are named.

The default file name convention is:

<table>
<thead>
<tr>
<th>Application</th>
<th>Default settings</th>
</tr>
</thead>
<tbody>
<tr>
<td>Fragment analysis</td>
<td><code>&lt;well&gt;_&lt;sample name&gt;_&lt;sample type&gt;_&lt;date and timestamp&gt;.fsa</code></td>
</tr>
<tr>
<td>Sequence analysis</td>
<td><code>&lt;well&gt;_&lt;sample name&gt;_&lt;date and timestamp&gt;.ab1</code></td>
</tr>
<tr>
<td>Sequence analysis with the Sanger variant analysis option selected</td>
<td><code>&lt;well&gt;_&lt;sample name&gt;_&lt;amplicon&gt;_&lt;specimen&gt;_&lt;date and timestamp&gt;.ab1</code></td>
</tr>
</tbody>
</table>

To change the default settings, in the Properties tab:

1. Select Actions » Edit the file name convention.
2. Click File attributes, then select the attributes to include in or exclude from the data file name.
3. (Optional) Click-drag to move an attribute to another position.
4. Click Save.

In the Properties screen:

- **Hidden**—Prevents other users from using or accessing the plate on the instrument. The last settings specified by the signed-in user are applied when a Hidden plate setup is opened or imported on the instrument.
- **Shared**—Allows other users to access and edit the plate on the instrument. Analysis settings saved in the plate setup.

Custom fields are text fields in which you can include additional sample attributes or identifiers. Custom fields can be used by some secondary analysis applications.

In the Plate tab:
1. Select **Action ▶ Add custom field**.

2. Enter information in the custom field in the table at the right of the plate.
Create or modify a plate setup from the instrument

- PSM and CSV plate setup files for import into the instrument ............... 63
- Shared (public), hidden (my plates), and guest plate setup files ........... 64
- Overview of plate setup settings ........................................ 65
- (Optional) Set up for auto export of sample data files (AB1 and FSA) .... 66
- Set up a plate using default settings (instrument) .......................... 66
- Set optional plate settings (instrument) .................................... 71
PSM and CSV plate setup files for import into the instrument

<table>
<thead>
<tr>
<th>Format</th>
<th>Contains...</th>
<th>When to use...</th>
</tr>
</thead>
</table>
| PSM    | • Size standard names and definitions  
        • Run module names and settings  
        • Dye set names and settings  
        • Analysis settings names and settings  
        • All remaining plate setup field settings: Well ID, Sample name, Application type and so on. | To create a plate setup that contains all the properties needed to save and run the plate setup.  
Note the following:  
• If the size standard, analysis settings, or run module in the PSM file do not exist on the instrument, they are automatically created when the PSM file is imported.  
• If the Plate setup security is set to Hidden:  
  – The plate setup is available for selection on the instrument only to the user who created the PSM file. |
| CSV    | • Size standard names only  
        • Dye set name only  
        • Run module names only  
        • All remaining plate setup field settings: Well ID, Sample name, Application type and so on. | To update properties of the plate setup [such as sample name] after the size standard, dye set, and run module for the plate setup have been created or imported on the instrument.  
When you import a CSV file:  
• If the size standard, dye set, or run module in the CSV file do not exist on the instrument:  
  – An error message is displayed.  
  – The CSV file is not imported on the instrument.  
• If the size standard or run module in the CSV file do exist on the instrument:  
  – The CSV file is imported on the instrument.  
  – The settings from the size standard, dye set, and run module that exist on the instrument are used [because the CSV file contains the names of these elements, but not the settings].  
  – The Plate setup security is set to Hidden. |
## Shared (public), hidden (my plates), and guest plate setup files

<table>
<thead>
<tr>
<th>Create by setting Plate setup security to...</th>
<th>Accessible to users...</th>
<th>Stored in folder on instrument...</th>
<th>Analysis settings used...</th>
<th>File name convention used...</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Shared</strong></td>
<td>All users, including guest</td>
<td>Public</td>
<td>Analysis settings saved in the plate setup</td>
<td>Last settings specified by the signed-in user (not saved with plate setup)</td>
</tr>
</tbody>
</table>

**Note:** If a guest user edits a shared plate setup, the plate must be saved under a new name, and the Plate setup security is set to Hidden and cannot be changed.

<table>
<thead>
<tr>
<th>Hidden</th>
<th>Only the user who created the plate setup</th>
<th><strong>My plates</strong></th>
<th>Last settings specified by the signed-in user (not saved with plate setup)</th>
<th>Last settings specified by the signed-in user (not saved with plate setup)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Guest plate setup security is automatically set to Hidden and cannot be changed</td>
<td>Guest user only</td>
<td><strong>My plates</strong></td>
<td>Last settings specified by the signed-in user (not saved with plate setup)</td>
<td>Last settings specified by the signed-in user (not saved with plate setup)</td>
</tr>
</tbody>
</table>
## Overview of plate setup settings

<table>
<thead>
<tr>
<th>Category</th>
<th>Setting</th>
<th>Notes</th>
</tr>
</thead>
<tbody>
<tr>
<td>Plate</td>
<td>• Plate properties</td>
<td>Analysis settings that are saved with the plate setup:</td>
</tr>
<tr>
<td></td>
<td>• Plate set up security (Shared or Hidden)</td>
<td>• Hidden plates—No analysis settings are saved with the plate setup. The last-used analysis settings for a user are applied to a plate setup when it is opened.</td>
</tr>
<tr>
<td></td>
<td>• File name convention</td>
<td>• Shared plates—The analysis settings specified for a plate setup when it is created are saved with the plate setup.</td>
</tr>
<tr>
<td></td>
<td>• Analysis settings</td>
<td>User-created analysis settings:</td>
</tr>
<tr>
<td></td>
<td></td>
<td>• Users can name and save analysis settings.</td>
</tr>
<tr>
<td></td>
<td></td>
<td>• In the instrument software and in the Plate Manager (Cloud), user-created analysis settings are accessible only to the user who saves them.</td>
</tr>
<tr>
<td></td>
<td></td>
<td>• In the Plate Manager (desktop), user-created analysis settings are accessible to all users.</td>
</tr>
<tr>
<td></td>
<td></td>
<td>User-created size standards and dye sets are accessible to all users.</td>
</tr>
<tr>
<td></td>
<td></td>
<td>User-created run modules:</td>
</tr>
<tr>
<td></td>
<td>• (Fragment analysis only) Size standard</td>
<td>• Users can name and save run modules.</td>
</tr>
<tr>
<td>Injection group</td>
<td>• Run module</td>
<td>• In the instrument software and in the Plate Manager (Cloud), user-created run modules are accessible only to the user who saves them.</td>
</tr>
<tr>
<td>(a set of 4 wells)</td>
<td>• Application type (mixed plate only)</td>
<td>• In the Plate Manager (desktop), user-created run modules are accessible to all users.</td>
</tr>
<tr>
<td></td>
<td>• Dye set</td>
<td></td>
</tr>
<tr>
<td>Well</td>
<td>• Sample name</td>
<td>Specimen and Amplicon fields are useful in secondary analysis software applications that organize sample data files based on amplicon and specimen information.</td>
</tr>
<tr>
<td></td>
<td>• (Fragment analysis only) Sample type</td>
<td>• Custom fields are text fields in which you can include additional sample attributes or identifiers. Custom fields can be used by some secondary analysis applications.</td>
</tr>
<tr>
<td></td>
<td>• (Sequencing only) Specimen and amplicon</td>
<td></td>
</tr>
<tr>
<td></td>
<td>• Custom fields 1–5</td>
<td></td>
</tr>
</tbody>
</table>
(Optional) Set up for auto export of sample data files (AB1 and FSA)

By default, sample data files (AB1 and FSA) are saved to the instrument. When you create a plate setup, you can also set the Save location to Cloud, Network Drive, and/or USB.

When the plate is run, the instrument automatically exports the sample data files to the save locations.

Before you can select these save locations, set up the instrument:

- “Link the instrument to your Thermo Fisher Cloud account” on page 50
- “Connect to a network drive” on page 115
- Insert a USB into the USB port on the front of the instrument (Figure 1 on page 13)

Set up a plate using default settings (instrument)

Create or import a plate setup

In the home screen:

1. Touch Set up run.

2. Create, open, or import a plate setup:
To | Procedure
--- | ---
Create a new plate setup | 1. Touch **Create new plate setup**.
2. See “Enter plate properties” on page 67.
Open an existing plate setup on the instrument | 1. Touch **My Instrument**.
2. Touch:
   - **My plates** folder to select hidden plates that you have created.
   - **Public** folder to select (1) shared plates that were created by any user or (2) any plates that were created by a Guest user.

For more information, see “Shared (public), hidden (my plates), and guest plate setup files” on page 64.
Import a plate setup | 1. Touch **Cloud**, **USB**, or **Network Drive**.
2. Select:
   - **PSM** file
   - **CSV** file

For more information, see “PSM and CSV plate setup files for import into the instrument” on page 63.

**Enter plate properties**

In the **Plate properties** screen:

1. Touch the **Plate name** field, then enter the plate name.

2. Touch **Applications**, then select Sequencing, Fragment analysis, or Mixed (allows you to specify fragment analysis and sequence analysis settings on the same plate).

3. **(Optional)** Touch the **Barcode** field, then use a scanner to scan the barcode.

4. **(Optional)** Touch the **Owner** field, then enter the plate owner name.
5. (Optional) Touch the More options to check the Plate setup security, Analysis settings, and File name convention.

6. If you want to save the plate to a location in addition to the instrument, touch Save location, then select a location for the run results.
   The plate setup is always saved to the instrument. In addition, you can save the plate to the Cloud, a network, or a USB, which will auto export the sample data files.

   **IMPORTANT!** To view analyzed data in the Remote Monitoring App on the Cloud, you must save the plate setup to the Cloud.

   **Note:** If you save a plate setup to the Cloud, a network, or a USB, then access the plate setup at a later time when the instrument is not linked to the Cloud, a network, or a USB, the save location is displayed with strikethrough text.

   ![Save location](image)

   1 Original location to which the plate was saved, but is no longer accessible by the instrument.

7. (Optional for Sequencing or Mixed plate)
   Touch the I am analyzing my data with Sanger variant analysis software checkbox.
   The amplicon and specimen fields are added to the Plate view, and the attributes are automatically added to the default file name conventions (see "Modify the default file name convention“ on page 72).
   This feature is useful in secondary analysis software applications that organize files based on amplicon and specimen information (Cloud applications: Variant Analysis (VA) module, Next-generation Confirmation (NGC) module; desktop applications: SeqScape™ Software, Variant Reporter™ Software, Minor Variant Finder Software).

Assign wells: run module, size standard, and dye set

In the Plate properties screen:
1. At the top-right of the screen, touch **Plate**.
   - **Plate tab**
   - **Save button is not enabled until you create an injection group**

   Each set of 4 wells on the plate is referred to as an injection group. An injection group is identified by the first well in the set of 4 (for example, Injection Group A1 contains wells A1–D1). The default injection order is: A1-D1, E1-H1, A2-D2, E2-H2,...A12-D12, E12-H12.

2. Select injection groups, then touch **Edit**.
   - Touch a well to select a single injection group.
   - Touch and drag to select multiple injection groups or the entire plate.

3. If you are creating a mixed plate, select the **Application type** for the wells.
Chapter 5 Create or modify a plate setup from the instrument
Set up a plate using default settings (instrument)

4. Touch Run modules, then select a run module.
   For more information, see “Run modules, read lengths, size ranges, and run times” on page 123.

5. Touch Dye set, then select a dye set for the injection group.

6. (Fragment analysis only) Touch Size standard, then select a size standard for the injection group.

Assign wells:
- sample name, sample type, and custom fields

In the Edit plate screen:

1. Touch Sample name to display the well attributes fields.

2. Touch a setting, then enter the definition for the selected wells:
   - (Fragment analysis only) **Sample type**—Sample, Positive Control, Negative Control, or Allelic Ladder.
   - **Custom fields**—Text fields to include additional sample attributes or identifiers that can be used by secondary analysis applications.
   - (Sequencing only) **Amplicon and Specimen**—Amplicon and Specimen names for Sanger Sequence analysis, if you selected the option in the Plate Properties screen.
3. Touch **Done** to close the screen then **Done** to close the **Edit Plate** screen.

![Plate Properties Screen]

1. Application type—Sequencing or Fragment, designated by S or F
2. Save the plate or start the run

4. Touch **Save** to save the plate to run at a later time, or touch **Start Run**.

### Set optional plate settings (instrument)

**Specify replicate injections**

In the **Plate properties** screen:

1. Touch **Injection options**.

2. Touch an injection group, then touch **Edit and re-inject** to add replicates to the injection list.

3. *(Optional)* Modify **Run module**, **Injection time**, **Injection voltage**, **Run time**, or **Run voltage** for the injections.

**IMPORTANT!** Changes to run conditions for replicate injections are not saved to the plate.

4. Touch **Done**.

**Modify analysis settings**

In the **Properties** tab of the **Plate properties** screen:

1. Touch **More options** ➔ **Analysis settings**.

2. Select a setting.
   
   See “Manage analysis settings” on page 125 for detailed information.
Note: The last setting selected is used as the default for new plates.

3. Touch Done.

Modify the default file name convention

The default file name convention determines how the data files (AB1 or FSA) associated with a plate are named.

The default file name convention is:

<table>
<thead>
<tr>
<th>Application</th>
<th>Default settings</th>
</tr>
</thead>
<tbody>
<tr>
<td>Fragment analysis</td>
<td>&lt;well&gt;<em>&lt;sample name&gt;</em>&lt;sample type&gt;_&lt;date and timestamp&gt;.fsa</td>
</tr>
<tr>
<td>Sequence analysis</td>
<td>&lt;well&gt;<em>&lt;sample name&gt;</em>&lt;date and timestamp&gt;.ab1</td>
</tr>
<tr>
<td>Sequence analysis with the Sanger variant analysis option selected</td>
<td>&lt;well&gt;<em>&lt;sample name&gt;</em>&lt;amplicon&gt;<em>&lt;specimen&gt;</em>&lt;date and timestamp&gt;.ab1</td>
</tr>
</tbody>
</table>

1. Access the File name convention screen:

<table>
<thead>
<tr>
<th>From</th>
<th>Action</th>
</tr>
</thead>
<tbody>
<tr>
<td>Plate properties screen</td>
<td>Select the Properties tab, then touch More options ▶ File name convention.</td>
</tr>
<tr>
<td>Home screen</td>
<td>Touch ⊗ Settings ▶ Run settings ▶ File name convention.</td>
</tr>
</tbody>
</table>

2. Touch Attributes.

3. Select the attributes to include in the data file name.

For information on creating custom fields to include in file name conventions, see “Define custom fields” on page 73.

4. Touch Done.
5. Touch and drag attributes up or down in the list.

6. Touch Done.

**Hide or share a plate (Plate setup security)**

For more information, see “Shared (public), hidden (my plates), and guest plate setup files” on page 64.

1. Touch More Options ▶ Plate Setup security.

2. Touch an option:
   - **Hidden** — Prevents other users from using or accessing the plate on the instrument. The last settings specified by the signed-in user are applied when a Hidden plate setup is opened or imported on the instrument.
   - **Shared** — Allows other users to access and edit the plate on the instrument. Analysis settings saved in the plate setup.

3. Touch Done, then touch Save.

**Define custom fields**

Custom fields are text fields in which you can include additional sample attributes or identifiers. Custom fields can be used by some secondary analysis applications.

In the **Plate** tab of the **Plate properties** screen:

1. Select injection groups, then touch **Edit**.
   - Touch a well to select a single injection group.
   - Touch and drag to select multiple injection groups or the entire plate.

2. Click **Edit**.
3. Touch **Sample name** to display the injection group and well attributes fields.

4. Touch a custom field, then enter the definition for the selected wells.

5. Click **Done**.

(Optional) View the injection list, change injection settings or order, or specify replicates and re-injections

In the **Plate properties** screen:
1. Touch **Injection options**.

2. Touch an injection group, then configure the injection list:
   - Touch and drag an injection group to a new location in the injection list.
   - Touch **Inject first**—Moves the selected injection group to the top of the injection list.
   - Touch **Edit and re-inject**—Adds replicates or re-injections to the injection list. You can also modify **Run module, Injection time, Injection voltage, Run time**, or **Run voltage** for these injections.

   **Note:** Changes to **Injection time, Injection voltage, Run time, or Run voltage** are not saved to the plate setup and will be used during the current plate run only.

3. Touch **Done**.
Start and monitor a run

- Load the plate or the tube assembly .......................................................... 76
- Select a plate setup and start a run .............................................................. 77
- Lock the touchscreen ................................................................................. 79
- Monitor a run from the Thermo Fisher Cloud ............................................ 79
- Monitor a run from a mobile device .............................................................. 87
- Monitor a run from the instrument ............................................................... 89
- Unload the plate or the tube assembly ......................................................... 92

Load the plate or the tube assembly

In the home screen:

1. Touch 🔄, touch ⏎ Eject plate, then open the instrument door when prompted.
2. Press the release button on the autosampler to open the lid.
3. Place the plate or tube assembly firmly in the autosampler.
4. Check the buffer fill level:
   a. Remove the CBC.
   b. Ensure that the level of buffer is above the fill line.
      If the buffer is at or below the fill line, see “Assemble the
      SeqStudio™ Genetic Analyzer Cathode Buffer Container
      (CBC)” on page 149 and “Insert the Cathode Buffer
      Container” on page 150.
      If the buffer is above the fill line, reinsert the CBC.
5. Place the plate or tube assembly firmly in the autosampler.
6. Close the autosampler lid: Press down on the center of the lid or press down on both sides of the lid with equal pressure until the lid clicks shut.

7. Touch Retract plate, then close the instrument door.

Select a plate setup and start a run

After you load the plate in the instrument (see “Load the plate or the tube assembly” on page 76):

1. In the instrument home screen, touch Setup run.

2. Select the location of your plate setup, then select the plate setup. For information on plate setup files, see “PSM and CSV plate setup files for import into the instrument” on page 63 and “Shared (public), hidden (my plates), and guest plate setup files” on page 64.

3. Verify that settings are as needed.
The **Save location** must specify **Cloud** if you want to view analyzed data when you monitor the run from the Cloud.

![Plate Properties](image)

4. Touch **Start run**.

When the run starts, the instrument automatically:

- Performs an optical alignment each time a cartridge is inserted.
- Performs an automatic spectral calibration adjustment (auto calibration) for each sample to correct for spectral overlap.

During a run, an administrator can lock the touchscreen to prevent other users from using the instrument. Only the user who started the run or an administrator can sign in to the instrument if the touchscreen is locked.

Proceed to:

- “Monitor a run from the Thermo Fisher Cloud” on page 79
- “Monitor a run from a mobile device” on page 87
- “Monitor a run from the instrument” on page 89

### Automatic file cleanup

Before starting a run, the instrument calculates the total amount of storage space required to save the run. If the required storage space is not available, the instrument deletes files associated with the oldest exported plates until sufficient space is available.

**Note:** Only complete plates that have been auto exported (saved to Cloud, network, or USB) or manually exported (using **Settings** ▸ **Run History** ▸ **plate name** ▸ **Export**) are deleted.

If the required storage space is not available and no plates have been exported, the instrument displays a notification indicating that there is not enough storage space. You can export plates and delete plates, then start the run again.
Lock the touchscreen

During a run, you can lock the touchscreen to prevent other users from using the instrument. This feature is not available to Guest users.

Only the user who locked the touchscreen or an administrator can sign in to the instrument if the touchscreen is locked.

1. Touch 🎨.
2. Touch Profile.
3. Touch Lock instrument.

Note: If a run is not in progress, Sign out is displayed instead of Lock instrument.

Monitor a run from the Thermo Fisher Cloud

A run is accessible from InstrumentConnect for 24 hours after the run is complete, or until another run is started.

1. Sign in to thermofisher.com/cloud.
2. Click 🎨 to access InstrumentConnect.
3. Click the run status dial to display the Remote Monitoring App.
Figure 11  Remote Monitoring App
A run is accessible from the Plate Manager for 24 hours after the run is complete, or until another run is started.

You can open the Remote Monitoring App immediately after you save a plate setup or at a later time.

In the Plate Manager on the Thermo Fisher Cloud:

- To open the Remote Monitoring App immediately after you save a plate setup and start the run, click **Monitor my run**.
To open the Remote Monitoring App at a later time, click **PM**, then select an instrument or click to access InstrumentConnect.

![Remote Monitoring App](image)

Select an instrument or click to access InstrumentConnect.

![Remote Monitoring App](image)

Figure 12  Remote Monitoring App
1. In any screen in the Thermo Fisher Cloud, click 🔍.

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

1. Open the Remote Monitoring App (see “Open the Remote Monitoring App from Instrument Connect App” on page 79).

2. Click an injection group in the injection list or the plate view.

   The status dials are color-coded for quality alerts:
   - ![Green](#) — All QC tests passed.
   - ![Yellow](#) — At least 1 warning quality alert was triggered.
   - ![Red](#) — At least 1 failing quality alert was triggered.

   For information on quality alerts, see:
   - “Data quality alerts” on page 102
   - “Sizecalling and basecalling quality alerts” on page 102

3. In the **Quality alerts** screen, click the **Raw**, **EPT**, or **Analyzed** tab to view data.

4. As needed, select **Actions** ➔ **Re-inject group**, select the **Run module** and settings, then click **Inject**.

**Pause or cancel an injection in the Remote Monitoring App**

Select:

- **Actions** ➔ **Pause plate** to pause the run after the current injection is complete.
- **Actions** ➔ **Stop current injection** to immediately stop the injection.

**Edit injection group run settings**

In the **Results** screen:
1. Select Actions ▶ Edit injection group.

2. Edit settings as needed, then click OK.

Re-inject or delete an injection group

In the Results screen:
Select Actions ▶ Re-inject group or Actions ▶ Delete injection group.

Export a QC report

The QC Report command is not available for an injection until the injection is complete. The QC Report command is not available for any injections if the plate setup Save location does not specify the Cloud.

In the Remote Monitor screen:
Select Actions ▶ QC Report.
A PDF of the plate QC report is generated.

Remote Monitoring App raw trace

Figure 13  Fragment analysis raw trace

1. Zoom in/out.
2. Raw trace.
3. Thumbnail trace—Click-drag to view another region of the trace.
4. Lock/unlock trace zooming for all traces in the injection group.
5. View Options—Select the dye color to display; set vertical scaling.
6. Cursor position indicator (red line).
Figure 14  Sequence analysis raw trace
① Zoom in/out.
② Raw trace.
③ Lock/unlock trace zooming for all traces in the injection group.
④ View Options—Select the basecalls to display; set vertical scaling.

Remote Monitoring App EPT trace
The EPT view (ElectroPhoresis Telemetry) shows instrument data conditions (currents, temperatures, electrophoresis voltage) as a function of time.
Remote Monitoring App analyzed trace

Figure 15 Fragment analysis analyzed trace
1. Lock/unlock trace zooming for all traces in the injection group.
2. Zoom in/out.
3. Analyzed trace.
4. Thumbnail trace—Click-drag to view another region of the trace.
5. View Options—Select the dye colors to display; set vertical scaling.
6. Cursor position indicator (red vertical and horizontal tick marks outside trace).
7. Size standard curve (red line).
8. Actions—Select commands to pause and cancel injections.

Figure 16 Sequence analysis analyzed trace
1. Zoom in/out.
2. Analyzed trace.
3. Thumbnail trace—Click-drag to view another region of the trace.
4. Lock/unlock trace zooming for all traces in the injection group.
5. View Options—Select the basecalls to display; show/hide quality bars and values; set vertical scaling.
6. Search for a sequence.
Monitor a run from a mobile device

Before you begin, see “Link the instrument from a mobile device” on page 168.

1. On your mobile device, launch InstrumentConnect.

2. Touch the instrument to monitor.

3. Swipe left to view consumable status.
4. Touch the status dial to view the injection list.

5. Touch an injection group to display quality alerts, then touch View raw plot to view the data.

- Swipe left to view the entire trace.
- Pinch-zoom to expand the trace.
Monitor a run from the instrument

(Optional) View the injection list, change injection settings or order, or specify replicates and re-injections

In the Plate properties screen:

1. Touch Injection options.
2. Touch an injection group, then configure the injection list:
   - Touch and drag an injection group to a new location in the injection list.
   - Touch **Inject first**—Moves the selected injection group to the top of the injection list.
   - Touch **Edit and re-inject**—Adds replicates or re-injections to the injection list.
   You can also modify Run module, Injection time, Injection voltage, Run time, or Run voltage for these injections.
   
   **Note:** Changes to Injection time, Injection voltage, Run time, or Run voltage are not saved to the plate setup and will be used during the current plate run only.
3. Touch Done.

View the run status

In the home screen:

View the run time information and the status dial for each capillary.

The status dials are color-coded for quality alerts:

- 💚—All QC tests passed.
- 🟢—At least 1 warning quality alert was triggered.
- 🟥—At least 1 failing quality alert was triggered.

If an injection group is set to re-inject, the number of the current injection is displayed on the status dials.

For information on quality alerts, see:

- “Data quality alerts” on page 102
- “Sizecalling and basecalling quality alerts” on page 102
View real-time results

During a run, in the home screen:

Touch one of the injection dials to display the trace for the selected capillary.

See “Fragment analysis trace” on page 96 or “Sequence analysis trace” on page 98 for information.

The status dials are color-coded for quality alerts:

- [ ] — All QC tests passed.
- [ ] — At least 1 warning quality alert was triggered.
- [ ] — At least 1 failing quality alert was triggered.

For information on quality alerts, see:

- “Data quality alerts” on page 102
- “Sizecalling and basecalling quality alerts” on page 102

Pause a plate or cancel or stop injections

In the home screen:

1. Touch [ ] Actions.
2. Manage the plate or injections:

<table>
<thead>
<tr>
<th>Touch</th>
<th>To</th>
</tr>
</thead>
<tbody>
<tr>
<td>View results</td>
<td>View the list of injections and status.</td>
</tr>
<tr>
<td>Edit plate</td>
<td>For injections that have not yet been run, edit <strong>Sample Name</strong>, <strong>Run Module</strong>, <strong>Dye Set</strong>, <strong>Size Standard</strong>, <strong>Sample Type</strong>, and custom fields.</td>
</tr>
<tr>
<td>Pause plate</td>
<td>Stop the run after the current injection is complete. Touch <strong>Resume</strong> to continue the run.</td>
</tr>
<tr>
<td>Stop current injection</td>
<td>Stop the current injection immediately. Touch <strong>Resume</strong> to continue the run.</td>
</tr>
<tr>
<td>Cancel remaining injections</td>
<td>Specify whether to cancel the run immediately or after the current injection is complete.</td>
</tr>
<tr>
<td>Injection options</td>
<td>Move an injection to the top of the injection list, edit run module information, and/or reinject samples.</td>
</tr>
</tbody>
</table>

When a run is complete, in the home screen:

1. Touch **View Results**.

2. Touch **List view**.

   Each injection group displays a QC color for each capillary:
   - **Green** — All QC tests passed.
   - **Yellow** — At least 1 warning quality alert was triggered.
   - **Red** — At least 1 failing quality alert was triggered.

   For information on quality alerts, see:
   - “Data quality alerts” on page 102
   - “Sizecalling and basecalling quality alerts” on page 102

3. Touch an injection group.

4. View the results in the **Run Result Details** screen, or touch **for well details.** See “Fragment analysis results” on page 96 or “Sequence analysis results” on page 98 for detailed information.

5. Touch a sample file name.

   If the data triggered any quality alerts, a QC alerts screen is displayed. See “Data quality alerts” on page 102 and “Sizecalling and basecalling quality alerts” on page 102 for detailed information.

   Touch **View data** to display the analyzed trace for the sample. See “Fragment analysis trace” on page 96 or “Sequence analysis trace” on page 98 for detailed information.

6. Touch and drag the thumbnail view of the analyzed trace (below the trace) to scroll left or right.
7. (Optional) Adjust the graphical view (see “Adjust the trace display” on page 92).

8. Touch › or ◀ to scroll to the raw data or EPT Plot (Electrophoresis Telemetry). See “EPT plot” on page 100.

Adjust the trace display

See “View results for the current plate” on page 91 to access results.

- Drag one finger to pan to the left or right.
- Zoom in and out by pinching and expanding with two fingers.
- Touch ▼ on the left border of the trace, then touch a dye to deselect.
- Touch ▲ on the right border of the trace, then touch Zoom In, Zoom Out, or Fit to screen to adjust the display.
- Drag the center of the pane in thumbnail view to scroll left or right.

Unload the plate or the tube assembly

When the run is complete:

1. Touch ⌁, touch Eject plate, then open the instrument door when prompted.

2. Press the release button on the autosampler to open the lid.

3. Remove the plate or tube assembly.
4. Close the autosampler lid: Press down on the center of the lid or press down on both sides of the lid with equal pressure until the lid clicks shut.

5. Touch Retract plate, then close the instrument door.
View and analyze results

- View results in the Remote Monitoring App on the Cloud ................. 94
- View results on the instrument ........................................... 95
- Export results from the instrument (sample data files and QC reports) ...... 104
- Analyze data ............................................................. 104

View results in the Remote Monitoring App on the Cloud

1. Open the Remote Monitoring App (see “Open the Remote Monitoring App from Instrument Connect App” on page 79).

2. Click an injection group in the injection list or the plate view.

   The status dials are color-coded for quality alerts:
   - Green — All QC tests passed.
   - Yellow — At least 1 warning quality alert was triggered.
   - Red — At least 1 failing quality alert was triggered.

   For information on quality alerts, see:
   - “Data quality alerts” on page 102
   - “Sizecalling and basecalling quality alerts” on page 102

![Injection Group Status Dials](image)

Note: The Analyzed tab is disabled if the Save location for the plate setup is not set to Cloud or if the injection group has not finished running.

3. In the Quality alerts screen, click the Raw, EPT, or Analyzed tab to view data.

4. As needed, select Actions ➔ Re-inject group, select the Run module and settings, then click Inject.
View results on the instrument

When a run is complete, in the home screen:

1. Touch View Results.

2. Touch List view.
   Each injection group displays a QC color for each capillary:
   • green — All QC tests passed.
   • yellow — At least 1 warning quality alert was triggered.
   • red — At least 1 failing quality alert was triggered.

   For information on quality alerts, see:
   • “Data quality alerts” on page 102
   • “Sizecalling and basecalling quality alerts” on page 102

3. Touch an injection group.

4. View the results in the Run Result Details screen, or touch for well details.
   See “Fragment analysis results” on page 96 or “Sequence analysis results” on page 98 for detailed information.

5. Touch a sample file name.
   If the data triggered any quality alerts, a QC alerts screen is displayed. See “Data quality alerts” on page 102 and “Sizecalling and basecalling quality alerts” on page 102 for detailed information.
   Touch View data to display the analyzed trace for the sample. See “Fragment analysis trace” on page 96 or “Sequence analysis trace” on page 98 for detailed information.

6. Touch and drag the thumbnail view of the analyzed trace (below the trace) to scroll left or right.

7. (Optional) Adjust the graphical view (see “Adjust the trace display” on page 92).

8. Touch to scroll to the raw data or EPT Plot (ElectroPhoresis Telemetry).
   See “EPT plot” on page 100.

Adjust the trace display

See “View results for the current plate” on page 91 to access results.

• Drag one finger to pan to the left or right.

• Zoom in and out by pinching and expanding with two fingers.

• Touch on the left border of the trace, then touch a dye to deselect.

• Touch on the right border of the trace, then touch or to adjust the display.
- Drag the center of the pane in thumbnail view to scroll left or right.

- Drag the right or left handle of the pane to zoom horizontally.

**Fragment analysis results**

**Fragment analysis trace**

1. Trace color hide/show—Touch to open, then touch a color to hide or show.
2. Analyzed trace
3. Size standard curve [red line]
4. Thumbnail trace—Drag the center of the pane in the thumbnail trace to display another trace area in the top pane. Drag the right or left handle of the pane to zoom horizontally.
5. Basepair or scan display selection.
6. Zoom tools—Touch to open.
7. Next trace tool—Touch to view the raw trace or EPT for the well.
## Fragment analysis results

<table>
<thead>
<tr>
<th>Setting</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Quality</strong></td>
<td>QC flags</td>
</tr>
<tr>
<td></td>
<td>• ![Green Circle]—All QC tests passed.</td>
</tr>
<tr>
<td></td>
<td>• ![Yellow Circle]—At least 1 warning quality alert was triggered.</td>
</tr>
<tr>
<td></td>
<td>• ![Red Circle]—At least 1 failing quality alert was triggered.</td>
</tr>
<tr>
<td><strong>SQ</strong></td>
<td>Size Quality</td>
</tr>
<tr>
<td></td>
<td>• If $\text{SQ}$ is $\leq 0.75$, it passes the QC test and does not trigger a quality alert ![Green Circle].</td>
</tr>
<tr>
<td></td>
<td>• If $\text{SQ}$ is $0.25$–$0.74$, it triggers a warning quality alert ![Yellow Circle].</td>
</tr>
<tr>
<td></td>
<td>• If $\text{SQ}$ is $&lt; 0.25$, it triggers a failing quality alert ![Red Circle].</td>
</tr>
</tbody>
</table>

### 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).

### Exported

The sample has been auto exported (saved to Cloud, network, or USB) or manually exported (using ![Settings] Run History > plate name > Export).

### Well details

Well details (see below).

| Well details | Sample file name, QC flag, sample name, sample type, settings used to acquire the data (size standard, run module and dye set), Sizing quality value, and export status. |
### Sequence analysis results

**Sequence analysis trace**

1. **Quality Value bars and values:**
   - Pure base with \( QV \geq 20 \)
   - Pure base with \( QV 15-19 \)
   - Pure base with \( QV < 15 \)
   - Mixed base

2. **Bases**—Mixed base calls are highlighted in red (if they exceed the **Mixed base threshold** specified in analysis settings; see “Sequencing settings (base calling)” on page 112).

3. **Trace color hide/show**—Touch to open, then touch a color to hide or show.

4. **Analyzed trace**

5. **Thumbnail trace**—Drag the center of the pane in the thumbnail trace to display another trace area in the top pane. Drag the right or left handle of the pane to zoom horizontally.

6. **Zoom tools**—Touch to open.

7. **Next trace tool**—Touch to view the raw trace or EPT for the well.

### Sequencing results

<table>
<thead>
<tr>
<th>Result</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Quality</strong></td>
<td>QC flags</td>
</tr>
<tr>
<td></td>
<td>• <img src="green.png" alt="Green" /> — All QC tests passed.</td>
</tr>
<tr>
<td></td>
<td>• <img src="orange.png" alt="Orange" /> — At least 1 warning quality alert was triggered.</td>
</tr>
<tr>
<td></td>
<td>• <img src="red.png" alt="Red" /> — At least 1 failing quality alert was triggered.</td>
</tr>
<tr>
<td>Result</td>
<td>Description</td>
</tr>
<tr>
<td>--------------------------------</td>
<td>------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------</td>
</tr>
<tr>
<td><strong>CRL (Contiguous Read Length)</strong></td>
<td>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 ±21-bp moving average to determine a contiguous read length based on quality values. <strong>Note:</strong> The contiguous read length passing criteria for install checks is an uninterrupted segment of bases with an average Quality Value (QV) of 30.</td>
</tr>
<tr>
<td>Exported</td>
<td>The sample has been auto exported (saved to Cloud, network, or USB) or manually exported (using Settings &gt; Run History &gt; plate name &gt; Export).</td>
</tr>
<tr>
<td>Well details</td>
<td>Well details (see below).</td>
</tr>
</tbody>
</table>

**Well details**

Sample file name, QC flag, sample name, CRL, signal strength, Median PUP, Trace score, run module and dye set used to acquire the data, and export status.

<table>
<thead>
<tr>
<th>Signal strength</th>
<th>The average relative fluorescence unit (RFU) for all dyes across the electropherogram in the raw data.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Trace score</td>
<td>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.</td>
</tr>
<tr>
<td>Median PUP (pull-up peak)</td>
<td>A measure of noise or pull-up that is determined by taking the mean of the ratios of signal strength calculated for each base-called peak: primary peak/secondary peak under the primary peak. A higher value indicates less baseline or secondary noise. A lower value indicates an elevated baseline or secondary noise. Example 1: Main called base signal strength is 1,000 RFU and the largest secondary peak beneath it is 10 RFU; PuP=100 Example 2: Main called base signal strength is 1,000 RFU and the largest secondary peak beneath it is 100 RFU; PuP=10</td>
</tr>
</tbody>
</table>

**Understanding Quality Values (QVs)**

**Quality value ranges**

The color of a QV bar indicates the QV of a base.

- Pure base with QV ≥ 20
- Pure base with QV 15–19
- Pure base with QV < 15
- Mixed base
Pure base versus mixed base QVs

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

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

<table>
<thead>
<tr>
<th>QV</th>
<th>Pe</th>
<th>QV</th>
<th>Pe</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>79.0%</td>
<td>30</td>
<td>0.10%</td>
</tr>
<tr>
<td>5</td>
<td>32.0%</td>
<td>35</td>
<td>0.032%</td>
</tr>
<tr>
<td>10</td>
<td>10.0%</td>
<td>40</td>
<td>0.010%</td>
</tr>
<tr>
<td>15</td>
<td>3.2%</td>
<td>45</td>
<td>0.0032%</td>
</tr>
<tr>
<td>20</td>
<td>1.0%</td>
<td>50</td>
<td>0.0010%</td>
</tr>
<tr>
<td>25</td>
<td>0.32%</td>
<td>60</td>
<td>0.00010%</td>
</tr>
</tbody>
</table>

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

EPT plot

The EPT view (ElectroPhoresis Telemetry) shows instrument data conditions (currents, temperatures, electrophoresis voltage) as a function of time.
Touch on the left border of the plot to display the legend.

**View results for a previously run plate (run history)**

In the home screen:

1. Touch **Settings** ➔ **Run history**.

2. Touch a plate name, then touch **View**.
   
   If you select more than one plate name, the **View** button is dimmed.
   
   The Run History screen is displayed.

![Run History Screen](image)

3. Touch a sample file name.

4. View the results in the **Run history** screen, or touch **View** to view well details.
   
   See “Fragment analysis results” on page 96 or “Sequence analysis results” on page 98 for information.
5. Touch a sample file name, then touch View.
If you select more than one sample file name, the View button is dimmed.
If the data triggered any quality alerts, a QC alerts screen is displayed.
For information on quality alerts, see:
Click View data to display the trace for the sample. See “Fragment analysis trace” on page 96 or “Sequence analysis trace” on page 98.

6. Touch and drag the thumbnail view of the analyzed trace (below the trace) to scroll left or right.

7. Touch › or ◀ to scroll to the raw data or EPT Plot.

Data quality alerts

<table>
<thead>
<tr>
<th>Quality alert</th>
<th>Description</th>
<th>Action</th>
</tr>
</thead>
<tbody>
<tr>
<td>Offscale peaks. Adjust the injection parameters and/or the sample</td>
<td>At least 10 scans have saturated the CCD camera.</td>
<td>• Reduce the injection voltage.</td>
</tr>
<tr>
<td>concentration.</td>
<td></td>
<td>• Dilute the sample.</td>
</tr>
<tr>
<td>No sample was detected.</td>
<td>Poor signal-to-noise ratio with low signal detected.</td>
<td>• Verify that the sample volume follows recommendations in the user</td>
</tr>
<tr>
<td></td>
<td></td>
<td>manual.</td>
</tr>
<tr>
<td></td>
<td></td>
<td>• Troubleshoot upstream PCR and sequencing steps.</td>
</tr>
</tbody>
</table>

Sizecalling and basecalling quality alerts

Table 5  Sizecalling quality alerts

<table>
<thead>
<tr>
<th>Quality alert</th>
<th>Description</th>
<th>Action</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sizing quality value is low due to poor size standard peak quality.</td>
<td>Low resolution or poor quality data is present.</td>
<td>• Re-inject the sample.</td>
</tr>
<tr>
<td>Peak height uniformity is low or the fitting quality in sizing is</td>
<td></td>
<td>• If the problem persists, check the sample quality.</td>
</tr>
<tr>
<td>poor.</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Sizecaller found broad peak(s) in the size standard peak(s).</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Sizing quality value is in the intermediate range; check size</td>
<td></td>
<td></td>
</tr>
<tr>
<td>standard data quality.</td>
<td></td>
<td></td>
</tr>
<tr>
<td>The number of size standard peaks detected is less than what is</td>
<td>Size standard definition includes peaks that are not present in the sample.</td>
<td>Use or create a size standard definition with the appropriate number</td>
</tr>
<tr>
<td>defined in the size standard.</td>
<td>Example: Sample peaks are detected up to 500 bp, but the size standard</td>
<td>of peaks and peak sizes.</td>
</tr>
<tr>
<td></td>
<td>definition includes peak sizes that are &gt;500 bp.</td>
<td></td>
</tr>
</tbody>
</table>
### Quality alert

<table>
<thead>
<tr>
<th>Quality alert</th>
<th>Description</th>
<th>Action</th>
</tr>
</thead>
<tbody>
<tr>
<td>The analysis range is too small. Correct the analysis range in analysis</td>
<td>Various causes.</td>
<td>• Analyze the data in a secondary analysis software with a corrected analysis range.</td>
</tr>
<tr>
<td>settings and re-analyze in secondary analysis software or re-inject sample.</td>
<td></td>
<td>• Re-inject the sample.</td>
</tr>
</tbody>
</table>

#### Table 6  Basecalling quality alerts

<table>
<thead>
<tr>
<th>Quality alert</th>
<th>Description</th>
<th>Action</th>
</tr>
</thead>
<tbody>
<tr>
<td>Basecalling failed due to poor quality data.</td>
<td>Poor quality data is present.</td>
<td>• Re-inject the sample.</td>
</tr>
<tr>
<td></td>
<td></td>
<td>• If the problem persists, prepare fresh sample.</td>
</tr>
<tr>
<td></td>
<td></td>
<td>• Troubleshoot upstream PCR and sequencing steps.</td>
</tr>
</tbody>
</table>

#### Edit injection parameters and re-inject samples

You can edit injection parameters and re-inject samples during a run or after a run is complete.

1. Access **Injection options**.
   - During a run—Touch Actions > Edit plate.
   - After a run—Touch Results.

2. Touch an injection group, then configure the injection list:
   - Touch and drag an injection group to a new location in the injection list.
   - Touch Inject first—Moves the selected injection group to the top of the injection list.
   - Touch Edit and re-inject—Adds replicates or re-injections to the injection list. You can also modify Run module, Injection time, Injection voltage, Run time, or Run voltage for these injections.

3. Touch Done.

   **Note:** The changes are not applied until you touch Done.

#### Export a report (QC report)

This function allows you to export a QC report for the current plate. To export a QC report for a previously run plate, export a run history (see “Export results from the instrument (sample data files and QC reports)” on page 104).

When a run is complete, in the home screen:

1. Touch Results.

2. Touch Export report.

3. Select a storage location.

4. Navigate to, then select a location, then touch Export.
Export results from the instrument (sample data files and QC reports)

In the home screen:

1. Touch Settings ▶ Run history.
2. Select one or more plates from the Run History table.
3. Touch Export.
4. Select a storage location.

The following data is exported for the plate:
• Fragment analysis—FSA file for each sample.
• Sequencing—AB1 file for each sample.
• Plate QC report in CSV and PDF format.

**Note:** If you select a plate, select View, then select Export, only an FSA or AB1 file for each analyzed sample is exported.

Analyze data

1. Export results (see “Export results from the instrument (sample data files and QC reports)” on page 104) or use auto exported data.
2. Use an appropriate fragment analysis or sequencing application to analyze the data.

**Note:** Data from the SeqStudio™ Genetic Analyzer may be labeled as "3200" in secondary analysis software.

For more information, see “Secondary analysis software” on page 28
Manage the software (Plate Manager)

- Add a custom dye calibration to the Plate Manager ...................... 105
- Download a plate setup template as a CSV file .......................... 105
- Save a plate setup as a PDF .............................................. 106
- Save a plate setup as a CSV file ........................................ 106
- Create a plate setup template .......................................... 106
- Delete plate setups .................................................. 107
- Manage email notifications in the Thermo Fisher Cloud ............... 107
- Manage run modules ................................................ 108
- Manage size standards ............................................... 108
- Manage analysis settings ............................................. 109

Add a custom dye calibration to the Plate Manager

On the instrument:

1. Open a plate setup that specifies the custom dye set of interest.

2. Export a plate setup that specifies the custom dye.

3. Open the exported plate setup in the Plate Manager.
   The custom dye is imported and is available for selection when you create new plates.

Download a plate setup template as a CSV file

1. Click [PM] to display the home screen.

2. Click New, select Create from template, then click Download for the template of interest.

Note: You cannot add plate setups to the list of templates. However, you can create a plate setup with "Template“ suffix, and use it as a starting point for creating new plate setups.
Save a plate setup as a PDF

In the Plate tab:
Select Actions  Print plate view.
The plate view and table view are exported.

Save a plate setup as a CSV file

In the Plate tab:

1. Select Actions  Save as CSV.
2. Navigate to and select a storage destination.

The plate setup is saved as a CSV file. The names of the dye set, run module, and size standard are included in the CSV file.

Create a plate setup template

Note: You cannot add templates to the list of templates you select when you create a plate setup. However, you can create a plate setup with “Template” suffix, then use it as a starting point for creating new plate setups.

1. Click New, select Create from template, then click Download for the template of interest.
2. Modify the CSV file as needed.
3. Save the plate setup with a “Template” suffix (example: Plate_FragAnalysis_Template), or other identifier.
## Delete plate setups

To delete plate setups from the Plate Manager:

<table>
<thead>
<tr>
<th>On the...</th>
<th>Use...</th>
</tr>
</thead>
</table>
| Desktop   | Windows™ Explorer to delete PSM or CSV files.  
**Note:** The location shown in the figure is an example. Users can save PSM files in any location. |
| Cloud     | Click ☑️ in the Thermo Fisher Cloud, then use DataConnect to delete PSM files. |

### Manage email notifications in the Thermo Fisher Cloud

1. In any screen in the Thermo Fisher Cloud, click ☑️.
2. Click **Settings**.

3. Select or deselect your email address.

**Manage run modules**

This function manages the list of run modules that you can select from when you create a plate setup.

To assign a run module to a plate, see “Assign wells: run module, size standard, and dye set” on page 68.

Factory-installed items cannot be edited or deleted. To create a new item from a factory-installed item, copy, edit, then save the new item.

For more information, see “Run modules, read lengths, size ranges, and run times” on page 123.

1. In the **Plate** tab, select **Actions** ➤ **Manage run modules**.

2. To create a new run module:
   a. Select a default run module or a user-created run module, then click **Copy**.
   
   b. Enter values, click **Advanced** to enter additional settings, then click **Save**.

   See “Run module settings” on page 123 for detailed information.

3. As needed, select a run module of interest, then click **Edit** or **Delete** (user-created run modules only).

**Manage size standards**

This function manages the list of size standard definitions that you can select from during plate set up.

To assign a size standard definition to a plate, see “Assign wells: run module, size standard, and dye set” on page 68.

A size standard defines the sizes in basepairs of known fragments. It is used to generate a standard curve. The standard curve is used to determine the sizing of fragments in unknown samples.

Factory-installed items cannot be edited or deleted. To create a new item from a factory-installed item, copy, edit, then save the new item.

Size standard definitions are accessible to all users.

1. In the **Plate** tab, select **Actions** ➤ **Manage size standards**.

2. To create a new size standard:
   a. Select a default size standard or a user-created size standard, then click **Copy**.

   b. Enter a name and select a dye color, then edit the fragment sizes (basepairs).
c. Click Save:

3. As needed, select a size standard of interest, then click Edit or Delete (user-created size standards only).

## Manage analysis settings

In the Properties tab:

1. Select Actions ➤ Analysis settings.

2. To create new analysis settings:
   a. Select the default analysis settings or user-created analysis settings, then click Copy.
   b. Enter a name and edit settings as needed (see “Fragment analysis settings (size calling)” on page 109 or “Sequencing settings (base calling)” on page 112).
   c. As needed, click Delete (user-created settings only).

3. Click Save.

### Fragment analysis settings (size calling)

<table>
<thead>
<tr>
<th>Setting</th>
<th>Description</th>
</tr>
</thead>
</table>
| **Size calling method** | • **Local Southern**—(default) Determines the fragment sizes using the reciprocal relationship between fragment length and electrophoretic mobility.  
                              • **Global Southern**—Compensates for standard fragments with anomalous electrophoretic mobility (similar to least squares methods).  
                              • **2nd LSQ** (2nd Order Least Squares)—Uses regression analysis to build a bestfit size calling curve.  
                              • **3rd LSQ** (3rd Order Least Squares)—Uses regression analysis to build a bestfit size calling curve.  
                              • **Cubic Spline Interpolation**—Forces the sizing curve through all the known points of the selected size standard. |
| **Analysis range**     | • **Full Range**—(default) 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. View 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.
<table>
<thead>
<tr>
<th>Setting</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Sizing range</strong></td>
<td>The size range (in base pairs) appropriate for the kit you are using:</td>
</tr>
<tr>
<td></td>
<td>• <strong>Full Range</strong> for the software to analyze fragments of all sizes in the Analysis Range.</td>
</tr>
<tr>
<td></td>
<td>• <strong>Partial Range</strong> for the software to analyze only fragments within a specified range. Enter a <strong>Start Size</strong> and a <strong>Stop Size</strong> appropriate for the size standard used.</td>
</tr>
<tr>
<td><strong>Peak amplitudes</strong></td>
<td>The peak height threshold (RFU) for peak detection for each dye color.</td>
</tr>
<tr>
<td></td>
<td>Peaks below the threshold are not detected. For example, if you use the default values of 175 RFU, peaks with heights equal to or greater than 175 RFU are detected. Peaks with heights below 175 RFU are still displayed in the electropherogram plots but are not detected or labeled.</td>
</tr>
<tr>
<td><strong>Primer peak</strong></td>
<td>If the primer peaks in your application obscure peaks of interest, select <strong>Present</strong>. This instructs the algorithm to ignore primer peaks. Primer peaks are still displayed in the trace.</td>
</tr>
<tr>
<td></td>
<td>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_LIZ_[60-600] or other size standards that include lower bp starting points may allow detection of the peaks.</td>
</tr>
<tr>
<td><strong>Common settings</strong></td>
<td></td>
</tr>
<tr>
<td><strong>Smoothing</strong></td>
<td>Select an option to smooth the outline of peaks and reduce the number of false peaks detected:</td>
</tr>
<tr>
<td></td>
<td>• <strong>None</strong> (default) to apply no smoothing. Best if the data display sharp, narrow peaks of interest.</td>
</tr>
<tr>
<td></td>
<td>• <strong>Light</strong> to provide the best results for typical data. Light smoothing slightly reduces peak height.</td>
</tr>
<tr>
<td></td>
<td>• <strong>Heavy</strong> for data with very sharp, narrow peaks of interest. Heavy smoothing can significantly reduce peak height.</td>
</tr>
<tr>
<td><strong>Baseline Window</strong></td>
<td>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:</td>
</tr>
<tr>
<td></td>
<td>• 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.</td>
</tr>
<tr>
<td></td>
<td>• 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.</td>
</tr>
<tr>
<td><strong>Minimum Peak Half Width</strong></td>
<td>Specify the minimum full peak width at half maximum <strong>Peak Height</strong> required for peak detection. The range is 2 to 99 data points.</td>
</tr>
<tr>
<td>Setting</td>
<td>Description</td>
</tr>
<tr>
<td>----------------------</td>
<td>-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------</td>
</tr>
</tbody>
</table>
| **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. |
| **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. |
| **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.  
  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. |
The default settings are optimized for sequencing of PCR amplicons from diploid genes, which are expected to have Mixed bases and which should end At PCR Stop. For sequencing from plasmid templates, which are of pure sequence (no Mixed bases) and have longer sequence read times than PCR products, create new analysis settings and disable (uncheck) At PCR Stop and Mixed base threshold checkboxes.

<table>
<thead>
<tr>
<th>Setting</th>
<th>Description</th>
</tr>
</thead>
</table>
| **Quality Threshold**  | • Basecall assignment (ambiguous bases):  
                          – Do not assign Ns to basecalls  
                          – Assign Ns to basecalls with QV<5— Bases with a QV less than the threshold display N instead of the base letter  
                          • End 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 checkbox. |
| **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. |
| **Clear range methods** | • **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 base positions**—Specifies the first and last base in the range to consider, or trims the specified number of bases from the 3’ end.  
                          • **Mask base positions before**—Specifies the base position before which to disregard bases. |
Manage the software (instrument)

- Connect the instrument to a network drive .................................. 113
- Link the instrument to your Thermo Fisher Cloud account ................. 119
- Lock the touchscreen .......................................................... 120
- Manage plate setups .................................................................. 121
- Manage run settings (instrument) .............................................. 122
- Manage instrument settings ...................................................... 130
- Manage instrument profiles on the instrument ........................... 134
- Manage storage space .............................................................. 136

Connect the instrument to a network drive

Determine IP address for a computer on a network

On the destination computer:

1. In the Windows™ desktop, click 📲.
2. In the search field at the bottom of the pane, type command prompt, then press Enter.

3. At the command prompt, type ipconfig, then press Enter.
4. Note the IP address listed.

   **Note:** The location and number of digits in your IP address may differ from the IPv4 Address example shown below.

   ![Command Prompt showing IP Configuration](image)

   **Create folders and enable network folder sharing**

   In the Windows™ desktop:

1. On a Windows™ computer, server, or network drive, create a folder to store your plates and results. Example: *C:/Users/Your Name/SharedData*.

2. Create subfolders in the *SharedData* folder. Example: *PlateSetups* and *Results*.

3. Right click on a folder, then select **Sharing ➤ Advanced** or **Share with ➤ Advanced sharing**.

4. Select the **Sharing** tab.

5. Click **Advanced sharing**.

6. Select **Share this folder**.

7. Click **Permissions**, then select **Full Control** or **Read, Write, and Delete** options.

   **IMPORTANT!** Without these permissions, the instrument cannot autoexport results when a run is complete.

8. Click **OK**, click **OK**, then click **Close**.
Connect to a network drive

See your laboratory administrator for the information you need to connect to a network drive.

From any screen that displays **Network drive** or **Save location** as an option, you can connect to the drive for the first time.

**IMPORTANT!** Before saving to the network drive, ensure that the folder is shared (see “Create folders and enable network folder sharing” on page 114).

1. Touch **Network drive** or **Save location** field.

2. Touch the **Destination** field, then touch the appropriate field to enter the IP address and shared folder name, then touch **Done**.

   For more information, see “Determine IP address for a computer on a network” on page 113.

3. If necessary, touch the appropriate fields to enter a domain name, username, and password.

4. Touch **Connect**.

Set up a default Cloud location for opening plate setups

Before you begin, create a plate setup (PSM file or CSV file) in the Cloud location that you want to set as the default location.

To set the default location, you must select a plate setup.

1. In the home screen of the instrument, touch **Setup run**, then touch **Cloud**. The **Setup Run** screen is displayed.

2. Select a folder (if needed), then select a plate file. The plate file is imported.

3. Touch **to return to the **Setup Run** screen.
Set up a default Cloud location for saving results (auto export)

1. In the home screen of the instrument, touch **Setup run**, then touch **Create new plate setup**.

2. Touch **Save location**.

3. Touch the Cloud **Destination** field. The **Select Directory** screen is displayed.

4. Select or create a folder.

5. Touch **Done**.

Before you begin, create a plate setup (PSM file or CSV file) in the shared directory on the computer that you want to set as the default location. To set the default location, you must select a plate setup.

1. Determine the IP address of the computer on which you created shared folders (see “Determine IP address for a computer on a network” on page 113 and “Create folders and enable network folder sharing” on page 114).

2. In the home screen of the instrument, touch **Setup run**, then touch **Network Drive**.

<table>
<thead>
<tr>
<th>If your instrument profile</th>
<th>This screen is displayed</th>
<th>How to proceed</th>
</tr>
</thead>
</table>
| Is not connected to a network drive | Connect                  | 1. In the **Network Destination** field, enter the IP address of the computer followed by the folder names you created. Example: 10.43.32.82/SharedData/Results.  
2. If required by your network, enter **Domain**, **User Name**, and **Password** to access the shared location.  
3. Touch **Connect**. The **Setup Run** screen is displayed. |
| Is connected to a network drive | **Select Directory**      | Proceed to step 3. |

3. In the **Setup Run** screen:

<table>
<thead>
<tr>
<th>Touch</th>
<th>To</th>
</tr>
</thead>
<tbody>
<tr>
<td>Set up import</td>
<td>Change the <strong>Network Destination</strong> you specified in the previous step.</td>
</tr>
<tr>
<td>A folder name</td>
<td>Navigate to the location you want to set as the default.</td>
</tr>
<tr>
<td>A plate name</td>
<td>Import the plate.</td>
</tr>
</tbody>
</table>
The Setup Run screen is displayed.

![Setup Run screen example](image)

**Figure 17** Setup Run screen example

1. Example IP address and folder locations
2. List of plates (will be blank if you have not saved plates to this location)

---

**Set up a default network location for saving results (auto export)**

1. Determine the IP address of the computer on which you created shared folders (see “Determine IP address for a computer on a network” on page 113 and “Create folders and enable network folder sharing” on page 114).

2. In the home screen of the instrument, touch **Setup run**, then touch **Create new plate setup**.

3. Touch **Save location**.

4. Touch the network **Destination** field.

<table>
<thead>
<tr>
<th>If your instrument profile</th>
<th>This screen is displayed</th>
<th>How to proceed</th>
</tr>
</thead>
</table>
| Is not connected to a network drive        | Connect                  | 1. In the **Network Destination** field, enter the IP address of the computer followed by the folder names you created. Example: 10.43.32.82/SharedData/Results.  
2. If required by your network, enter **Domain**, **User Name**, and **Password** to access the shared location.  
3. Touch **Connect**. The **Select Directory** screen is displayed. |
| Is connected to a network drive            | Select Directory         | Proceed to step 5.                                                            |
5. In the **Select Directory** screen:

<table>
<thead>
<tr>
<th>Touch</th>
<th>To</th>
</tr>
</thead>
<tbody>
<tr>
<td>New folder</td>
<td>Create a subfolder.</td>
</tr>
<tr>
<td>Set up export</td>
<td>Change the <strong>Network Destination</strong> you specified in the previous step.</td>
</tr>
<tr>
<td>Select this folder</td>
<td>Select the directory shown at the top of the screen.</td>
</tr>
</tbody>
</table>

![Select Directory screen example](image)

**Figure 18**  **Select Directory** screen example

1. Example IP address and folder locations
2. List of folders

6. In the **Save Destination** screen, touch **Done**.
Link the instrument to your Thermo Fisher Cloud account

**Note:** For detailed information on linking the instrument to your Cloud account, see Appendix B, “Link the instrument to your Cloud account—detailed instructions”.

1. If a user is signed in, touch 🔄, then touch **Sign out**.
2. In the **Sign In** screen, touch **Get started** → **Connect**.

3. In the Connect to the Thermo Fisher Cloud screen, touch a connection option.
### Lock the touchscreen

During a run, you can lock the touchscreen to prevent other users from using the instrument. This feature is not available to Guest users.

Only the user who locked the touchscreen or an administrator can sign in to the instrument if the touchscreen is locked.

1. Touch ✏.
2. Touch Profile.
3. Touch Lock instrument.

**Note:** If a run is not in progress, Sign out is displayed instead of Lock instrument.
Manage plate setups

Export or delete a plate setup (PSM file)

1. Touch **Set up run**, then touch **My instrument**.
2. Touch **Manage** at the bottom left of the screen.
3. Touch a plate, then touch **Export** or **Delete**.
4. If you touched:
   - **Export**, select a storage location, then touch **Export**.
   - **Delete**, then touch **Yes** to delete the plate setup.
Import a plate setup from a CSV or PSM file

Note: You can create a plate setup in CSV or PSM file in the Plate Manager (desktop or Cloud).

Before importing a CSV file, see “PSM and CSV plate setup files for import into the instrument” on page 63.

In the home screen:

1. Touch Set up run, then touch  Cloud,  Network, or  USB.

2. Navigate to, then select a CSV or PSM file.

Manage run settings (instrument)

Manage run modules

This function manages the list of run modules that you can select from when you create a plate setup.

To assign a run module to a plate, see “Assign wells: run module, size standard, and dye set” on page 68.

Factory-installed items cannot be edited or deleted. To create a new item from a factory-installed item, copy, edit, then save the new item.

Run modules are accessible only to the user who creates them.

For more information, see “Run modules, read lengths, size ranges, and run times” on page 123.

1. Access the Manage run modules screen:

<table>
<thead>
<tr>
<th>From</th>
<th>Action</th>
</tr>
</thead>
<tbody>
<tr>
<td>Plate properties tab</td>
<td>Touch More options ▶ Manage run modules.</td>
</tr>
<tr>
<td>Home screen</td>
<td>Touch  Settings ▶ Run settings ▶ Run modules.</td>
</tr>
</tbody>
</table>
2. To create a new run module:
   a. Touch a default run module or a user-created run module to use as a starting point, then touch Copy.
   b. Enter values, then touch Next.
   c. Enter a name, touch Advanced to enter additional settings, then Done.

See “Run module settings” on page 123 for detailed information.

3. As needed, touch a run module of interest, then touch Edit or View.
   Note: The Edit button is dimmed if a run is in progress.

### Run module settings

<table>
<thead>
<tr>
<th>Setting</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Run module name</td>
<td>Name of the module</td>
</tr>
<tr>
<td>Capillary temperature (°C)</td>
<td>Temperature setting for the capillary array throughout run</td>
</tr>
<tr>
<td>Prerun voltage (Volts)</td>
<td>Voltage setting for pre-run before sample injection</td>
</tr>
<tr>
<td>Prerun time (seconds)</td>
<td>Prerun time</td>
</tr>
<tr>
<td>Injection voltage (Volts)</td>
<td>Voltage for sample injection</td>
</tr>
<tr>
<td>Injection time (seconds)</td>
<td>Sample injection time</td>
</tr>
<tr>
<td>Run voltage (Volts)</td>
<td>Final sample electrophoresis separation run voltage</td>
</tr>
<tr>
<td>Run ramp duration (seconds)</td>
<td>Time required to reach the Run voltage</td>
</tr>
<tr>
<td></td>
<td>Note: Data collection does not start until this time elapses.</td>
</tr>
<tr>
<td>Run time (seconds)</td>
<td>Length of time that data is collected after the Run ramp duration elapses</td>
</tr>
</tbody>
</table>

### Run modules, read lengths, size ranges, and run times

**Table 7** Sequencing run modules for standard sequencing

<table>
<thead>
<tr>
<th>Run module</th>
<th>Contiguous read length (CRL)</th>
<th>QV threshold</th>
<th>Approximate run time</th>
</tr>
</thead>
<tbody>
<tr>
<td>ShortSeq</td>
<td>≥350</td>
<td>QV30</td>
<td>30 minutes</td>
</tr>
<tr>
<td>ShortSeq_BDX</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>MediumSeq</td>
<td>≥500</td>
<td>QV30</td>
<td>45 minutes</td>
</tr>
<tr>
<td>MediumSeq_BDX</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
important! Use BDX run modules only if you prepare samples with BigDye XTerminator™ Purification Kit. Use non-BDX run modules for samples purified with other methods.

<table>
<thead>
<tr>
<th>Run module</th>
<th>Contiguous read length (CRL)[1]</th>
<th>QV threshold</th>
<th>Approximate run time</th>
</tr>
</thead>
<tbody>
<tr>
<td>LongSeq</td>
<td>≥800</td>
<td>QV20</td>
<td>~ 2 hours</td>
</tr>
<tr>
<td>LongSeq_BDX</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

[1] CRL was determined using the Long Read Sequencing standard. A minimum of 90% of analyzed sequences with an average QV > QV threshold were observed.

Table 8  Fragment analysis run modules

<table>
<thead>
<tr>
<th>Run module</th>
<th>Resolution range</th>
<th>Approximate run time</th>
<th>Sizing precision</th>
<th>Compatible size standards</th>
</tr>
</thead>
<tbody>
<tr>
<td>SNaPshot</td>
<td>40–120 bp</td>
<td>25 minutes</td>
<td>40–120: &lt;0.5</td>
<td>GeneScan™ 120 LIZ™ Size Standard</td>
</tr>
<tr>
<td>FragAnalysis</td>
<td>60–460 bp[1]</td>
<td>45 minutes</td>
<td>60–460: &lt;0.15</td>
<td>All except GeneScan™ 1200 LIZ™ Size Standard</td>
</tr>
<tr>
<td>LongFragAnalysis[2]</td>
<td>60–600 bp[1]</td>
<td>&lt; 2 hours</td>
<td>60–600: &lt;0.15</td>
<td>• GeneScan™ 600 LIZ™ Size Standard v2.0</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>461–600: &lt;0.3</td>
<td>• GeneScan™ 1200 LIZ™ Size Standard</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>601–800: &gt;0.45</td>
<td></td>
</tr>
</tbody>
</table>

[1] 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.

[2] Load a maximum of 48 samples per plate if you use a long run module.

Note: The following size standards have not been validated for use with the instrument. A default size standard definition is not provided in the software.

- GeneScan™ 500 LIZ™ Size Standard
- GeneScan™ 350 ROX™ Size Standard
- GeneScan™ 400HD ROX™ dye Size Standard

Manage size standard definitions

This function manages the list of size standard definitions that you can select from during plate set up.

To assign a size standard definition to a plate, see “Assign wells: run module, size standard, and dye set” on page 68.

A size standard defines the sizes in basepairs of known fragments. It is used to generate a standard curve. The standard curve is used to determine the sizing of fragments in unknown samples.

Factory-installed items cannot be edited or deleted. To create a new item from a factory-installed item, copy, edit, then save the new item.

Size standard definitions are accessible to all users.
1. Access the **Manage size standards** screen:

<table>
<thead>
<tr>
<th>From</th>
<th>Actions</th>
</tr>
</thead>
<tbody>
<tr>
<td>Plate properties</td>
<td>Touch More options &gt; Manage size standards.</td>
</tr>
<tr>
<td>Home screen</td>
<td>Touch Settings &gt; Run settings &gt; Size standards.</td>
</tr>
</tbody>
</table>

2. To create a new size standard:
   a. Touch a default size standard or a user-created size standard, then touch **Copy**.
   b. Enter a name and select a dye color.
   c. As needed, touch any of the following, then touch **Done**:
      
      **Note:** To change an existing value, add a new value, then delete the original value.
      
      - One or more fragment size values, then touch **Delete**.
      - **Add** to add a value.

3. As needed, touch a size standard of interest, then touch **Edit** or **View**.

### Manage analysis settings

#### Edit fragment analysis settings

Factory-installed items cannot be edited or deleted. To create a new item from a factory-installed item, copy, edit, then save the new item.

Analysis settings are accessible only to the user who creates them.

1. Access the **Analysis settings** screen:

<table>
<thead>
<tr>
<th>From</th>
<th>Action</th>
</tr>
</thead>
<tbody>
<tr>
<td>Plate properties</td>
<td>Touch More options &gt; Analysis settings, then select the settings to assign to the plate setup.</td>
</tr>
<tr>
<td>Home screen</td>
<td>Touch Settings &gt; Run settings &gt; Analysis settings, then manage the list of settings that you can select from during plate set up.</td>
</tr>
</tbody>
</table>

2. To create new analysis settings:
   a. Touch the default analysis settings or user-created analysis settings, then touch **Copy**.
   b. Enter a name and edit settings as needed (see “Fragment analysis settings (size calling)” on page 109 or “Sequencing settings (base calling)” on page 112).
   c. As needed, touch **View** or **Delete** (user-created settings only).

3. Touch **Done**.
Edit sequencing settings

Factory-installed items cannot be edited or deleted. To create a new item from a factory-installed item, copy, edit, then save the new item.

Analysis settings are accessible only to the user who creates them.

1. Access the Analysis settings screen:

<table>
<thead>
<tr>
<th>From</th>
<th>Action</th>
</tr>
</thead>
<tbody>
<tr>
<td>Plate properties tab</td>
<td>Touch More options ➤ Analysis settings, then select the settings to assign to the plate setup.</td>
</tr>
<tr>
<td>Home screen</td>
<td>Touch ➤ Settings ➤ Run settings ➤ Analysis settings, then manage the list of settings that you can select from during plate set up.</td>
</tr>
</tbody>
</table>

2. To create new analysis settings:
   a. Touch the default analysis settings or user-created analysis settings, then touch Copy.
   b. Enter a name and edit settings as needed (see “Sequencing settings (base calling)” on page 112).
   c. As needed, touch View or Delete (user-created settings only).

3. Touch Done.

Fragment analysis settings (size calling)

<table>
<thead>
<tr>
<th>Setting</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Size calling method</td>
<td>• <strong>Local Southern</strong>—<em>(default)</em> Determines the fragment sizes using the reciprocal relationship between fragment length and electrophoretic mobility.</td>
</tr>
<tr>
<td></td>
<td>• <strong>Global Southern</strong>—Compensates for standard fragments with anomalous electrophoretic mobility (similar to least squares methods).</td>
</tr>
<tr>
<td></td>
<td>• <strong>2nd LSQ</strong> <em>(2nd Order Least Squares)</em>—Uses regression analysis to build a bestfit size calling curve.</td>
</tr>
<tr>
<td></td>
<td>• <strong>3rd LSQ</strong> <em>(3rd Order Least Squares)</em>—Uses regression analysis to build a bestfit size calling curve.</td>
</tr>
<tr>
<td></td>
<td>• <strong>Cubic Spline Interpolation</strong>—Forces the sizing curve through all the known points of the selected size standard.</td>
</tr>
</tbody>
</table>
### Setting | Description
--- | ---
#### Analysis range
- **Full Range** *(default)* 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. View 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**.

#### Sizing range
The size range (in base pairs) appropriate for the kit you are using:
- **Full Range** for the software to analyze fragments of all sizes in the **Analysis Range**.
- **Partial Range** 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.

#### Peak amplitudes
The peak height 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 RFU, peaks with heights equal to or greater than 175 RFU are detected. Peaks with heights below 175 RFU are still displayed in the electropherogram plots but are not detected or labeled.

**Note:** Use the same peak amplitude thresholds in secondary analysis software.

#### Primer peak
If the primer peaks in your application obscure peaks of interest, select **Present**. This instructs the algorithm to ignore primer peaks. Primer peaks are still displayed in the trace.

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_LIZ_(60-600) or other size standards that include lower bp starting points may allow detection of the peaks.

#### Common settings
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.
<table>
<thead>
<tr>
<th>Setting</th>
<th>Description</th>
</tr>
</thead>
</table>
| **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. |
| **Minimum 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.                                                                               |
| **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. |
| **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. |
| **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.  
  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. |
Sequencing settings (base calling)

The default settings are optimized for sequencing of PCR amplicons from diploid genes, which are expected to have Mixed bases and which should end At PCR Stop.

For sequencing from plasmid templates, which are of pure sequence (no Mixed bases) and have longer sequence read times than PCR products, create new analysis settings and disable (uncheck) At PCR Stop and Mixed base threshold checkboxes.

<table>
<thead>
<tr>
<th>Setting</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Quality Threshold</td>
<td>• Basecall assignment (ambiguous bases):</td>
</tr>
<tr>
<td></td>
<td>- Do not assign Ns to basecalls</td>
</tr>
<tr>
<td></td>
<td>- Assign Ns to basecalls with QV&lt;5— Bases with a QV less than the threshold display N instead of the base letter</td>
</tr>
<tr>
<td></td>
<td>• End base—Last base on which to perform basecalling:</td>
</tr>
<tr>
<td></td>
<td>- At PCR Stop</td>
</tr>
<tr>
<td></td>
<td>- After X number of bases</td>
</tr>
<tr>
<td></td>
<td>- After X number of Ns in X number of bases</td>
</tr>
<tr>
<td></td>
<td>- After X number of Ns</td>
</tr>
<tr>
<td>Note:</td>
<td>If you have PCR products with sequences that end while data is still being collected, select the At PCR Stop checkbox.</td>
</tr>
<tr>
<td>Mixed bases threshold</td>
<td>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.</td>
</tr>
<tr>
<td>Clear range methods</td>
<td>• Use quality values—Sets a window with a specified number of allowed low-quality bases by removing bases until there are &lt;X number of bases per Z number of bases with QV &lt;Y.</td>
</tr>
<tr>
<td></td>
<td>• Use base positions—Specifies the first and last base in the range to consider, or trims the specified number of bases from the 3’ end.</td>
</tr>
<tr>
<td></td>
<td>• Mask base positions before—Specifies the base position before which to disregard bases.</td>
</tr>
</tbody>
</table>

Modify the default file name convention

The default file name convention determines how the data files (AB1 or FSA) associated with a plate are named.

The default file name convention is:

<table>
<thead>
<tr>
<th>Application</th>
<th>Default settings</th>
</tr>
</thead>
<tbody>
<tr>
<td>Fragment analysis</td>
<td>&lt;well&gt;<em>&lt;sample name&gt;</em>&lt;sample type&gt;_&lt;date and timestamp&gt;.fsa</td>
</tr>
<tr>
<td>Sequence analysis</td>
<td>&lt;well&gt;<em>&lt;sample name&gt;</em>&lt;date and timestamp&gt;.abl</td>
</tr>
<tr>
<td>Sequence analysis with the Sanger variant analysis option selected</td>
<td>&lt;well&gt;<em>&lt;sample name&gt;</em>&lt;amplicon&gt;<em>&lt;specimen&gt;</em>&lt;date and timestamp&gt;.abl</td>
</tr>
</tbody>
</table>
1. Access the **File name convention** screen:

<table>
<thead>
<tr>
<th>From</th>
<th>Action</th>
</tr>
</thead>
<tbody>
<tr>
<td>Plate properties screen</td>
<td>Select the <strong>Properties</strong> tab, then touch More options  File name convention.</td>
</tr>
<tr>
<td>Home screen</td>
<td>Touch 📜 <strong>Settings</strong>  Run settings  File name convention.</td>
</tr>
</tbody>
</table>

2. Touch **Attributes**.

3. Select the attributes to include in the data file name.

   ![Select Attributes](image)

   For information on creating custom fields to include in file name conventions, see “Define custom fields” on page 73.

4. Touch **Done**.

5. Touch and drag attributes up or down in the list.

6. Touch **Done**.

### Manage instrument settings

**Display instrument hardware and software information**

In the home screen:

1. Touch 📜 **Settings**  Instrument settings  About to access the instrument information:
   - Model name
   - Ethernet IP address
   - Ethernet MAC address
   - Wireless IP address
   - Wireless MAC address
2. *(Optional)* Touch **EULA** to display the end-user licence agreement or touch **Details** to display additional instrument information.

### Change the instrument name

If the instrument is linked to the Cloud, only a Cloud administrator for the instrument can change the instrument name. The instrument name can be changed by a Cloud administrator on the instrument or in InstrumentConnect.

In the home screen:

1. Touch **Settings** → **Instrument Settings** → **Instrument name**.
2. Touch the **Instrument Name** field, enter an instrument name, then touch **Done**.
3. Touch **OK**.

When you change the instrument name, the software unlinks all instrument profiles.

### Enable Demo mode

Demo mode allows you to use all features of the system and provides simulated real-time data and results. You cannot save plates or settings in Demo mode.

In the home screen:

1. Touch **Settings** → **Instrument settings** → **Turn Demo mode on**.
2. Touch **OK** to allow the instrument to restart.
   - The instrument automatically restarts in Demo mode.

### Manage date and time settings

In the home screen:

1. Touch **Settings** → **Instrument settings** → **Date and Time**.
2. Slide the control to select a time-setting option:
   - The instrument automatically detects the time via the network.
   - Enter the time manually.
3. Touch **Time zone**, then select a time zone.
4. Touch **Date/Format**, then select the display order for the month, day, and year.
5. Touch **Time/Format**, then select a 12-Hour or 24-Hour time display format.
6. Click **OK**.

### Manage the network configuration

**Note:** For a direct connection between the instrument and a computer, set up a wired connection.

In the home screen:

2. Touch Edit, or touch one of the network settings fields.

3. *(Optional)* Edit the Wireless network settings.
   a. Select a Network that was automatically detected by instrument.
   b. Enter a password, if prompted.
   c. Click Join.
   d. Click OK when the authentication is completed.

4. *(Optional)* Edit the Wired network settings.
   a. Select DHCP or Static IP.
      An IP address is automatically assigned if DHCP is selected.
   b. *(Static IP only)* Enter an IP address, Subnet mask, Default gateway, Primary DNS server, and Secondary DNS server.
      For more information, see “Determine IP address for a computer on a network” on page 113.

5. Touch OK.

Check for software updates (administrator only)

In the home screen:
1. Touch Settings → Instrument settings → About.

2. Touch Check for updates.
   If the software update is located on a USB, it may take 10–15 seconds for the instrument to recognize the USB.

3. Touch:
   - Update if an update is available.
   - Cancel if there is no update available.

   A message is displayed during the software updated, then the instrument automatically restarts.
Manage instrument profiles on the instrument

Local instrument profile roles and functions

<table>
<thead>
<tr>
<th>Instrument profile</th>
<th>Location</th>
<th>Functions allowed</th>
</tr>
</thead>
</table>
| Standard           | Local[1] | • Create, save, open, import, and run plate setups  
|                    |          | • Create and modify run settings 
|                    |          | • View and export results |
| Administrator      | Local[1] | All standard user functions, plus:  
|                    |          | • Create or delete an instrument profile 
|                    |          | • Change an instrument profile from Standard to Administrator access 
|                    |          | • Reset an instrument profile PIN for another user 
|                    |          | • Unlock instrument touchscreen 
|                    |          | • Backup user data (plates and results) 
|                    |          | • Delete Cloud instrument profile from the instrument, which removes the instrument from the InstrumentConnect. The user can link the instrument to the Cloud again using a local instrument profile. After a user relinks to the Cloud, the Cloud instrument profile is displayed on the home screen and the instrument is listed in the InstrumentConnect. |
| Guest              | Local    | All standard user functions, except:  
|                    |          | • Cannot link to the Thermo Fisher Cloud 
|                    |          | • Cannot modify a public plate setup 

**Note:** Standard instrument profiles cannot access Guest instrument profile plate setups unless the Plate Setup Security is set to Shared.

[1] The first user who signs in to the instrument is assigned a local profile with administrator role.

For more information, see Chapter 3, “Use the instrument with the Thermo Fisher Cloud”

Create a local instrument profile for another user (administrator only)

An instrument profile can be assigned standard or administrator roles. For more information, see “Change the role of a local instrument profile (administrator only)” on page 135.

In the home screen:

1. Touch 📅.
2. Touch All accounts.
3. Touch Add Profile.
4. Touch **User name**, enter an instrument profile name, then touch **Done**.
5. Touch **PIN (4 digits required)**, enter a four-digit numerical PIN, then touch **Enter**.
6. Touch **Confirm PIN**, reenter the PIN, then touch **Enter**.

7. Touch **Create profile**.

8. Touch **Done**.

In the home screen:

1. Touch 🔄.

2. Touch **All accounts**.

3. Touch the account of interest.

4. Slide the control from **Standard** to **Administrator** or from **Administrator** to **Standard**.

5. Touch **Done**.

Local administrators and Cloud administrators can delete local and Cloud profiles.

**IMPORTANT!** Before proceeding, back up user data to retain plates and results (“Back up user data (plates and results) (administrator only)” on page 138).

In the home screen:

1. Touch 🔄.

2. Touch **All accounts**.

3. Touch the instrument profile to delete.

4. Touch **Delete account**.

5. Touch **Yes** to confirm.

6. Touch **Done**.

Local administrators and Cloud administrators can delete the PIN for a local instrument profile.

In the home screen:

1. Touch 🔄.

2. Touch **All accounts**.

3. Touch the instrument profile of interest.

4. Touch **Delete PIN**.

The user will be prompted for a new pin upon the next sign in.
5. Touch Yes to confirm.

6. Touch Done.

Create your own local instrument profile

If you are not signed in to the instrument when you link the instrument to your Cloud account, the software creates a local instrument profile with Standard role using the FirstName LastInitial of your Cloud account.

For more information, see “Link the instrument to your Thermo Fisher Cloud account” on page 50.

Change your own local instrument profile PIN

Sign in to access these features (see “Sign in” on page 33).

1. Touch .

2. Touch Edit.

3. Touch Old PIN, enter your current PIN, then touch Enter.

   Touch the Show PIN checkbox to switch the PIN display on or off.

4. Touch PIN (4 digits required), enter a new four-digit numerical PIN, then touch Enter.

5. Touch Confirm PIN, reenter your new PIN, then touch Enter.

6. Touch Done.

Manage storage space

Automatic file cleanup

Before starting a run, the instrument calculates the total amount of storage space required to save the run. If the required storage space is not available, the instrument deletes files associated with the oldest exported plates until sufficient space is available.

Note: Only complete plates that have been auto exported (saved to Cloud, network, or USB) or manually exported (using Settings ▶ Run History ▶ plate name ▶ Export) are deleted.

If the required storage space is not available and no plates have been exported, the instrument displays a notification indicating that there is not enough storage space.

You can export plates and delete plates, then start the run again.
Export or delete a plate setup (PSM file)

1. Touch **Set up run**, then touch 🖐️ **My instrument**.
2. Touch **Manage** at the bottom left of the screen.
3. Touch a plate, then touch **Export** or **Delete**.
4. If you touched:
   - **Export**, select a storage location, then touch **Export**.
   - **Delete**, then touch **Yes** to delete the plate setup.

Export results from the instrument (sample data files and QC reports)

In the home screen:
1. Touch 🏛️ **Settings › Run history**.
2. Select one or more plates from the **Run History** table.
3. Touch **Export**.
4. Select a storage location.

The following data is exported for the plate:
- Fragment analysis—FSA file for each sample.
- Sequencing—AB1 file for each sample.
- Plate QC report in CSV and PDF format.

**Note:** If you select a plate, select **View**, then select **Export**, only an FSA or AB1 file for each analyzed sample is exported.

Delete a run history

In the home screen:
1. Touch Settings ➤ Run history.

2. Select one or more plates from the Run History table.

3. Touch Delete, then touch OK to confirm.

**Note:** Run histories for the oldest exported plates are automatically deleted if sufficient storage space is not available when you start a run.

---

### Back up user data (plates and results) (administrator only)

1. Select Settings ➤ Maintenance and service ➤ Back up user data.

2. Enter a name for the folder that will contain the backup data.

3. Touch the instrument profiles for which you want to back up plate and result information.

4. Touch Backup.

5. Specify a storage location, then touch Export.

   A folder containing plate setup and sample data file is backed up to the specified location.

*(Optional)* After backing up, you can:

- Delete the plates (see “Delete a run history” on page 137).
- Open the CSV files in the folder on another instrument or in the Plate Manager.
Maintain the instrument

- Regular maintenance tasks ........................................... 139
- Manage the cartridge ................................................ 141
- Install cathode buffer ................................................ 149

Regular maintenance tasks

Check the cathode buffer fill level

When a cartridge is installed in the instrument, the volume of buffer in the Cathode Buffer Container (CBC) must be above the fill line.

Check the cathode buffer fill level before each run. It is recommended to check one time each week if the instrument is not in use.

In the home screen:

1. Touch , touch Eject plate, then open the instrument door when prompted.

2. Press the release button on the autosampler to open the lid, then remove the CBC.

3. Ensure that the level of buffer is above the fill line.
   If the buffer is at or below the fill line, see “Assemble the SeqStudio™ Genetic Analyzer Cathode Buffer Container (CBC)” on page 149 and “Insert the Cathode Buffer Container” on page 150.
4. Reinstall the CBC.

5. Close the autosampler lid: Press down on the center of the lid or press down on both sides of the lid with equal pressure until the lid clicks shut.

6. Touch **Retract plate**, close the instrument door, then touch **Done** when the **Consumables Status** screen is displayed.

**Clean the instrument exterior and touchscreen**

Power off the instrument before cleaning.

**IMPORTANT!** The instrument does not maintain the correct temperature conditions for the cartridge when it is powered off. Avoid cartridge exposure to ambient temperature.

- Wipe the exterior of the instrument with a lint-free cloth and deionized water.

**IMPORTANT!** Do not allow any moisture to reach the interior of the instrument through the door.

- Wipe the touchscreen with a lint-free cloth and glass cleaner.

**Clean the autosampler**

The autosampler is attached to the instrument.

Clean spills to prevent a build-up of crystallized polymer or dried salt from the buffers.

Power off the instrument before cleaning the autosampler.

1. Wipe the exterior of the autosampler with a lint-free cloth and deionized water.

**IMPORTANT!** Do not pour liquid directly on to the autosampler. This will damage the heater at the bottom of the cathode buffer reservoir.

**Note:** Do not use detergents or solvents.

2. Use a lint-free cloth to absorb any liquid spilled in the individual wells of the autosampler.
# Manage the cartridge

## Cartridge storage

<table>
<thead>
<tr>
<th>Condition</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Shipping</strong></td>
<td>Shipped at 2–8°C. Store upright at 2–8°C upon receipt. Save the white storage box and optical cover for off-instrument cartridge storage.</td>
</tr>
</tbody>
</table>
| **On-instrument storage** | For routine use, can be used and stored on the instrument for up to 4 months. If you store the cartridge on-instrument:  
  • The instrument must be powered on.  
  • A Cathode Buffer Container must also be installed.  
  The instrument keeps the components under the following conditions when it is powered on and in **Cartridge storage mode**:  
  • **Optical detection window**—Covered  
  • **Capillary array electrodes**—Submerged in cathode buffer (buffer must be above the fill line in the Cathode Buffer Container)  
  • **Polymer**—Chilled  
  • **Anode buffer**—Ambient temperature  
  **IMPORTANT!** The instrument does not maintain the correct temperature conditions for the cartridge when it is powered off. Avoid cartridge exposure to ambient temperature. |
| **Off-instrument storage** | For intermittent use, can be stored off-instrument until the expiry date on the label or up to 4 months after first use. Store upright at 2–8°C, with an integrated capillary protector (ICP) and optical cover installed (see “Store the cartridge” on page 146).  
  **Note:** After you remove the cartridge from the instrument, install an ICP within a few minutes. Avoid cartridge exposure to ambient temperature. |
| **Reuse**          | Can be removed from an instrument then inserted again on the same instrument or a different instrument, if it was stored properly at 2–8°C and has not expired or exceeded 125 injections.  
  Information about the cartridge installation and usage is retained in the cartridge history [Settings ➤ Cartridge ➤ Instrument–cartridge history]. |
### Table 10  Storage information for the SeqStudio™ Genetic Analyzer Cartridge v2 (Cat. No. A41331)

<table>
<thead>
<tr>
<th>Condition</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Shipping</strong></td>
<td>Shipped at 2–8°C. Store upright at 2–8°C upon receipt. Save the white storage box and optical cover for off-instrument cartridge storage.</td>
</tr>
<tr>
<td><strong>On-instrument storage</strong></td>
<td>For routine use, can be used and stored on the instrument for up to 6 months. If you store the cartridge on-instrument:</td>
</tr>
<tr>
<td></td>
<td>• The instrument must be powered on.</td>
</tr>
<tr>
<td></td>
<td>• A Cathode Buffer Container must also be installed.</td>
</tr>
<tr>
<td></td>
<td>The instrument keeps the components under the following conditions when it is powered on and in <strong>Cartridge storage mode</strong>:</td>
</tr>
<tr>
<td></td>
<td>• Optical detection window—Covered</td>
</tr>
<tr>
<td></td>
<td>• Capillary array electrodes—Submerged in cathode buffer (buffer must be above the fill line in the Cathode Buffer Container)</td>
</tr>
<tr>
<td></td>
<td>• Polymer—Chilled</td>
</tr>
<tr>
<td></td>
<td>• Anode buffer—Ambient temperature</td>
</tr>
<tr>
<td><strong>IMPORTANT!</strong></td>
<td>The instrument does not maintain the correct temperature conditions for the cartridge when it is powered off. Avoid cartridge exposure to ambient temperature.</td>
</tr>
<tr>
<td><strong>Off-instrument storage</strong></td>
<td>For intermittent use, can be stored off-instrument until the expiry date on the label or up to 6 months after first use. Store upright at 2–8°C, with an integrated capillary protector (ICP) and optical cover installed (see “Store the cartridge” on page 146).</td>
</tr>
<tr>
<td></td>
<td><strong>Note:</strong> After you remove the cartridge from the instrument, install an ICP within a few minutes. Avoid cartridge exposure to ambient temperature.</td>
</tr>
<tr>
<td><strong>Reuse</strong></td>
<td>Can be removed from an instrument then inserted again on the same instrument or a different instrument, if it was stored properly at 2–8°C and has not expired or exceeded 250 injections.</td>
</tr>
<tr>
<td></td>
<td>Information about the cartridge installation and usage is retained in the cartridge history (Settings &gt; Cartridge &gt; Instrument–cartridge history).</td>
</tr>
</tbody>
</table>

### Set cartridge storage mode (administrator only)

If a cartridge is installed on the instrument, the instrument will enter **Cartridge storage mode** after the time you specify.

The instrument keeps the components under the following conditions when it is powered on and in **Cartridge storage mode**:

- **Optical detection window**—Covered
- **Capillary array electrodes**—Submerged in cathode buffer (buffer must be above the fill line in the Cathode Buffer Container)
- **Polymer**—Chilled
- **Anode buffer**—Ambient temperature

In the home screen:
1. Touch Settings → Cartridge → Cartridge Storage Mode.

2. Select the duration of instrument inactivity before the instrument enters Cartridge Storage Mode.

3. Touch OK.

This function lists the cartridges that have been installed on this instrument.

1. Touch Settings → Cartridge → Instrument-cartridge history.

2. (Optional) Touch Export.

This function lists the instruments on which the cartridge has been installed.

Touch Settings → Consumables status, then touch Cartridge history.
Chapter 10 Maintain the instrument

Manage the cartridge

Fill the capillary array and refresh the polymer delivery system

The functions accessed from Cartridge maintenance are performed automatically during a run. Do not use these commands to manually perform these functions unless instructed to do so in troubleshooting or by Support.

In the home screen:

1. Touch 🛠 Settings ➔ Cartridge ➔ Cartridge maintenance.

2. Select Fill array or Refresh PDS.

3. Touch ✕ to close the screen when the function ends.

Remove the cartridge

Perform these steps if you are replacing the cartridge or storing it off-instrument. Removal of the cartridge after each run is not required.

For appropriate off-instrument storage conditions, see the following tables:
• For the SeqStudio™ Genetic Analyzer Cartridge, see Table 1 on page 17
• For the SeqStudio™ Genetic Analyzer Cartridge v2, see Table 2 on page 18

1. Touch 🛠, touch 🚹 Eject cartridge, then open the instrument door when prompted.

2. Hold the cartridge at the hand hold above the capillaries, then pull to remove it from the instrument.

3. Close the instrument door.

For more information, see “Store the cartridge” on page 146.

Insert the cartridge

1. If a cartridge is installed:
   a. Touch 🛠, touch 🚹 Eject cartridge, then open the instrument door when prompted.

   b. Remove the used cartridge.
2. Prepare the cartridge.
   a. Remove the cartridge from the box.
      
      **Note:** Save the box for off-instrument cartridge storage.

   b. Remove the optical cover from the cartridge by grasping the finger holds, then pulling toward you.
      
      **Note:** Save the optical cover for off-instrument cartridge storage. Avoid touching the capillaries that are protected by the optical cover.

   c. Pinch the clamp on the SeqStudio™ Integrated Capillary Protector, then pull down.
      
      Discard the SeqStudio™ Integrated Capillary Protector. The SeqStudio™ Integrated Capillary Protector is single-use. Use a new SeqStudio™ Integrated Capillary Protector if you store the cartridge.
3. Grasp the cartridge above the capillaries.

4. Position the cartridge:
   a. Orient the cartridge with the embossed arrow pointing toward the rear of the instrument.
   b. Align the guides at the top of the cartridge with the insertion rails in the instrument.

5. Slide the cartridge into the instrument until it clicks into place.

6. Close the instrument door, then touch Done when the Consumables Status screen is displayed.

   The cartridge is initialized.

---

**Store the cartridge**

1. Touch ②, touch Eject cartridge, then open the instrument door when prompted.

2. Hold the cartridge at the hand holds above the capillaries, then pull to remove it from the instrument.

3. Close the instrument door.

4. Carefully place the optical cover on the cartridge to avoid damage to the capillaries.
5. Place a new SeqStudio™ Integrated Capillary Protector on the cartridge: pinch the clamp on the ICP, then push up on to the capillaries.

6. Place the cartridge in the white storage box.

7. Store upright at 2–8°C.
   
   **Note:** Avoid cartridge exposure to ambient temperature.

   **IMPORTANT!** Do not freeze the cartridge. It cannot be used after freezing.

---

The SeqStudio™ Integrated Capillary Protector (ICP) is a single-use protective cover that clamps onto the SeqStudio™ Genetic Analyzer Cartridge or the SeqStudio™ Genetic Analyzer Cartridge v2. The ICP prevents the capillary array from drying out during off-instrument storage of the cartridge, and is removed before insertion of the cartridge into the SeqStudio™ Genetic Analyzer.

Each cartridge is supplied with an ICP for shipping and one additional ICP for off-instrument cartridge storage.

**Figure 19** SeqStudio™ Integrated Capillary Protector

![Clamp mechanism for attaching to cartridge](image)

**IMPORTANT!** Remove the Integrated Capillary Protector before installing the cartridge into the instrument. Installing the cartridge with the ICP in place can damage the capillary array.
SeqStudio™ Integrated Capillary Protector storage

<table>
<thead>
<tr>
<th>Condition</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Shipping</td>
<td>Is shipped at 2–8°C.</td>
</tr>
<tr>
<td></td>
<td>Before opening, can be stored until expiry date on label at 2–8°C.</td>
</tr>
<tr>
<td></td>
<td>Discard the shipping ICP when you insert a new cartridge in the instrument.</td>
</tr>
<tr>
<td>Reuse</td>
<td>Do not reuse.</td>
</tr>
<tr>
<td></td>
<td>Use a new ICP for off-instrument cartridge storage.</td>
</tr>
<tr>
<td></td>
<td><strong>IMPORTANT!</strong> If an ICP is used for off-instrument cartridge storage more than one time, the capillary array will not be kept fully hydrated.</td>
</tr>
</tbody>
</table>

Long-term on-instrument cartridge storage

You can leave the cartridge installed in the instrument if the instrument is powered on and a CBC is installed. Replace the CBC every 2 weeks.

**IMPORTANT!** If the instrument will be idle for longer than the shelf life of the cartridge components, remove the cartridge and cathode buffer, then power off the instrument.

Table 11  Cartridge storage

<table>
<thead>
<tr>
<th>Cartridge</th>
<th>Storage</th>
</tr>
</thead>
<tbody>
<tr>
<td>SeqStudio™ Genetic Analyzer Cartridge [Cat. No. A33671]</td>
<td>See Table 1 on page 17</td>
</tr>
<tr>
<td>SeqStudio™ Genetic Analyzer Cartridge v2 [Cat. No. A41331]</td>
<td>See Table 2 on page 18</td>
</tr>
</tbody>
</table>

**IMPORTANT!** The instrument does not maintain the correct temperature conditions for the cartridge when it is powered off. Avoid cartridge exposure to ambient temperature.
Install cathode buffer

SeqStudio™ Genetic Analyzer Cathode Buffer Container storage

<table>
<thead>
<tr>
<th>Condition</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Shipping</td>
<td>Is shipped at ambient temperature. Store at 2–8°C upon receipt.</td>
</tr>
<tr>
<td>On-instrument storage</td>
<td>After installation, can be stored for up to 2 weeks when the instrument is powered on and in <em>Cartridge storage mode</em>.</td>
</tr>
<tr>
<td>Off-instrument storage</td>
<td>Before opening, can be stored until expiry date on label at 2–8°C.</td>
</tr>
<tr>
<td>Reuse</td>
<td>Do not remove the CBC from the instrument for storage. Do not reuse.</td>
</tr>
</tbody>
</table>

Remove the SeqStudio™ Genetic Analyzer Cathode Buffer Container

Perform these steps if you are replacing the Cathode Buffer Container. It is not necessary to remove the CBC after each run.

1. Touch 🔄, touch 🔄 Eject plate, then open the instrument door when prompted.
2. Press the release button on the autosampler to open the lid.
3. Lift the CBC out of the autosampler.

Assemble the SeqStudio™ Genetic Analyzer Cathode Buffer Container (CBC)

Equilibrate the CBC to room temperature (15 minutes to overnight) before assembling.

On a clean and level surface:

1. Ensure that the buffer is above the fill line.
2. Carefully peel off the seal.
3. Wipe off any buffer on top of the CBC with a lint-free tissue. Ensure that the top of the container is dry.
4. Place the reservoir septa on the CBC, then press firmly to seat the septa.

Note: The CBC is filled significantly above Fill Line to account for evaporation. Replace the CBC when the fluid level is at or below the fill line.

**Insert the Cathode Buffer Container**

Perform these steps if the Cathode Buffer Container has not been installed, if the CBC on the instrument has expired, or if the buffer level is at or below the fill line.

Install the CBC before you install the cartridge.

See Figure 2 on page 13 for the position of the cathode buffer on the instrument.

1. Touch 📡, touch ➤ Eject plate, then open the instrument door when prompted.

2. Press the release button on the autosampler to open the lid.

3. Insert the cathode buffer in the autosampler with the notch positioned in the back right.

See Figure 8 on page 19.
4. Press the autosampler lid until it clicks shut.

5. Touch Retract plate, then close the instrument door.
Troubleshooting

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- Troubleshooting workflow ........................................... 153
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Troubleshooting resources

<table>
<thead>
<tr>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>Troubleshooting Sanger sequencing data User Bulletin</td>
<td>MAN0014435</td>
</tr>
<tr>
<td>DNA Sequencing by Capillary Electrophoresis Chemistry Guide Second Edition</td>
<td>4305080</td>
</tr>
<tr>
<td>DNA Fragment Analysis by Capillary Electrophoresis User Guide</td>
<td>4474504</td>
</tr>
</tbody>
</table>
Troubleshooting workflow

Follow this general workflow when you are troubleshooting:

Review the analyzed data.

▼

Review the raw data, then review the EPT plot.

▼

(Fragment analysis) Check size standard quality ("Check size standard quality" on page 155).

▼

Check the CBC buffer fill level.

▼

Check that the cartridge is installed and engaged, and that capillary tips are not bent or damaged.

▼

Check that the sample plate is installed, confirm that samples are in the wells that are specified in the plate setup, and make sure that samples are at bottom of wells (no bubbles are visible).

Export log files for plates, install runs, injections, and instrument

Export log files and provide them to Thermo Fisher Scientific if directed to do so by Technical Support.

In the home screen:

1. Touch Settings ➔ Maintenance and Service ➔ Export logs.

2. Select one of the following options.
   - **Export logs for the last injection**—Includes all run types: analysis run, install run, and calibration run.
   - **Export logs for the last / current plate**—Includes all run types.
   - **Export logs for selected plates**—Includes options to export logs for regular runs and install check runs for the analysis run for the current user.
   - **Export recent instrument server logs**—Includes instrument export logs only.

3. Touch Export.

4. Select a storage location.
   
   **Note:** Log files can be large. Select a location with adequate storage space.
   
   A ZIP file containing log information is exported.
View the raw data and the EPT plot

The EPT view (ElectroPhoresis Telemetry) shows instrument data conditions (currents, temperatures, electrophoresis voltage) as a function of time.

When a run is complete, in the home screen:

1. Touch Results.
2. Touch List view.
3. Touch an injection group.
4. Touch a sample file name.
   If the data triggered any quality alerts, a QC alerts screen is displayed.
   Click View data to display the trace for the sample.
5. Touch or to scroll to the raw data or EPT Plot.

Data quality alerts

<table>
<thead>
<tr>
<th>Quality alert</th>
<th>Description</th>
<th>Action</th>
</tr>
</thead>
<tbody>
<tr>
<td>Offscale peaks. Adjust the injection parameters and/or the sample</td>
<td>At least 10 scans have saturated the CCD camera.</td>
<td>• Reduce the injection voltage.</td>
</tr>
<tr>
<td>concentration.</td>
<td></td>
<td>• Dilute the sample.</td>
</tr>
<tr>
<td>No sample was detected.</td>
<td>Poor signal-to-noise ratio with low signal detected.</td>
<td>• Verify that the sample volume follows recommendations in the user manual.</td>
</tr>
<tr>
<td></td>
<td></td>
<td>• Troubleshoot upstream PCR and sequencing steps.</td>
</tr>
</tbody>
</table>

Sizecalling and basecalling quality alerts

Table 12 Sizecalling quality alerts

<table>
<thead>
<tr>
<th>Quality alert</th>
<th>Description</th>
<th>Action</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sizing quality value is low due to poor size standard peak quality. Peak</td>
<td>Low resolution or poor quality data is present.</td>
<td>• Re-inject the sample.</td>
</tr>
<tr>
<td>height uniformity is low or the fitting quality in sizing is poor.</td>
<td></td>
<td>• If the problem persists, check the sample quality.</td>
</tr>
<tr>
<td>Sizecaller found broad peak(s) in the size standard peak(s).</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Sizing quality value is in the intermediate range; check size standard data</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
Quality alert | Description | Action
--- | --- | ---
The number of size standard peaks detected is less than what is defined in the size standard. | Size standard definition includes peaks that are not present in the sample. Example: Sample peaks are detected up to 500 bp, but the size standard definition includes peak sizes that are >500 bp. | Use or create a size standard definition with the appropriate number of peaks and peak sizes.
The analysis range is too small. Correct the analysis range in analysis settings and re-analyze in secondary analysis software or re-inject sample. | Various causes. | • Analyze the data in a secondary analysis software with a corrected analysis range. • Re-inject the sample.

Table 13 Basecalling quality alerts

<table>
<thead>
<tr>
<th>Quality alert</th>
<th>Description</th>
<th>Action</th>
</tr>
</thead>
<tbody>
<tr>
<td>Basecalling failed due to poor quality data.</td>
<td>Poor quality data is present.</td>
<td>• Re-inject the sample. • If the problem persists, prepare fresh sample. • Troubleshoot upstream PCR and sequencing steps.</td>
</tr>
</tbody>
</table>

Check size standard quality

1. Touch 🎎 Settings ➔ Run history.
2. Touch a plate name, then touch View.
3. Touch a sample file name, then touch View.
   If the data triggered any quality alerts, a QC alerts screen is displayed.
4. Touch View data to display the trace.
5. Touch on the left border of the trace, then deselect all dyes except the size standard dye (red or orange).

6. As needed, touch on the right border of the trace to zoom on the trace.

Instrument troubleshooting

<table>
<thead>
<tr>
<th>Observation</th>
<th>Possible cause</th>
<th>Recommended action</th>
</tr>
</thead>
<tbody>
<tr>
<td>There was a loss of power to the instrument</td>
<td>There was a power failure.</td>
<td>Restart the instrument. The Sign In screen is displayed. A run that was in progress at the time of the power failure must be restarted.</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Run a control sample to ensure that the consumables have not degraded, especially if the consumables reached room temperature. Replace the consumables if the results with a control sample show that the consumables have degraded.</td>
</tr>
<tr>
<td>The RFID tags on the cartridge or the cathode buffer are not read</td>
<td>The label on the cartridge or the Cathode Buffer Container is damaged, not positioned properly, or has been removed.</td>
<td>Ensure that the labels are present and not visibly damaged. Ensure that the consumables are installed correctly. The Cathode Buffer Container should be firmly seated in the autosampler. The cartridge will click into place when it is installed correctly. Insert consumables that have previously had RFID tags read. Contact technical support if the RFID tags are not read.</td>
</tr>
<tr>
<td>The run stopped and Resume is displayed</td>
<td>A user paused the run.</td>
<td>Touch Resume to continue the run.</td>
</tr>
<tr>
<td>The amber light is blinking</td>
<td>The run was paused.</td>
<td>Touch Resume to continue the run.</td>
</tr>
<tr>
<td></td>
<td>The instrument door is open.</td>
<td>Close the instrument door.</td>
</tr>
<tr>
<td></td>
<td>There was an instrument error.</td>
<td>Follow the instructions in the error message. Restart the instrument.</td>
</tr>
<tr>
<td>The electrophoresis failed or Current check failed is displayed</td>
<td>There is insufficient cathode buffer.</td>
<td>Check the fill line on the Cathode Buffer Container. Replace the Cathode Buffer Container if the buffer is at or below the fill line.</td>
</tr>
</tbody>
</table>
### Cartridge troubleshooting

<table>
<thead>
<tr>
<th>Observation</th>
<th>Possible cause</th>
<th>Recommended action</th>
</tr>
</thead>
<tbody>
<tr>
<td>The electrophoresis failed or <strong>Current check failed</strong> is displayed</td>
<td>The Cathode Buffer Container has been installed on the instrument for more than two weeks or used for more than 125 injections.</td>
<td>Replace the Cathode Buffer Container.</td>
</tr>
<tr>
<td></td>
<td>The septum on either the Cathode Buffer Container or the sample plate is not installed correctly.</td>
<td>Ensure that the septa are fully inserted into both the Cathode Buffer Container and the sample plate.</td>
</tr>
<tr>
<td></td>
<td>Buffer or other liquid was spilled on top of the reservoir septum or on top of the autosampler.</td>
<td>Wipe the spill with a lint-free cloth.</td>
</tr>
<tr>
<td></td>
<td>There is condensation on the Cathode Buffer Container or around the reservoir septum.</td>
<td>Wipe the condensation with a lint-free cloth. Ensure that the humidity in the lab is non-condensing.</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Observation</th>
<th>Possible cause</th>
<th>Recommended action</th>
</tr>
</thead>
<tbody>
<tr>
<td>There are crystals on the cartridge capillary array</td>
<td>Small amounts of leakage around the cartridge capillary array are normal.</td>
<td>No action is required.</td>
</tr>
<tr>
<td>There are crystals on the cartridge polymer delivery system</td>
<td>There is a leak in the polymer delivery system.</td>
<td>Run a control sample to determine if the cartridge function is affected.</td>
</tr>
<tr>
<td>Poor-quality data is observed after prolonged drying of the capillary tips</td>
<td>The capillary tips develop blockages if they are allowed to dry out.</td>
<td>Use an Integrated Capillary Protector when the cartridge is off the instrument to prevent the capillary tips from drying out. Clear the blockage by running polymer through the capillaries.</td>
</tr>
<tr>
<td></td>
<td></td>
<td>1. Touch 🗯️ <strong>Settings</strong> ➞ <strong>Cartridge</strong> ➞ <strong>Cartridge maintenance</strong> ➞ <strong>Fill array</strong>.</td>
</tr>
<tr>
<td></td>
<td></td>
<td>2. Touch 🕒 when the function ends.</td>
</tr>
<tr>
<td></td>
<td></td>
<td>3. Run a control sample.</td>
</tr>
<tr>
<td></td>
<td></td>
<td>4. Replace the cartridge if there is poor-quality data with the control sample.</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Follow the recommendations for cartridge storage to prevent drying of the capillary tips. See “Cartridge storage” on page 17.</td>
</tr>
</tbody>
</table>
## Sample and data troubleshooting

See also “Data quality alerts” on page 102, “Sizecalling and basecalling quality alerts” on page 102, and Troubleshooting Sanger sequencing data User Bulletin (Pub. No. MAN0014435).

<table>
<thead>
<tr>
<th>Observation</th>
<th>Possible cause</th>
<th>Recommended action</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Offscale signal is detected</strong> is displayed</td>
<td>The sample concentration is too high.</td>
<td>Dilute the sample, prepare a new plate, and start a new run.</td>
</tr>
<tr>
<td><strong>Note:</strong> Samples are stable on the instrument for 16–24 hours. Determine if samples will be stable if a re-injection is recommended, then plan the re-injection accordingly.</td>
<td>The injection conditions are too strong for the sample.</td>
<td>Re-inject the samples with adjusted injection conditions. Injection time, voltage, or a combination of these conditions can be adjusted.</td>
</tr>
<tr>
<td><strong>There is no signal or a low signal</strong></td>
<td>The sample concentration was too low.</td>
<td>Re-inject the samples with adjusted injection conditions. Injection time, voltage, or a combination of these conditions can be adjusted.</td>
</tr>
<tr>
<td><strong>Note:</strong> Samples are stable on the instrument for 16–24 hours. Determine if samples will be stable if a re-injection is recommended, the plan the re-injection accordingly.</td>
<td>The sample volume was insufficient.</td>
<td>Use the recommended sample volume. See “Sample preparation guidelines” on page 36.</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>There were bubbles in the sample wells.</strong></td>
<td>Centrifuge the sample plate or tubes to remove the bubbles before loading onto the instrument.</td>
<td>If the samples have been run, centrifuge the plate or tubes, then set up a re-injection.</td>
</tr>
<tr>
<td><strong>The sequence reaction failed.</strong></td>
<td>Review the sequence analysis protocol, the template quality, and the template quantity. Set up a new plate and repeat the reaction. See Troubleshooting Sanger sequencing data User Bulletin (Pub. No. MAN0014435).</td>
<td></td>
</tr>
<tr>
<td><strong>The Hi-Di™ Formamide used to prepare the samples was degraded.</strong></td>
<td>Prepare the samples with fresh Hi-Di™ Formamide and repeat the experiment. See “Sample preparation guidelines” on page 36.</td>
<td></td>
</tr>
<tr>
<td><strong>The sample was prepared with the BigDye X Terminator™ Purification Kit but a BDX run module was not selected.</strong></td>
<td>Re-inject the sample with the correct module.</td>
<td></td>
</tr>
<tr>
<td><strong>The sample was degraded.</strong></td>
<td>Prepare the sample according to the protocol provided with the kits for sample preparation. See “Sample preparation guidelines” on page 36 for sample preparation guidelines.</td>
<td></td>
</tr>
<tr>
<td><strong>IMPORTANT!</strong> Do not resuspend samples in water.</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Observation</td>
<td>Possible cause</td>
<td>Recommended action</td>
</tr>
<tr>
<td>-----------------------------------------------------------------------------</td>
<td>--------------------------------------------------------------------------------</td>
<td>----------------------------------------------------------------------------------</td>
</tr>
<tr>
<td>There is no signal or a low signal</td>
<td>The sample had a high concentration of salt.</td>
<td>Dilute or desalt the samples.</td>
</tr>
<tr>
<td><strong>Note:</strong> Samples are stable on the instrument for 16–24 hours. Determine if samples will be stable if a re-injection is recommended, the plan the re-injection accordingly.</td>
<td>There was an excess of unlabeled template competing with the fragments labeled with dye during the injection.</td>
<td>Dilute or desalt the samples. See: - <em>DNA Sequencing by Capillary Electrophoresis Chemistry Guide Second Edition</em> (Pub. No. 4305080) - <em>DNA Fragment Analysis by Capillary Electrophoresis User Guide</em> (Pub. No. 4474504)</td>
</tr>
<tr>
<td>A capillary array tip is blocked.</td>
<td>Flush the capillary array.</td>
<td></td>
</tr>
<tr>
<td>The cartridge is damaged.</td>
<td>Inspect the cartridge for damage. Replace the cartridge if there is damage.</td>
<td></td>
</tr>
<tr>
<td>There was poor resolution, poor size quality, or a poor sequencing result</td>
<td>The samples degraded over time while on the instrument.</td>
<td>Analyze a maximum of 48 samples on a plate for long run modules. Additional samples will take more than 24 hours and the samples can degrade. <strong>Note:</strong> Thermal breakdown of samples is normal. Samples are stable for 16–24 hours on the instrument. Use Hi-Di™ Formamide to prepare the samples. Sample stability is optimal in Hi-Di™ Formamide.</td>
</tr>
<tr>
<td>The temperature and/or humidity in the lab is too high for optimal sample stability.</td>
<td>Ensure that the conditions in the lab are within the operating range for the instrument (15–30°C and 20–80% relative humidity). Sample stability can be lower near the high end of the operating range of the instrument for temperature and humidity. Use 20 µL of sample instead of 10 µL. A larger sample volume can reduce sample breakdown under hot and humid conditions.</td>
<td></td>
</tr>
<tr>
<td>There was a sporadic data quality failure.</td>
<td>Repeat the injection.</td>
<td></td>
</tr>
<tr>
<td><strong>Note:</strong> A sporadic data quality failure can happen occasionally.</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Poor resolution in some capillaries</td>
<td>Poor-quality samples were used.</td>
<td>See “Sample preparation guidelines” on page 36.</td>
</tr>
<tr>
<td>Observation</td>
<td>Possible cause</td>
<td>Recommended action</td>
</tr>
<tr>
<td>-------------------------------------------</td>
<td>-------------------------------------------------------------------------------</td>
<td>------------------------------------------------------------</td>
</tr>
<tr>
<td>Poor resolution in some capillaries</td>
<td>A capillary was damaged or is blocked.</td>
<td>Use a control sample to determine if the poor resolution is due to the samples are another factor.</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Try to clear the capillary, then replace the cartridge if the poor resolution is due to the cartridge and not the sample.</td>
</tr>
<tr>
<td></td>
<td></td>
<td>1. Touch • Settings • Cartridge • Cartridge maintenance • Fill array.</td>
</tr>
<tr>
<td></td>
<td></td>
<td>2. Touch • when the function ends.</td>
</tr>
<tr>
<td></td>
<td></td>
<td>3. Run a control sample.</td>
</tr>
<tr>
<td>Poor resolution in all the capillaries</td>
<td>The cartridge has been used for more than the stated number of injections, is past the labeled expiration date, or has degraded polymer from incorrect storage.</td>
<td>Replace the cartridge.</td>
</tr>
<tr>
<td></td>
<td>The Hi-Di™ Formamide that was used to prepare the samples was degraded.</td>
<td>Prepare the samples with fresh Hi-Di™ Formamide and repeat the reaction.</td>
</tr>
<tr>
<td></td>
<td></td>
<td>See:</td>
</tr>
<tr>
<td></td>
<td></td>
<td>• ”Sample preparation guidelines” on page 36</td>
</tr>
<tr>
<td></td>
<td></td>
<td>• <em>DNA Fragment Analysis by Capillary Electrophoresis User Guide</em> (Pub. No. 4474504)</td>
</tr>
<tr>
<td></td>
<td>There was too much sample injected.</td>
<td>Dilute the sample and re-inject it.</td>
</tr>
<tr>
<td>Spikes are present in raw and/or analyzed fluorescence data</td>
<td>Trace impurities passed the detector.</td>
<td>For fragment analysis, increasing the Minimum peak half width setting in the analysis settings (under Common settings) can reduce the identification of spikes as peaks.</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Note: Secondary sequencing and fragment analysis software can recognize and ignore spikes.</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Repeat the injection if necessary.</td>
</tr>
<tr>
<td>There is noise in the baseline</td>
<td>Fluorescent contamination has built up in the CBC.</td>
<td>Replace the CBC. Use a new reservoir septum when assembling the new CBC.</td>
</tr>
<tr>
<td>Sample carryover from a previous injection</td>
<td>Sample carryover on the SeqStudio™ Genetic Analyzer can occur in trace amounts when previous injections are off-scale. Very strong peaks, for example, primer peaks in a fragment analysis sample, are typically visible in subsequent injections.</td>
<td>Replace the reservoir septum on the CBC before the next injection to minimize the carryover effect.</td>
</tr>
<tr>
<td>Observation</td>
<td>Possible cause</td>
<td>Recommended action</td>
</tr>
<tr>
<td>-----------------------------------------</td>
<td>-------------------------------------------------------------------------------</td>
<td>------------------------------------------------------------------------------------</td>
</tr>
<tr>
<td>Dye blobs are seen in the sequencing data</td>
<td>Impurities remained in the sample after the sample purification. The impurities cause dye blobs to appear in the sequencing data.</td>
<td>Improve the sample purification method. See “Sample preparation guidelines” on page 36 for guidelines.</td>
</tr>
<tr>
<td>Extra peaks are present in the sequencing traces</td>
<td>There was renaturation of the sample.</td>
<td>Heat-denature the samples prepared with fresh Hi-Di™ Formamide, then immediately place the samples on ice.</td>
</tr>
<tr>
<td>There is low signal. With very low signal, the peaks are barely visible in the baseline noise.</td>
<td></td>
<td>Check the raw data, the raw data signal intensity, and average raw signal-to-noise ratio, then:</td>
</tr>
<tr>
<td></td>
<td>• Increase the injection time and reinject.</td>
<td></td>
</tr>
<tr>
<td></td>
<td>• Remake the sample. Ensure that you are using:</td>
<td></td>
</tr>
<tr>
<td></td>
<td>– Enough sequencing template</td>
<td></td>
</tr>
<tr>
<td></td>
<td>– Enough primer and/or a sufficient concentration of primer</td>
<td></td>
</tr>
<tr>
<td>There is a heterozygous insertion-deletion (het indel) that is causing multiple peaks to appear at the same basecall position. The sequence can appear “clean” for some number of bases until the het indel is encountered.</td>
<td></td>
<td>Examine the analyzed trace. A het indel typically has single peaks at the 5’ end, then part-way through the trace, two peaks appear in almost every position to the end of the trace. This pattern occurs when one copy of the gene has an insertion or deletion relative to the other copy of the gene. When aligning your sequence to a reference sequence, a series of bases may have been inserted or deleted in an allele. These indels can be encountered in any number of bases after the gene-specific priming region. To confirm that the het indel is present in both directions of your target, check the sequencing in the opposite direction.</td>
</tr>
<tr>
<td>Observation</td>
<td>Possible cause</td>
<td>Recommended action</td>
</tr>
<tr>
<td>-------------</td>
<td>---------------</td>
<td>--------------------</td>
</tr>
<tr>
<td>Extra peaks are present in the sequencing traces</td>
<td>Primer-dimer has occurred.</td>
<td>You can often diagnose primer-dimer by looking at the raw trace data for questionable sequences. When primer-dimer exists, the 5’ sequence signal may be significantly higher for a region of bases spanning the length of the forward and reverse gene-specific primers. Primer-dimer is the annealing of the 3’ end of primers during PCR. The resulting short annealed fragment may amplify more efficiently than fully extended template. Primer-dimer fragments amplified during PCR can display increased 5’ signal and extra peaks when multiple PCR products are sequenced simultaneously. In some instances, the secondary or extra peaks can be read as the reverse compliment of the PCR primers in this noisy 5’ region. The secondary sequence or multiple PCR product sequences appear as far as 100–200 bp into the sequence, then suddenly disappear.</td>
</tr>
<tr>
<td>The PCR amplification primers do not have specificity and are sequencing two different regions of the genome. The analyzed trace shows extra peaks throughout the entire length of the trace.</td>
<td>Redesign the primers or increase the amplification temperature.</td>
<td></td>
</tr>
<tr>
<td>You accidentally contaminated the DNA and are sequencing two templates at the same time. The analyzed trace shows extra peaks throughout the entire length of the trace.</td>
<td>Repeat the amplification and sequencing reactions with uncontaminated DNA.</td>
<td></td>
</tr>
<tr>
<td>There were impure or contaminated primers.</td>
<td>Primer stocks may have inadvertently had other primer solution introduced. For best results, use HPLC to purify the primers.</td>
<td></td>
</tr>
<tr>
<td>There was a contaminated sample well.</td>
<td>Use a new sample plate and buffer/wash septa whenever possible. To avoid getting sample into adjacent wells, centrifuge the plates before you remove the adhesive seal.</td>
<td></td>
</tr>
<tr>
<td>There are pull-up or pull-down peaks in the data</td>
<td>The manual dye calibration is not current or is not matched to the samples, or a high-quality sample was not run with the dye set for the first time in the absence of a manual calibration.</td>
<td>If the dye set is a fragment analysis dye set that is being used for the first time, run a manual dye calibration. Alternatively, if a high-quality sample is run with an uncalibrated dye set, and the automated spectral calibration successfully generates an optimized matrix, manual calibration is not absolutely required. See “Determine if manual calibration is required” on page 177.</td>
</tr>
<tr>
<td>Observation</td>
<td>Possible cause</td>
<td>Recommended action</td>
</tr>
<tr>
<td>-------------</td>
<td>---------------</td>
<td>--------------------</td>
</tr>
<tr>
<td>There are pull-up or pull-down peaks in the data</td>
<td>The incorrect dye set was selected in the Plate setup. <strong>Note:</strong> This is applicable to both sequence analysis and fragment analysis.</td>
<td>Correct the dye set and repeat the injection.</td>
</tr>
<tr>
<td>There are error messages about spectral issues</td>
<td>A high-quality sample has not been run with the dye set.</td>
<td>If the dye set is a fragment analysis dye set that is being used for the first time, run a manual dye calibration. Alternatively, if a high-quality sample is run with an uncalibrated dye set, and the automated spectral calibration successfully generates an optimized matrix, manual calibration is not absolutely required. See “Determine if manual calibration is required” on page 177.</td>
</tr>
<tr>
<td>There is a short read length and uneven peak spacing in sequence data</td>
<td>The incorrect dye set was selected in the Plate setup.</td>
<td>Correct the dye set and repeat the injection. Select from the following: • E_BigDye™ Terminator v1.1 • Z_BigDye™ Terminator v3.1 • Z_BigDye™ Direct Reanalyze the data in the Sequencing Analysis Software, using the correct mobility file.</td>
</tr>
<tr>
<td>Fragment analysis peaks are sized differently than previously observed</td>
<td>Aging of the polymer in the cartridge, which can cause small (≤0.5 bp) changes in fragment size.</td>
<td>• Use a reference marker (for example, an allelic ladder) for auto bin adjustment. <em>Or</em> • Manually adjust the fragment bin positions to account for the size change.</td>
</tr>
</tbody>
</table>

### EPT data

<table>
<thead>
<tr>
<th>Observation</th>
<th>Possible cause</th>
<th>Recommended action</th>
</tr>
</thead>
<tbody>
<tr>
<td>There is a fluctuating or unstable electrophoresis current, or <strong>Current check failed</strong> is displayed</td>
<td>There is a bubble in the polymer system.</td>
<td>Flush the capillary array. 1. Touch @ Settings → Cartridge → Cartridge maintenance. 2. Touch Refresh PDS. 3. Touch @ to close the screen when the function ends. Replace the cartridge if the problem persists.</td>
</tr>
<tr>
<td>The cartridge is damaged.</td>
<td>Inspect the cartridge for damage and replace the cartridge.</td>
<td></td>
</tr>
</tbody>
</table>
# Software troubleshooting

<table>
<thead>
<tr>
<th>Observation</th>
<th>Possible cause</th>
<th>Recommended action</th>
</tr>
</thead>
<tbody>
<tr>
<td>Strikethrough text is displayed in <strong>Save location</strong> in <strong>Plate properties</strong> screen</td>
<td>The original location to which the plate was saved is no longer accessible by the instrument.</td>
<td>No action.</td>
</tr>
<tr>
<td><img src="image1" alt="Save location screen" /></td>
<td><img src="image2" alt="Save location screen" /></td>
<td></td>
</tr>
<tr>
<td>Import failed message when you select a CSV plate setup on the instrument.</td>
<td>The CSV file specifies the name of a run module, dye set, and/or size standard that does not exist on the instrument.</td>
<td>Add the run module, dye set, and/or size standard to the instrument by selecting a PSM file that contains the items, or by creating the items manually.</td>
</tr>
<tr>
<td>The message also indicates that a valid run module, dye set, and/or size standard is not present.</td>
<td><strong>IMPORTANT!</strong> A CSV file contains only the name of the run module, dye set, and/or size standard, it does not contain the settings.</td>
<td></td>
</tr>
<tr>
<td>Import CSV fails but import PSM with same settings imports with no errors</td>
<td>The size standard, dye set, or run module specified in the CSV file does not exist on the instrument.</td>
<td>Create the size standard, dye set, or run module on the instrument.</td>
</tr>
<tr>
<td>The CSV file contains the <em>names only</em> of the size standard, dye set, or run module, it does not contain the settings.</td>
<td>The PSM file contains the <em>names and settings</em> of the size standard, dye set, or run module. The size standard, dye set, or run module are automatically created when the PSM file is imported.</td>
<td></td>
</tr>
<tr>
<td>When saving a PSM file in Plate Manager (Cloud), &quot;You do not have edit permission to the cloud group&quot; message is displayed</td>
<td>You are saving to a Thermo Fisher Cloud group and you do not have edit permissions for the group.</td>
<td>Save to a different location, or request edit permissions from the group administrator.</td>
</tr>
<tr>
<td>Observation</td>
<td>Possible cause</td>
<td>Recommended action</td>
</tr>
<tr>
<td>----------------------------------------------------------------------------</td>
<td>--------------------------------------------------------------------------------</td>
<td>-------------------------------------------------------------------------------------</td>
</tr>
<tr>
<td>Analysis settings or run module is not available for selection by some users</td>
<td>Analysis settings and run modules are saved per user. If the analysis settings or run modules are associated with a hidden plate setup, the analysis settings or run modules are not listed for selection unless the user who created the plate setup is signed in.</td>
<td>Change the plate setup security from Hidden to Shared (see “Hide or share a plate (Plate setup security)” on page 73). Create the analysis settings or run modules manually.</td>
</tr>
<tr>
<td>This situation is seen on the instrument.</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Your local instrument profile name is not available for sign in</td>
<td>Your local instrument profile is linked to your Cloud account and is replaced by your Cloud profile.</td>
<td>See “Local instrument profile roles and functions” on page 134. Sign in with your Cloud profile.</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Cloud account is already linked to a local profile message</td>
<td>You have a local instrument profile that has previously been linked to Cloud account. You touched Get Started Connect, then typed in your Cloud account email and password.</td>
<td>Return to Sign in screen, then select your local profile from the Sign in list. Return to Sign in screen, touch , touch Sign out, then select your local profile from the Sign in list.</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>The Notifications button is not displayed in Instrument Settings</td>
<td>You are signed in to the instrument with a local instrument profile.</td>
<td>Sign in to the instrument with a Cloud instrument profile.</td>
</tr>
<tr>
<td>A button is dimmed</td>
<td>The function is available to users with administrator role only.</td>
<td>None.</td>
</tr>
<tr>
<td>Sample data files from the SeqStudio™ Genetic Analyzer can be opened but not analyzed in secondary analysis software</td>
<td>An updated version of the secondary analysis software is required.</td>
<td>Download and run the latest version of secondary analysis software. See “Secondary analysis software” on page 28. Note: The SeqStudio™ Genetic Analyzer instrument model is listed as 3200.</td>
</tr>
<tr>
<td>• Sequencing Analysis Software</td>
<td></td>
<td></td>
</tr>
<tr>
<td>• GeneMapper™ Software</td>
<td></td>
<td></td>
</tr>
<tr>
<td>• SeqScape™ Software</td>
<td></td>
<td></td>
</tr>
<tr>
<td>• Variant Reporter™ Software</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Files cannot be imported into Thermo Fisher Cloud applications or cannot be analyzed in Thermo Fisher Cloud sequencing apps</td>
<td>The sample name or file name used a special character.</td>
<td>Rename the sample name or file name. Note: Special characters (/,, @, %) will impact file import into Thermo Fisher Cloud applications.</td>
</tr>
<tr>
<td>Observation</td>
<td>Possible cause</td>
<td>Recommended action</td>
</tr>
<tr>
<td>------------------------------</td>
<td>-----------------------------------</td>
<td>-----------------------------------------------------------------------------------</td>
</tr>
<tr>
<td>Unexpected error is displayed</td>
<td>There was a software error.</td>
<td>Follow the instructions in the error message.</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Export the log files to determine the potential source of the unexpected error. See “Export log files for plates, install runs, injections, and instrument” on page 153.</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Restart the system using the On/Off switch on the rear panel. See “Power on the instrument” on page 33.</td>
</tr>
</tbody>
</table>

## Service tools

The **Service tools** function is password-protected and for service use only.

![Service tools screenshot](image_url)
Link the instrument to your Cloud account—detailed instructions

■ Workflow: Set up the instrument for Thermo Fisher Cloud access ............... 167
■ Network requirements .......................................................... 167
■ Link the instrument from a mobile device ................................. 168
■ Link the instrument using a link code .................................... 169
■ Link the instrument using your Cloud account ............................ 173
■ Set up email notifications from the instrument ............................ 174

Workflow: Set up the instrument for Thermo Fisher Cloud access

Register and obtain a Thermo Fisher Connect account
(page 49)

▼

Link the instrument to the Thermo Fisher Cloud in any of the following ways:

• Link the instrument from a mobile device
  (page 168)
• Link the instrument using a link code
  (page 169)
• Link the instrument using your Cloud account
  (page 173)

Network requirements

The instrument is factory-configured for IPv4 TCP/IP communication and includes a fast Ethernet adapter (10/100 Mbps) with a RJ45-type connector for integrating the device into a local area network (LAN).

By default, the instrument is configured to use the Dynamic Host Configuration Protocol (DHCP) but can use a static IP address.

The instrument should be configured behind a firewall. Contact Support for information on required firewall exceptions.
Link the instrument from a mobile device

Create a Cloud PIN and generate the QR code on the instrument

1. Sign in to thermofisher.com/cloud.

2. Click 🆕 to access InstrumentConnect.

3. If you have not previously set up a PIN, click Update PIN, then enter a PIN that you will use to sign in to the instrument.

4. From the instrument Sign In screen, navigate to the Connect to the Thermo Fisher Cloud screen:

<table>
<thead>
<tr>
<th>Do you have a local instrument profile?</th>
<th>Description</th>
</tr>
</thead>
</table>
| Yes                                    | 1. Touch Sign in, then enter your PIN.  
                                          2. In the home screen, touch Setup run.  
                                          3. In the Setup run screen, touch Cloud. |
| No                                     | Touch Get started ➔ Connect. |

5. Touch Mobile devices.
Register the instrument with the Instrument Connect App

1. On your mobile device, download the InstrumentConnect from the Apple Store or from Google™ Play.
2. Launch, then sign in to the mobile app on your mobile device.
3. Register the instrument:
   a. Touch ☰, then touch Register Instrument.
   b. Touch QR code on your mobile device.
   c. With your mobile device, scan the QR code displayed in the instrument touchscreen.

Link the instrument using a link code

1. From the instrument Sign In screen, navigate to the Connect to the Thermo Fisher Cloud screen:

<table>
<thead>
<tr>
<th>Do you have a local instrument profile?</th>
<th>Description</th>
</tr>
</thead>
</table>
| Yes                                    | 1. Touch Sign in, then enter your PIN.  
                                          2. In the home screen, touch Setup run.  
                                          3. In the Setup run screen, touch Cloud. |
| No                                     | Touch Get started + Connect.            |
2. Touch PC.

A unique link code is displayed.

3. Sign into your Thermo Fisher Cloud on a separate computer.
   Go to thermofisher.com/cloud.
4. Click 🔄, then click **Add an Instrument**.

5. Select **SeqStudio™**, then click **Next**.
6. Enter the link code from the instrument touchscreen (from step 2), then click **Send**.

![Add an instrument](image)

7. If you have not previously set up a PIN, enter a PIN to use when you sign in to an instrument, then click **Send**.

![Set your pin to proceed](image)

A start linking message is displayed.
A confirmation message is displayed on the instrument touchscreen when the instrument is linked and connected to the Thermo Fisher Cloud.

The first time the instrument is linked, the software automatically:
- Creates a Cloud instrument profile with the First Name and Last Name from your Thermo Fisher Cloud account.
- Registers the instrument in the InstrumentConnect software.
Link the instrument using your Cloud account

1. From the instrument **Sign In** screen, navigate to the **Connect to the Thermo Fisher Cloud** screen:

<table>
<thead>
<tr>
<th>Do you have a local instrument profile?</th>
<th>Description</th>
</tr>
</thead>
</table>
| Yes                                    | 1. Touch **Sign in**, then enter your PIN.  
2. In the home screen, touch **Setup run**.  
3. In the **Setup run** screen, touch **Cloud**. |
| No                                     | Touch **Get started • Connect**. |

2. Touch **Instrument**.

3. Enter your Thermo Fisher Cloud account username (email address) and password, then touch **Link account**.
4. If you have not previously set up a PIN, enter a PIN to use when you sign in to an instrument, then touch **Done**.

![Enter PIN](image)

A confirmation message is displayed when the instrument is linked and connected to the Thermo Fisher Cloud.

The first time the instrument is linked, the software automatically:

- Creates a Cloud instrument profile with the First Name and Last Name from your Thermo Fisher Cloud account.
- Registers the instrument in the InstrumentConnect software.

**Set up email notifications from the instrument**

When an instrument is linked to your Cloud account, email notifications are automatically sent to your Cloud account email address.

Perform this procedure to disable any of the default notifications.
1. Sign in to the instrument with your Cloud instrument profile and PIN.

2. In the home screen of the instrument, touch 📜 Settings ➔ Instrument settings ➔ Email notifications.

3. In the Email notifications screen, select or deselect the options for which you want to receive email notifications, then touch Done.

**Note:** If you are signed in with a local instrument profile instead of a Cloud instrument profile, the Email notifications button is not displayed on the Instrument Settings screen.
Dye calibration and install standard checks

- Calibrate dyes ............................................................... 176
- Perform an install run ................................................ 187

Calibrate dyes

Overview of system dye set and custom dye set calibration

Dye calibration compensates for dye emission spectral overlap.

![Dye emission spectra for the J6 (DS-36) dye set showing spectral overlap](image)

Figure 20  Dye emission spectra for the J6 (DS-36) dye set showing spectral overlap

System dye sets are available from Thermo Fisher Scientific.

<table>
<thead>
<tr>
<th>System dye sets</th>
<th>Sequence analysis dye sets</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Fragment analysis dye sets</strong></td>
<td><strong>E_BigDye™ Terminator v1.1</strong></td>
</tr>
<tr>
<td>• D (DS-30, DS-31)</td>
<td>• Z_BigDye™ Terminator v3.1</td>
</tr>
<tr>
<td>• E5 (DS-02)</td>
<td>• Z_BigDye™ Direct</td>
</tr>
<tr>
<td>• F (DS-32)</td>
<td></td>
</tr>
<tr>
<td>• G5 (DS-33)</td>
<td></td>
</tr>
<tr>
<td>• J6 (DS-36)</td>
<td></td>
</tr>
</tbody>
</table>

Custom dye sets are any dyes that are not available from Thermo Fisher Scientific. Custom dye sets require manual calibration.
Three types of calibration can occur on the instrument:

- **Factory calibration** — Default calibration provided with the instrument. It is not optimized for a specific instrument.

- **Manual calibration** — Manual procedure performed by the user that provides a baseline calibration for the instrument on which it is run. Reduces pull-up (false secondary peaks under a true peak).

- **Auto calibration** — Automatic adjustment of the baseline calibration to optimally reduce pull-up (false secondary peaks under a true peak). The instrument performs an auto calibration for system and custom dyes.

- Sequence analysis dye sets — Do not typically require manual calibration.

- Fragment analysis dye sets — Manual calibration is recommended one time before use.

  **Note:** With high-quality sample data, it is possible for auto calibration to pass using the factory calibration.

To determine if a dye set requires manual calibration, review the calibration history for the dye set.

In the home screen:
1. Touch  

   - Settings 
   - Maintenance and Service 
   - Calibration 
   - Calibration history.

2. Examine the entry for the dye set of interest. If the dye set does not list a date and a cartridge serial number for a manual calibration or a date for auto calibration, the dye set requires manual calibration.

   ![Calibration History](image)

   **Figure 21** Fragment analysis dye sets example

   1. Manual calibration is recommended—No auto calibration or manual calibration has been performed.
   2. Manual calibration is not required—A manual calibration has been performed.
   3. Manual calibration is not required—The factory calibration has been optimized for the instrument by auto calibration.
   4. Manual calibration is recommended—Auto calibration has been performed, but only 2 capillaries passed.
   5. Manual calibration is not required—A manual calibration and an auto calibration have been performed.

**Perform a system dye calibration**

A system dye calibration requires ~30 minutes to complete.

Prepare the dye set calibration standards and plate as described in the product information sheet for the dye set.

In the home screen:

2. Touch the injection group for the dye set in the plate, then touch Dye set.

3. Touch Sequence Standard or Matrix Standard, then select a system dye calibration standard provided with the instrument.

4. Touch Calibrate. The calibration run starts.

**IMPORTANT!** If the dye calibration fails:

- The results of the calibration are not saved, and the calibration plate is not moved to Run History.
- The instrument does not allow you to rerun the plate setup for a failed calibration. Close the calibration screen, then start a new calibration.
**Spectral Quality Value**

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

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

**Condition number**

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

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

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

<table>
<thead>
<tr>
<th>Dye Set</th>
<th>Quality Value Minimum</th>
<th>Condition Number Maximum</th>
</tr>
</thead>
<tbody>
<tr>
<td>AnyDye</td>
<td>0.8 (default)</td>
<td>20.0 (default)</td>
</tr>
<tr>
<td>D</td>
<td>0.8</td>
<td>8.5</td>
</tr>
<tr>
<td>E</td>
<td>0.95</td>
<td>5.5</td>
</tr>
<tr>
<td>E5</td>
<td>0.95</td>
<td>6.0</td>
</tr>
<tr>
<td>F</td>
<td>0.95</td>
<td>8.5</td>
</tr>
<tr>
<td>G5</td>
<td>0.95</td>
<td>13.5</td>
</tr>
<tr>
<td>J6</td>
<td>0.95</td>
<td>8.0</td>
</tr>
<tr>
<td>Z</td>
<td>0.95</td>
<td>5.5</td>
</tr>
</tbody>
</table>

---

**Perform a custom dye calibration**

Add a custom dye set to the software based on a system dye

In the home screen:
1. Touch Settings › Maintenance and Service › Calibration › Dye calibration.

2. Touch Custom Dye.

3. Touch Add.

4. Touch the system dye to use as a starting point for the custom dye settings.

5. Modify the settings as needed then touch Next.

6. Enter a Dye set name, then touch Done.

Add a custom dye set to the software using the Any Dye template

In the home screen:
1. Touch ☰ **Settings** › **Maintenance and Service** › **Calibration** › **Dye calibration.**

2. Touch **Custom Dye.**

3. Touch **Add.**

4. Select **Any Dye** to use as a starting point for the custom dye settings. All dyes are selected by default.

5. Touch a dye color, then manage the dye set arrangement:
   - Touch **Dye selection** to deselect the dye.
   - Touch **Move up** or **Move down** to organize the dyes in the order in which they occur as peaks in the electropherogram of the custom dye set standard.
   - Touch **Reduce selection** to exclude it from the calibration.
• **Note:** If you are calibrating with a system dye set, but will not run all system dyes in your application:
  - Enable (select) the **Dye selection** checkbox (to indicate that the system dye is present in the matrix standard)
  - Disable (deselect) the **Reduce selection** checkbox (to indicate that the system dye should not be analyzed, reported, or used for auto calibration)

6. Touch **Next**, enter dye set parameters, then touch **Next**.

7. Enter a **Dye set name**, then touch **Save**.

**Perform a custom dye calibration**

Before you begin:
- Prepare the dye set calibration standards and plate as described in the product information sheet for the dye set.
- Add a custom dye set to the software (see “Add a custom dye set to the software based on a system dye” on page 180).

In the home screen:
1. Touch ☰ Settings ▶ Maintenance and Service ▶ Calibration ▶ Dye calibration.

2. Touch the injection group for the dye set in the plate, then touch Dye set.

3. Touch a custom dye set.

4. Touch Calibrate.

5. When the run is complete, touch View results.

6. Ensure that all capillaries passed the calibration, then click Done.

**IMPORTANT!** If the dye calibration fails:

- The results of the calibration are not saved, and the calibration plate is not moved to Run History.
- The instrument does not allow you to rerun the plate setup for a failed calibration. Close the calibration screen, then start a new calibration.

**Add a custom dye to the Plate Manager or another instrument**

- To add a custom dye set to the Plate Manager:
  a. Open a plate setup that specifies the custom dye set of interest.
  b. Export a plate setup that specifies the custom dye (see “Export or delete a plate setup (PSM file)” on page 121).
  c. Open the exported plate setup in the Plate Manager.

- To transfer a custom dye set to another instrument:
  a. Touch Settings ▶ Maintenance and Service ▶ Calibration ▶ Calibration history.
  b. Touch Custom dye.
  c. Touch Manage.
d. Touch a custom dye, then touch Export.

e. Select a location, then touch Export.

f. Import the custom dye on another instrument (Settings > Maintenance and Service > Calibration > Dye calibration > Custom dye > Manage > Import).

View the dye calibration history

In the home screen:

1. Touch Settings > Maintenance and Service > Calibration history.

A thumbnail of each capillary calibration spectrum is displayed, with the q, α, and c values (see “Spectral Quality Value” on page 180 and “Condition number” on page 180).

2. Touch a dye set.

A thumbnail of each capillary calibration spectrum is displayed, with the q, α, and c values (see “Spectral Quality Value” on page 180 and “Condition number” on page 180).

2. Touch a dye set.

A thumbnail of each capillary calibration spectrum is displayed, with the q, α, and c values (see “Spectral Quality Value” on page 180 and “Condition number” on page 180).

3. Touch >> and << to view a full-screen calibration spectrum for each capillary.

4. Touch ◀ to return to the list of dye sets on the Calibration History screen.

5. (Optional) Touch Filter to narrow the dye set list down by dye sets.
   a. Select or deselect the dyes listed.
b. (Optional) Touch Desselect All to clear the dye set selections.

c. Touch Done.

6. Touch OK.

In the home screen:

- Touch 📋 Settings › Maintenance and Service › Calibration › Dye calibration › Custom dye › Manage.
  1. Touch the custom dye set.
  
  2. Touch Import or Export.
Perform an install run

Overview of install checks

Install checks are performed by a Thermo Fisher Scientific Field Service Engineer at the time of installation.

An install check can be run at any time with the following reagents to ensure instrument performance:

<table>
<thead>
<tr>
<th>Install check type</th>
<th>Reagent</th>
</tr>
</thead>
</table>
| Sequencing         | • 3500/3500xL Sequencing Standards, BigDye™ Terminator v3.1 (Cat. No. 4404312)  
                      • 3500/3500xL Sequencing Standards, BigDye™ Terminator v1.1 (Cat. No. 4404314) |
| Fragment           | DS-33 GeneScan™ Installation Standards with GeneScan™ 600 LIZ™ Size Standard v2.0 (Cat. No. 4376911) |

You can include multiple injection groups, multiple applications, and/or multiple chemistries on an install run plate. For example, you can prepare an install run plate that contains replicate injections of the fragment install standard and both sequencing standards.

![Figure 22 Example install run plate with multiple applications and replicate injections](image)

An install run requires ~45 minutes to complete each injection group.

Prepare the installation standard and plate as described in the product information sheet for the installation standard.

In the home screen:
Appendix C Dye calibration and install standard checks

Perform an install run

1. Touch Settings > Maintenance and service > Install run > Install run.

2. Touch an injection group on the plate to select a location for the install standards.

3. Touch Chemistry, then select the type of install run.
   Select None to cancel the selection.

4. Repeat the steps above for additional injection groups and/or multiple chemistries.

5. Touch Start Run.
1. Open the install run results summary:
   - To view results immediately after the install run completes, touch **Results**.
   - To view results for a previous install run, touch **Settings ➤ Maintenance and Service ➤ Install run ➤ Install run history**.
2. Touch an install run to display the results, including the pass/fail results.

Each injection group displays a QC color for each capillary:
- ![Green](image)
  - All QC tests passed.
- ![Yellow](image)
  - At least 1 warning quality alert was triggered.
- ![Red](image)
  - At least 1 failing quality alert was triggered.

For information on quality alerts, see:
- “Data quality alerts” on page 102
- “Sizecalling and basecalling quality alerts” on page 102
3. Touch **Detail** to see allele-specific details for fragment analysis and basecall accuracy for sequencing.

4. Touch **Export report** (see “Export the install run report” on page 192).

### Fragment analysis install run pass/fail criteria

<table>
<thead>
<tr>
<th>Result</th>
<th>Acceptance criteria</th>
</tr>
</thead>
<tbody>
<tr>
<td># Allele peaks</td>
<td>15 for all four capillaries</td>
</tr>
<tr>
<td># Size standard peaks</td>
<td>34 for all four capillaries</td>
</tr>
<tr>
<td>Standard deviation of the observed allele fragment sizes for all 4 capillaries</td>
<td>&lt;0.15 base pairs (bp)</td>
</tr>
</tbody>
</table>
Sequence analysis install run pass/fail criteria

<table>
<thead>
<tr>
<th>Result</th>
<th>Acceptance criteria</th>
</tr>
</thead>
<tbody>
<tr>
<td>QV30 CRL (contiguous read length)</td>
<td>BigDye™ Terminator v3.1</td>
</tr>
<tr>
<td></td>
<td>Capillaries with QV30 CRL ≥500 bp pass.</td>
</tr>
<tr>
<td><strong>Note</strong>: The contiguous read length passing criteria for install checks is an uninterrupted segment of bases with an average Quality Value (QV) of 30.</td>
<td>BigDye™ Terminator v1.1</td>
</tr>
<tr>
<td></td>
<td>Capillaries with a QV30 CRL ≥500 bp pass.</td>
</tr>
</tbody>
</table>

The remaining results on the screen are for information only.

Export the install run report

1. Touch ☰ Settings ➔ Maintenance and Service ➔ Install run ➔ Install run history.
2. Touch the install run of interest.
3. Touch Export report.
4. Select a destination for the report.
5. Touch OK.
## Example fragment analysis run report

**Install run report**

### System Information
- **Instrument Name:** SeqStudio-SVT2
- **Instrument Serial Number:** 122000009Z
- **Instrument Software Version:** SVT1.4.21-1306+12852
- **Buffer Installation Date:** 2017/03/04
- **Buffer Expiration Date:** 2017/03/18

### Install Run Result

<table>
<thead>
<tr>
<th>Capillary</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
</tr>
</thead>
<tbody>
<tr>
<td># of Allele Peaks</td>
<td>15</td>
<td>15</td>
<td>15</td>
<td>15</td>
</tr>
<tr>
<td># of Size Standard Peaks</td>
<td>34</td>
<td>34</td>
<td>34</td>
<td>34</td>
</tr>
</tbody>
</table>

### Running info

<table>
<thead>
<tr>
<th>Dye</th>
<th>Allele</th>
<th>Nominal Size</th>
<th>Mean</th>
<th>Average Peak height</th>
<th>Peak height% &gt; Min</th>
<th>Sizing precision</th>
<th>Sizing accuracy</th>
<th>Pass/Fail</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>D56445</td>
<td>85.06</td>
<td>85.1</td>
<td>1851.75</td>
<td>100.0</td>
<td>0.02</td>
<td>0.04</td>
<td>Pass</td>
</tr>
<tr>
<td>2</td>
<td>D56445</td>
<td>96.89</td>
<td>96.92</td>
<td>1184.0</td>
<td>100.0</td>
<td>0.03</td>
<td>0.03</td>
<td>Pass</td>
</tr>
<tr>
<td>3</td>
<td>D205111</td>
<td>113.7</td>
<td>113.67</td>
<td>1393.25</td>
<td>100.0</td>
<td>0.0</td>
<td>0.03</td>
<td>Pass</td>
</tr>
<tr>
<td>4</td>
<td>D205111</td>
<td>119.6</td>
<td>119.56</td>
<td>1308.5</td>
<td>100.0</td>
<td>0.05</td>
<td>0.04</td>
<td>Pass</td>
</tr>
<tr>
<td>5</td>
<td>D56288</td>
<td>137.5</td>
<td>137.38</td>
<td>1545.0</td>
<td>100.0</td>
<td>0.02</td>
<td>0.12</td>
<td>Pass</td>
</tr>
<tr>
<td>6</td>
<td>D56288</td>
<td>145.24</td>
<td>145.09</td>
<td>1044.75</td>
<td>100.0</td>
<td>0.04</td>
<td>0.15</td>
<td>Pass</td>
</tr>
<tr>
<td>7</td>
<td>D56288</td>
<td>171.49</td>
<td>171.35</td>
<td>1677.0</td>
<td>100.0</td>
<td>0.05</td>
<td>0.14</td>
<td>Pass</td>
</tr>
<tr>
<td>8</td>
<td>D56288</td>
<td>173.41</td>
<td>173.25</td>
<td>1084.0</td>
<td>100.0</td>
<td>0.03</td>
<td>0.16</td>
<td>Pass</td>
</tr>
<tr>
<td>9</td>
<td>D56242</td>
<td>216.39</td>
<td>216.26</td>
<td>1457.5</td>
<td>100.0</td>
<td>0.04</td>
<td>0.13</td>
<td>Pass</td>
</tr>
<tr>
<td>10</td>
<td>D56242</td>
<td>218.27</td>
<td>218.14</td>
<td>955.75</td>
<td>100.0</td>
<td>0.03</td>
<td>0.13</td>
<td>Pass</td>
</tr>
<tr>
<td>11</td>
<td>D56242</td>
<td>236.74</td>
<td>236.48</td>
<td>2030.0</td>
<td>100.0</td>
<td>0.06</td>
<td>0.26</td>
<td>Pass</td>
</tr>
<tr>
<td>12</td>
<td>D56242</td>
<td>238.67</td>
<td>238.38</td>
<td>1300.5</td>
<td>100.0</td>
<td>0.04</td>
<td>0.29</td>
<td>Pass</td>
</tr>
<tr>
<td>13</td>
<td>D15561</td>
<td>303.06</td>
<td>302.86</td>
<td>1718.25</td>
<td>100.0</td>
<td>0.06</td>
<td>0.2</td>
<td>Pass</td>
</tr>
<tr>
<td>14</td>
<td>D15561</td>
<td>336.81</td>
<td>336.71</td>
<td>1331.0</td>
<td>100.0</td>
<td>0.02</td>
<td>0.1</td>
<td>Pass</td>
</tr>
<tr>
<td>15</td>
<td>D15561</td>
<td>338.73</td>
<td>338.63</td>
<td>914.25</td>
<td>100.0</td>
<td>0.01</td>
<td>0.1</td>
<td>Pass</td>
</tr>
</tbody>
</table>

**Capillary (Raman) Uniformity:** 0.4

The spectral dye matrix has not been updated.
Appendix C Dye calibration and install standard checks

Perform an install run

Example sequencing run report

In the home screen:

1. Touch Settings → Maintenance and Service → Install run history.

<table>
<thead>
<tr>
<th>Capillary</th>
<th>Signal Strength Sample file name</th>
<th>G</th>
<th>A</th>
<th>T</th>
<th>C</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>A2_A2_20170424_104040.ab1</td>
<td>792</td>
<td>1275</td>
<td>968</td>
<td>917</td>
</tr>
<tr>
<td>2</td>
<td>B2_B2_20170424_104041.ab1</td>
<td>1016</td>
<td>1625</td>
<td>1193</td>
<td>1108</td>
</tr>
<tr>
<td>3</td>
<td>C2_C2_20170424_104042.ab1</td>
<td>751</td>
<td>1326</td>
<td>1126</td>
<td>978</td>
</tr>
<tr>
<td>4</td>
<td>D2_D2_20170424_104043.ab1</td>
<td>635</td>
<td>1087</td>
<td>901</td>
<td>742</td>
</tr>
</tbody>
</table>

View the install run history

Install run report

System Information

- Instrument Name: SeqStudio/VT1
- Instrument Serial Number: 122000021
- Instrument Software Version: 0.6.10
- Buffer Installation Date: 2016/12/05
- Buffer Expiration Date: 2016/12/19

Install Run Result

- Contiguous Read Length (CRL) range:
  - 1: 530 (26-555), 535 (29-563), 531 (29-569), 530 (32-561)
  - Mean: 531.5
  - SD: 2.1

- CRL Pass/Fail: Pass

- Basecall Accuracy:
  - %CRL: 99.8
  - %RL: 99.1

- Alignment Read Length (range): 562 (5-566), 557 (19-575), 556 (15-570), 562 (5-566)

Legend:
- Passed
- Failed

Signal Strength

- Capillary Uniformity: 0.0

SeqStudio™ Genetic Analyzer Instrument and Software User Guide
2. *Optional* Touch **Filter**, select the install run type, then touch **Done**.

![Filter by chemistry screen]

**Note:** If the screen is blank when you click **Done**, no install runs are present for the chemistry you selected.
Run modules, read lengths, size ranges, and run times

Table 14  Sequencing run modules for standard sequencing

<table>
<thead>
<tr>
<th>Run module</th>
<th>Contiguous read length (CRL)(^1)</th>
<th>QV threshold</th>
<th>Approximate run time</th>
</tr>
</thead>
<tbody>
<tr>
<td>ShortSeq</td>
<td>≥350</td>
<td>QV30</td>
<td>30 minutes</td>
</tr>
<tr>
<td>ShortSeq_BDX</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>MediumSeq</td>
<td>≥500</td>
<td>QV30</td>
<td>45 minutes</td>
</tr>
<tr>
<td>MediumSeq_BDX</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>LongSeq</td>
<td>≥800</td>
<td>QV20</td>
<td>~ 2 hours</td>
</tr>
<tr>
<td>LongSeq_BDX</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

\(^{1}\) CRL was determined using the Long Read Sequencing standard. A minimum of 90% of analyzed sequences with an average QV ≥ QV threshold were observed.

IMPORTANT! Use BDX run modules only if you prepare samples with BigDye XTerminator™ Purification Kit. Use non-BDX run modules for samples purified with other methods.

Table 15  Fragment analysis run modules

<table>
<thead>
<tr>
<th>Run module</th>
<th>Resolution range</th>
<th>Approximate run time</th>
<th>Sizing precision</th>
<th>Compatible size standards</th>
</tr>
</thead>
<tbody>
<tr>
<td>SNaPshot</td>
<td>40–120 bp</td>
<td>25 minutes</td>
<td>40–120: &lt;0.5</td>
<td>GeneScan™ 120 LIZ™ Size Standard</td>
</tr>
<tr>
<td>FragAnalysis</td>
<td>60–460 bp(^1)</td>
<td>45 minutes</td>
<td>60–460: &lt;0.15</td>
<td>All except GeneScan™ 1200 LIZ™ Size Standard</td>
</tr>
<tr>
<td>LongFragAnalysis(^2)</td>
<td>60–600 bp(^1)</td>
<td>&lt; 2 hours</td>
<td>60–460: &lt;0.15</td>
<td>• GeneScan™ 600 LIZ™ Size Standard v2.0</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>461–600: &lt;0.3</td>
<td>• GeneScan™ 1200 LIZ™ Size Standard</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>601–800: &gt;0.45</td>
<td></td>
</tr>
</tbody>
</table>

\(^{1}\) 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.

\(^{2}\) Load a maximum of 48 samples per plate if you use a long run module.
**Note:** The following size standards have not been validated for use with the instrument. A default size standard definition is not provided in the software.

- GeneScan™ 500 LIZ™ Size Standard
- GeneScan™ 350 ROX™ Size Standard
- GeneScan™ 400HD ROX™ dye Size Standard
### Parts and materials

#### Required materials not supplied

Unless otherwise indicated, all materials are available through [thermofisher.com](http://thermofisher.com). MLS: Fisher Scientific ([fisherscientific.com](http://fisherscientific.com)) or other major laboratory supplier.

<table>
<thead>
<tr>
<th>Item</th>
<th>Source</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Software</strong></td>
<td></td>
</tr>
<tr>
<td><em>(Optional)</em> SeqStudio™ Plate Manager and App</td>
<td>Available on the Thermo Fisher Cloud or for download at <a href="http://thermofisher.com">thermofisher.com</a></td>
</tr>
<tr>
<td><em>(Optional)</em> SeqStudio™ Remote Monitoring App</td>
<td>Available on the Thermo Fisher Cloud</td>
</tr>
<tr>
<td><em>(Optional)</em> InstrumentConnect</td>
<td></td>
</tr>
<tr>
<td><strong>Equipment</strong></td>
<td></td>
</tr>
<tr>
<td><em>(Optional)</em> Handheld Barcode Scanner</td>
<td>4488442</td>
</tr>
<tr>
<td><strong>Consumables for SeqStudio™ Genetic Analyzer</strong></td>
<td></td>
</tr>
<tr>
<td>SeqStudio™ Genetic Analyzer Cartridge</td>
<td>A33671</td>
</tr>
<tr>
<td>SeqStudio™ Genetic Analyzer Cartridge v2</td>
<td>A41331</td>
</tr>
<tr>
<td>SeqStudio™ Genetic Analyzer Cathode Buffer Container</td>
<td>A33401</td>
</tr>
<tr>
<td>Reservoir Septa (for Cathode Buffer Container)</td>
<td>A35640</td>
</tr>
<tr>
<td>SeqStudio™ Integrated Capillary Protector</td>
<td>A31923</td>
</tr>
<tr>
<td><strong>Tubes, plates, and other consumables</strong></td>
<td></td>
</tr>
<tr>
<td>MicroAmp™ Optical 96-Well Reaction Plate</td>
<td>4316813</td>
</tr>
<tr>
<td>MicroAmp™ Optical 96-Well Reaction Plate with Barcode</td>
<td>4326659</td>
</tr>
<tr>
<td>MicroAmp™ Optical 8-Tube Strip, 0.2 mL</td>
<td>4316567</td>
</tr>
<tr>
<td>Septa for SeqStudio™ Genetic Analyzer, 96 well</td>
<td>A36541</td>
</tr>
<tr>
<td>Septa for SeqStudio™ Genetic Analyzer, 8 strip</td>
<td>A36543</td>
</tr>
<tr>
<td>MicroAmp™ 96-Well Tray/Retainer Set (Adapter for 8-Tube Strip)</td>
<td>403081</td>
</tr>
<tr>
<td><strong>Reagents</strong></td>
<td></td>
</tr>
<tr>
<td>Hi-Di™ Formamide</td>
<td>4401457</td>
</tr>
</tbody>
</table>
## Required materials not supplied

### Sequencing kits

<table>
<thead>
<tr>
<th>Item</th>
<th>Source</th>
</tr>
</thead>
<tbody>
<tr>
<td>BigDye XTerminator™ Purification Kit</td>
<td>4376486</td>
</tr>
<tr>
<td><strong>BigDye™ Terminator v1.1 Cycle Sequencing Kit</strong></td>
<td>4337449</td>
</tr>
<tr>
<td><strong>BigDye™ Terminator v3.1 Cycle Sequencing Kit</strong></td>
<td>4337454</td>
</tr>
<tr>
<td><strong>BigDye™ Direct Cycle Sequencing Kit</strong></td>
<td>4458689</td>
</tr>
</tbody>
</table>

### Fragment analysis dye calibration standards and installation standard

<table>
<thead>
<tr>
<th>Item</th>
<th>Source</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>GeneScan™ 600 LIZ™ Size Standard v2.0</strong></td>
<td>4408399</td>
</tr>
<tr>
<td><strong>GeneScan™ 120 LIZ™ Size Standard</strong></td>
<td>4324287</td>
</tr>
<tr>
<td><strong>GeneScan™ 1200 LIZ™ Size Standard</strong></td>
<td>4379950</td>
</tr>
<tr>
<td><strong>GeneScan™ 500 ROX™ Size Standard</strong></td>
<td>401734</td>
</tr>
<tr>
<td><strong>GeneScan™ 500 LIZ™ Size Standard</strong></td>
<td>4322682</td>
</tr>
<tr>
<td><strong>GeneScan™ 350 ROX™ Size Standard</strong></td>
<td>401735</td>
</tr>
<tr>
<td><strong>GeneScan™ 400HD ROX™ dye Size Standard</strong></td>
<td>402985</td>
</tr>
<tr>
<td><strong>DS-33 GeneScan™ Installation Standards with GeneScan™ 600 LIZ™ Size Standard v2.0</strong></td>
<td>4376911</td>
</tr>
</tbody>
</table>

[1] This size standard has not been validated for use with the instrument. A default size standard definition is not provided in the software.
Instrument specifications and layout

- Instrument dimensions ............................................... 200
- Instrument clearances ................................................ 200
- Environmental requirements .......................................... 201
- Electrical requirements ............................................... 202
- Electrical protective devices ........................................... 202
- Network requirements ............................................... 203
- Safety requirements ................................................. 203

Instrument dimensions

Ensure that the installation site bench space can accommodate the dimensions and support the weight.

<table>
<thead>
<tr>
<th>Configuration</th>
<th>Height</th>
<th>Length (depth)</th>
<th>Width</th>
<th>Weight</th>
</tr>
</thead>
<tbody>
<tr>
<td>(Door Closed)</td>
<td>44.2 cm (17.4 in.)</td>
<td>64.8 cm (25.5 in.)</td>
<td>49.5 cm (19.5 in.)</td>
<td>53.5 kg (118 lbs)</td>
</tr>
<tr>
<td>(Door Open)</td>
<td>56.9 cm (22.4 in.)</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

**WARNING! PHYSICAL INJURY HAZARD.** Do not attempt to lift or move the instrument without professional assistance. The crated instrument is heavy. Any incorrect lifting or moving of the crated instrument can cause serious injury.

Instrument clearances

During instrument setup and maintenance, it is necessary to access the back and sides of the instrument. If the back of the instrument faces a wall, it will be necessary to have enough space to rotate the instrument on the bench for access.

**IMPORTANT!** For safety, the power outlet used for powering the instrument must be accessible at all times.

<table>
<thead>
<tr>
<th>Component</th>
<th>Top</th>
<th>Front</th>
<th>Left</th>
<th>Right</th>
<th>Back</th>
</tr>
</thead>
<tbody>
<tr>
<td>SeqStudio™ Genetic Analyzer</td>
<td>30.5 cm (12.0 in)</td>
<td>30.5 cm (12.0 in)</td>
<td>10.0 cm (4.0 in)</td>
<td>20.0 cm (8.0 in)</td>
<td>10.0 cm (4.0 in)</td>
</tr>
</tbody>
</table>
Environmental requirements

Ensure that the installation room is maintained under correct environmental conditions.

<table>
<thead>
<tr>
<th>Condition</th>
<th>Acceptable range</th>
</tr>
</thead>
<tbody>
<tr>
<td>Installation site</td>
<td>Indoor use only</td>
</tr>
<tr>
<td>Electromagnetic interference</td>
<td>Do not use this device in close proximity to sources of strong electromagnetic radiation (for example, unshielded intentional RF sources). Strong electromagnetic radiation may interfere with the proper operation of the device. This equipment has been designed and tested to CISPR 11 Class A. In a domestic environment it may cause radio interference. You may need to take measures to mitigate the interference.</td>
</tr>
<tr>
<td>Altitude</td>
<td>Located between sea level and 2000 m (6500 ft.) above sea level</td>
</tr>
</tbody>
</table>
| Humidity (instrument and computer)| • Operation: 20%–80% (noncondensing)  
• Transport and storage: 15%–80% (noncondensing)                                                                                       |
| Temperature (instrument and computer) | • Operation: 15°C to 30°C (60°F to 85°F)  
• Transport and storage: −20°C to 60°C (−4°F to 140°F)  
**Note**: The room temperature must not fluctuate more than 2°C over a 2-hour period. |
| Transient category               | Installation categories II                                                                                                                                 |
| Overvoltage category             | Installation categories II                                                                                                                                 |
| Vibration                        | Ensure that the instrument is not adjacent to strong vibration sources, such as a centrifuge, pump, or compressor. Excessive vibration will affect instrument performance. |
| Pollution degree                 | II  
Install the instrument in an environment designated pollution degree II (only non-conductive pollution [e.g., dust] occurs except that occasionally a temporary conductivity caused by condensation is to be expected). Typical pollution degree II environments are laboratories and office spaces. |
| Liquid waste collection          | Dispose of the polymer, buffer, reagents and any liquid waste as hazardous waste in compliance with local and national regulations. |
| Other conditions                 | Ensure the installation site is away from any vents that could expel particulate material on the system components.  
Avoid placing the instrument and computer adjacent to heaters, cooling ducts, or in direct sunlight. |
Electrical requirements

**CAUTION!** Do not unpack or plug in any components until the Field Service Engineers (FSEs) have configured the system for the proper operating voltage.

**WARNING!** For safety, the power outlet used for powering the instrument must be accessible at all times. See “Instrument clearances” on page 200 for information about the space needed between the wall and the instrument. In case of emergency, you must be able to immediately disconnect the main power supply to all the equipment. Allow adequate space between the wall and the equipment so that the power cords can be disconnected in case of emergency.

- Electric receptacle required: 2-prong with ground pin
- Maximum power dissipation: 380 W (approximately, not including computer and monitor)
- Mains AC line voltage tolerances must be up to ±10 percent of nominal voltage

<table>
<thead>
<tr>
<th>Rated voltage</th>
<th>Circuit required</th>
<th>Rated frequency</th>
<th>Rated power</th>
</tr>
</thead>
<tbody>
<tr>
<td>100–240 ±10% VAC[1]</td>
<td>10 A</td>
<td>50–60 Hz</td>
<td>400 W</td>
</tr>
</tbody>
</table>

[1] If the supplied power fluctuates beyond the rated voltage, a power line regulator may be required. High or low voltages can adversely affect the electronic components of the instrument.

Electrical protective devices

We recommend several protective devices to protect the system in environments with large voltage and power fluctuations.

<table>
<thead>
<tr>
<th>Device</th>
<th>Description</th>
</tr>
</thead>
</table>
| Power line regulator    | We recommend the use of a 1.5-kVA power line regulator in areas where the supplied power fluctuates in excess of ±10% of the normal voltage. Power fluctuations can adversely affect the function of the instrument and computer.  
**Note:** A power line regulator monitors the input current and adjusts the power supplied to the instrument or computer. It does not protect against a power surge or failure. |
<table>
<thead>
<tr>
<th>Device</th>
<th>Description</th>
</tr>
</thead>
</table>
| Uninterruptible power supply (UPS) | We recommend the use of a 1.5-kVA uninterruptible power supply (UPS), especially in areas prone to power failure. Power failures and other events that abruptly terminate the function of the instrument and computer can corrupt data and possibly damage the system.  
**WARNING! PHYSICAL INJURY HAZARD.** Do not attempt to lift the UPS unit without assistance of at least two people. Improper lifting can cause painful and permanent back injury. Refer to the UPS manufacturer user guide for more information.  
**IMPORTANT!** UPSs provide power for a limited time. They are meant to delay the effects of a power outage, not to serve as replacement power sources. In the event of a power loss, power off the instrument and computer unless you expect to regain power within the battery life of the UPS.  
**Note:** A dedicated line and ground between the instrument, computer, and the building's main electrical service can also prevent problems caused by power fluctuations. |
| Surge protector              | We recommend the use of a 10-kVA surge protector (line conditioner) in areas with frequent electrical storms or near devices that are electrically noisy, such as refrigerators, air conditioners, or centrifuges. Short-duration, high-voltage power fluctuations can abruptly terminate the function of, and thereby damage the components of, the computer and the instrument. |

## Network requirements

The instrument is factory-configured for IPv4 TCP/IP communication and includes a fast Ethernet adapter (10/100 Mbps) with a RJ45-type connector for integrating the device into a local area network (LAN). If the instrument will be connected to a LAN, an active, tested network jack must be in place before the scheduled installation date. Also, a representative from your information technologies department must complete and return the *SeqStudio™ Genetic Analyzer IT Checklist* (Pub. No. MAN0016055) before installation, and be available during the installation to help connect the instrument to your network.

## Safety requirements

### Safety practices

A safety representative from your facility must ensure that:

- Personnel establish and follow all applicable safety practices and policies to protect laboratory personnel from potential hazards.
- All applicable safety devices and equipment are available at all times.
Your laboratory has specific safety practices and policies designed to protect laboratory personnel from potential hazards that are present. Follow all applicable safety-related procedures at all times.

The following safety equipment and protection from hazards must be available at the installation site:

- Protection from any sources of hazardous chemicals, radiation (for example, lasers, radioisotopes, radioactive wastes, and contaminated equipment), and potentially infectious biological material that may be present in the area where the service representative will work.
- Appropriate fire extinguisher:
  - You are responsible for providing an appropriate fire extinguisher for use on or near the equipment.
  - The types and sizes of fire extinguishers shall be suitable for use on electrical and chemical fires as specified in current codes, regulations, and/or standards, and with approval of the Fire Marshall or other authority having jurisdiction.
  - The installation of appropriate fire extinguishers shall be in addition to other fire-protection systems and not as a substitute or alternative to them.
- Eyewash
- Safety shower
- Eye and hand protection
- Adequate ventilation, including vent line/fume hood, if applicable
- Biohazard waste container, if applicable
- First-aid equipment
- Spill cleanup equipment
- Applicable Safety Data Sheets (SDSs)
WARNING! GENERAL SAFETY. Using this product in a manner not specified in the user documentation may result in personal injury or damage to the instrument or device. Ensure that anyone using this product has received instructions in general safety practices for laboratories and the safety information provided in this document.

- Before using an instrument or device, read and understand the safety information provided in the user documentation provided by the manufacturer of the instrument or device.
- Before handling chemicals, read and understand all applicable Safety Data Sheets (SDSs) and use appropriate personal protective equipment (gloves, gowns, eye protection, and so on). To obtain SDSs, 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.

<table>
<thead>
<tr>
<th>Symbol</th>
<th>English</th>
<th>Français</th>
</tr>
</thead>
<tbody>
<tr>
<td><img src="image" alt="Caution, risk of danger" /></td>
<td>Caution, risk of danger&lt;br&gt;Consult the manual for further safety information.</td>
<td>Attention, risque de danger&lt;br&gt;Consulter le manuel pour d'autres renseignements de sécurité.</td>
</tr>
<tr>
<td><img src="image" alt="Caution, risk of electrical shock" /></td>
<td>Caution, risk of electrical shock</td>
<td>Attention, risque de choc électrique</td>
</tr>
<tr>
<td><img src="image" alt="Caution, piercing hazard" /></td>
<td>Caution, piercing hazard</td>
<td>Attention, danger de perforation</td>
</tr>
<tr>
<td>Symbol</td>
<td>English</td>
<td>Français</td>
</tr>
<tr>
<td>--------</td>
<td>---------</td>
<td>---------</td>
</tr>
<tr>
<td>![Triangle]</td>
<td>Caution, hot surface</td>
<td>Attention, surface chaude</td>
</tr>
<tr>
<td>![Biohazard]</td>
<td>Potential biohazard</td>
<td>Danger biologique potentiel</td>
</tr>
<tr>
<td>![On]</td>
<td>On</td>
<td>On (marche)</td>
</tr>
<tr>
<td>![Off]</td>
<td>Off</td>
<td>Off (arrêt)</td>
</tr>
<tr>
<td>![On/Off]</td>
<td>On/Off</td>
<td>On/Off (marche/arrêt)</td>
</tr>
<tr>
<td>![Protective conductor terminal]</td>
<td>Protective conductor terminal (main ground)</td>
<td>Borne de conducteur de protection (mise à la terre principale)</td>
</tr>
<tr>
<td>![Alternating current or voltage]</td>
<td>Terminal that can receive or supply alternating current or voltage</td>
<td>Borne pouvant recevoir ou envoyer une tension ou un courant de type alternatif</td>
</tr>
<tr>
<td>![Do not dispose of this product]</td>
<td>Do not dispose of this product in unsorted municipal waste</td>
<td>Ne pas éliminer ce produit avec les déchets usuels non soumis au tri sélectif.</td>
</tr>
</tbody>
</table>

**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.

**MISE EN GARDE !** 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

<table>
<thead>
<tr>
<th>Conformity mark</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>![Conformity mark]</td>
<td>Indicates conformity with safety requirements for Canada and U.S.A.</td>
</tr>
</tbody>
</table>
Appendix G Safety

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.

<table>
<thead>
<tr>
<th>Conformity mark</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>⭐️ ⭐️</td>
<td>Indicates conformity with Australian standards for electromagnetic compatibility.</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>English</th>
<th>Français</th>
</tr>
</thead>
<tbody>
<tr>
<td>CAUTION! Hazardous waste. Refer to SDS[s] and local regulations for handling and disposal.</td>
<td>MISE EN GARDE ! Déchets dangereux. Lire les fiches signalétiques [FS] et la réglementation locale associées à la manipulation et à l’élimination des déchets.</td>
</tr>
<tr>
<td>DANGER! Class 3B (III) visible and/or invisible laser radiation present when open and interlocks defeated. Avoid exposure to beam.</td>
<td>DANGER ! Rayonnement laser ou DEL visible ou invisible de classe 3B (III) présent en position ouverte et avec les dispositifs de sécurité non enclenchés. Eviter toute exposition au faisceau.</td>
</tr>
</tbody>
</table>
Safety information for instruments not manufactured by Thermo Fisher Scientific

Some of the accessories provided as part of the instrument system are not designed or built by Thermo Fisher Scientific. Consult the manufacturer’s documentation for the information needed for the safe use of these products.

Instrument safety

General

⚠️ CAUTION! Do not remove instrument protective covers. If you remove the protective instrument panels or disable interlock devices, you may be exposed to serious hazards including, but not limited to, severe electrical shock, laser exposure, crushing, or chemical exposure.

Physical injury

⚠️ CAUTION! Moving Parts. Moving parts can crush, pinch and cut. Keep hands clear of moving parts while operating the instrument. Disconnect power before servicing.

Electrical safety

⚠️ WARNING! Ensure appropriate electrical supply. For safe operation of the instrument:

- Plug the system into a properly grounded receptacle with adequate current capacity.
- Ensure the electrical supply is of suitable voltage.
- Never operate the instrument with the ground disconnected. Grounding continuity is required for safe operation of the instrument.

⚠️ 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.

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.

Laser

**WARNING! LASER HAZARD.** Under normal operating conditions, the SeqStudio™ Genetic Analyzer is categorized as a Class 1 laser product. However, removing the protective covers and defeating the interlock(s) may result in exposure to the internal Class 3B laser. Lasers can burn the retina, causing permanent blind spots. To ensure safe laser operation:

- Never look directly into the laser beam.
- Do not remove safety labels, instrument protective panels, or defeat safety interlocks.
- The system must be installed and maintained by a Thermo Fisher Scientific Technical Representative.
- Remove jewelry and other items that can reflect a laser beam into your eyes or those of others
- Wear proper eye protection and post a laser warning sign at the entrance to the laboratory if the laser protection is defeated for servicing
- DO NOT operate the laser when it cannot be cooled by its cooling fan; an overheated laser can cause severe burns on contact.
Safety and electromagnetic compatibility (EMC) standards

The instrument design and manufacture complies with the following standards and requirements for safety and electromagnetic compatibility.

Safety compliance

<table>
<thead>
<tr>
<th>Reference</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>EN 61010-1</td>
<td>Safety requirements for electrical equipment for measurement, control, and laboratory use – Part 1: General requirements</td>
</tr>
<tr>
<td>UL 61010-1</td>
<td>Safety requirements for electrical equipment for measurement, control, and laboratory use – Part 1: General requirements</td>
</tr>
<tr>
<td>CSA C22.2 No. 61010-1</td>
<td>Safety requirements for electrical equipment for measurement, control, and laboratory use – Part 1: General requirements</td>
</tr>
<tr>
<td>EN 61010-2-010</td>
<td>Safety requirements for electrical equipment for measurement, control and laboratory use – Part 2-010: Particular requirements for laboratory equipment for the heating of materials</td>
</tr>
<tr>
<td>EN 61010-2-081</td>
<td>Safety requirements for electrical equipment for measurement, control, and laboratory use – Part 2-010: Particular requirements for automatic and semi-automatic laboratory equipment for analysis and other purposes</td>
</tr>
<tr>
<td>EN 60825-1</td>
<td>Safety of lasers products – Part 1: Equipment classification and requirements</td>
</tr>
</tbody>
</table>

EMC

<table>
<thead>
<tr>
<th>Reference</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>EN 61326-1</td>
<td>Electrical equipment for measurement, control and laboratory use – EMC requirements – Part 1: General requirements</td>
</tr>
<tr>
<td>AS/NZS CISPR 22</td>
<td>Limits and Methods of Measurement of Electromagnetic Disturbance Characteristics of Industrial, Scientific, and Medical (ISM) Radiofrequency Equipment</td>
</tr>
<tr>
<td>ICES-003, Issue 5</td>
<td>Industrial, Scientific and Medical (ISM) Radio Frequency Generators</td>
</tr>
</tbody>
</table>
### Environmental design

<table>
<thead>
<tr>
<th>Reference</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>SJ/T 11364-2014</td>
<td>“China RoHS” Standard—Marking for the Restricted Use of Hazardous Substances in Electronic and Electrical Products</td>
</tr>
</tbody>
</table>

### Radio compliance

<table>
<thead>
<tr>
<th>Reference</th>
<th>Description</th>
</tr>
</thead>
</table>
WARNING! GENERAL CHEMICAL HANDLING. To minimize hazards, ensure laboratory personnel read and practice the general safety guidelines for chemical usage, storage, and waste provided below. Consult the relevant SDS for specific precautions and instructions:

- Read and understand the Safety Data Sheets (SDSs) provided by the chemical manufacturer before you store, handle, or work with any chemicals or hazardous materials. To obtain SDSs, see the “Documentation and Support” section in this document.
- Minimize contact with chemicals. Wear appropriate personal protective equipment when handling chemicals (for example, safety glasses, gloves, or protective clothing).
- Minimize the inhalation of chemicals. Do not leave chemical containers open. Use only with adequate ventilation (for example, fume hood).
- Check regularly for chemical leaks or spills. If a leak or spill occurs, follow the manufacturer’s cleanup procedures as recommended in the SDS.
- Handle chemical wastes in a fume hood.
- Ensure use of primary and secondary waste containers. (A primary waste container holds the immediate waste. A secondary container contains spills or leaks from the primary container. Both containers must be compatible with the waste material and meet federal, state, and local requirements for container storage.)
- After emptying a waste container, seal it with the cap provided.
- Characterize (by analysis if necessary) the waste generated by the particular applications, reagents, and substrates used in your laboratory.
- Ensure that the waste is stored, transferred, transported, and disposed of according to all local, state/provincial, and/or national regulations.
- IMPORTANT! Radioactive or biohazardous materials may require special handling, and disposal limitations may apply.
Biological hazard safety

**WARNING! BIOHAZARD.** Biological samples such as tissues, body fluids, infectious agents, and blood of humans and other animals have the potential to transmit infectious diseases. Conduct all work in properly equipped facilities with the appropriate safety equipment (for example, physical containment devices). Safety equipment can also include items for personal protection, such as gloves, coats, gowns, shoe covers, boots, respirators, face shields, safety glasses, or goggles. Individuals should be trained according to applicable regulatory and company/institution requirements before working with potentially biohazardous materials. Follow all applicable local, state/provincial, and/or national regulations. The following references provide general guidelines when handling biological samples in laboratory environment.

Documentation and support

Related documentation

<table>
<thead>
<tr>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>SeqStudio™ Genetic Analyzer Instrument and Software User Guide</td>
<td>MAN0016138</td>
</tr>
<tr>
<td>SeqStudio™ Genetic Analyzer with Data Collection Software v 1.1 Getting Started Guide</td>
<td>MAN0017464</td>
</tr>
<tr>
<td>DNA Fragment Analysis by Capillary Electrophoresis User Guide</td>
<td>4474504</td>
</tr>
<tr>
<td>DNA Sequencing by Capillary Electrophoresis Chemistry Guide Second Edition</td>
<td>4305080</td>
</tr>
<tr>
<td>Troubleshooting Sanger sequencing data</td>
<td>MAN0014435</td>
</tr>
<tr>
<td>SeqStudio™ Genetic Analyzer Site Preparation Guide</td>
<td>MAN0016143</td>
</tr>
</tbody>
</table>

Customer and technical support

Visit thermofisher.com/support for the latest service and support information.

- Worldwide contact telephone numbers
- Product support information
  - Product FAQs
  - Software, patches, and updates
  - Training for many applications and instruments
- Order and web support
- Product documentation
  - User guides, manuals, and protocols
  - Certificates of Analysis
  - Safety Data Sheets (SDSs; also known as MSDSs)

**Note:** For SDSs for reagents and chemicals from other manufacturers, contact the manufacturer.

Limited product warranty

Life Technologies Corporation and/or its affiliate(s) warrant their products as set forth in the Life Technologies' General Terms and Conditions of Sale at www.thermofisher.com/us/en/home/global/terms-and-conditions.html. If you have any questions, please contact Life Technologies at www.thermofisher.com/support.
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