Spectrum Compact CE System Remote Access Software Manual

Instructions for Using the Spectrum Compact CE System with Remote Access Software

TMD064 | REVISED 8/23

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All technical literature is available at: **www.promega.com/protocols/**

Visit the web site to verify that you are using the most current version of this Technical Manual.

E-mail Promega Technical Services if you have questions on use of this system: **genetic@promega.com**

Description 1

1.1 Spectrum Compact CE System Remote Access Software

The Spectrum Compact CE System Remote Access Software enables the user to create/edit/review/delete strip IDs for sample strips, create/edit/review/delete protocols and assays, view analysis results, monitor a Spectrum Compact CE System run in progress as well as completed runs, and download completed runs using a web browser on a PC connected to the instrument either directly or over a lab network. The application must be operated in Microsoft® Internet Explorer® 11, Microsoft Edge, Google Chrome or Mozilla Firefox.

Note: The Spectrum Compact CE System Remote Access Software allows the user to create, edit, review and delete strip IDs, protocols and assays located on the Spectrum Compact CE System. That is, any changes made using the Spectrum Compact CE System Remote Access Software are immediately viewable locally on the Spectrum Compact CE System.

Safety information, operational precautions, operation methods, maintenance methods, and troubleshooting are described in the *Spectrum Compact CE System Operating Manual* #TMD058. Please make sure to read all manuals carefully before using the Spectrum Compact CE System.

Warning

To avoid injury or harm, review all system and safety information before use.

- Review all safety precautions
- Follow all instructions outlined in the relevant Technical Manuals

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1.2 System Requirements

Operating Environment	Description
Standalone environment	Use the integrated touch panel of the Spectrum Compact CE System for electrophoresis, data analysis viewing reports. Transfer primary analysis data via an external storage medium such as USB Memory.
Network environment	Connect the Spectrum Compact CE System via your local area network or directly to a PC.
Regulatory Compliance	For Research Use Only. Not for use in Diagnostic Procedures.

- Connecting to a local area network and setup is the responsibility of the user.
- Only wired local network connections are possible.
- Wireless connections are not supported.

1.3 Minimum PC and Monitor Specifications

Item	Specification
CPU	32bit (x86) or 64bit, 1GHz
Operating System	Windows® 7 Service Pack 1 or higher or Windows® 10
Memory	512MB
Storage for	Windows® 7 32-bit—70 MB Windows® 7 64-bit—120 MB
Display	SVGA over (800×600) 256 colors. Minimum resolution of 1360x768 is recommended
Internet Browser	Internet Explorer® 11, Microsoft Edge, Google Chrome or Mozilla Firefox

1.4 PC Setting (Sleep Mode/Hibernation Mode)

If the PC enters sleep or hibernate mode while using the Spectrum Compact CE System Remote Access Software, the connection to the Spectrum Compact CE System may be terminated, requiring the user to login to the instrument/software again.

Note: We recommend disabling sleep/hibernation mode on the PC.

If the connection with the Spectrum Compact CE System has been lost, perform the following procedure.

- Restart the web browser. You can log into the system by using the Force Login function.
- Log into the system 1 hour after closing the web browser. Normal login is possible.

1.5 Installing the Certificate

This section explains how to export the certificate from the Spectrum Compact CE System and import it to the PC using the web browser Google Chrome. When using Microsoft Edge or Mozilla Firefox, refer to the brower-specific instruction manual.

The certificate must be installed after any of the following operations.

- Connecting to Remote Access for the first time
- Changing the IP address of the instrument
- Changing the mode of the instrument IP address (by enabling/disabling Use DHCP)
- Changing the instrument name

1.5.1 Exporting the Certificate

1. Enter the following URL in the web browser:

https://IP address of the instrument/CCERemoteAccess

2. Select the “Not secure” warning in the browser address bar. Choose **Certificate (Invalid)**.

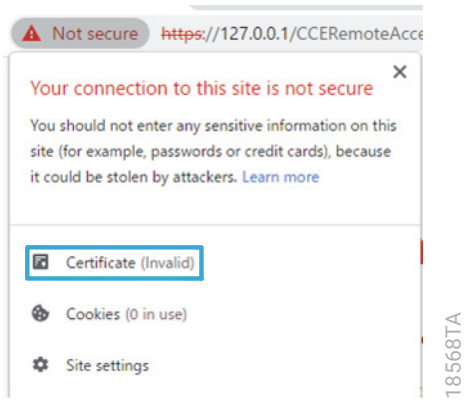

Figure 1. Screen displayed when the “Not secure” warning Is selected in Google Chrome.

3. Select the ‘Details’ tab of the Certificate window and choose **Copy to File...**.

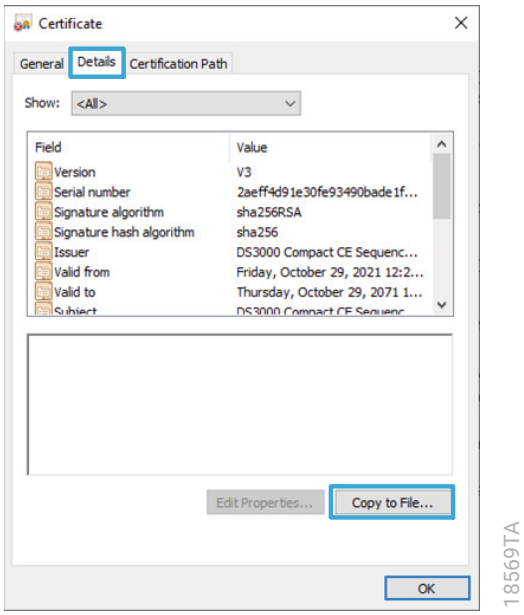

Figure 2. Certificate window shown in Google Chrome.

4. The Certificate Export Wizard starts. Follow the wizard to export the certificate file.

In the Export File Format section of the wizard, select **DER encoded binary X.509 (.CER)**.

1.5.2 Importing the Certificate

1. On the Control Panel, select **Internet Options**.
2. Select the 'Content' tab and then **Certificates**.

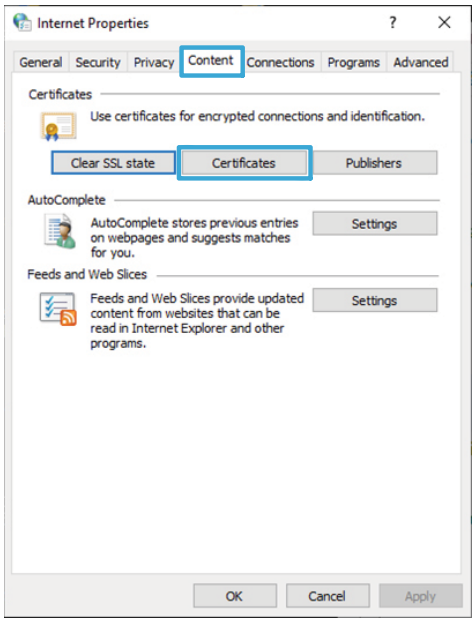

Figure 3. 'Internet Properties' screen.

3. On the 'Certificates' window, select the 'Trusted Root Certification Authorities' tab and choose **Import**.

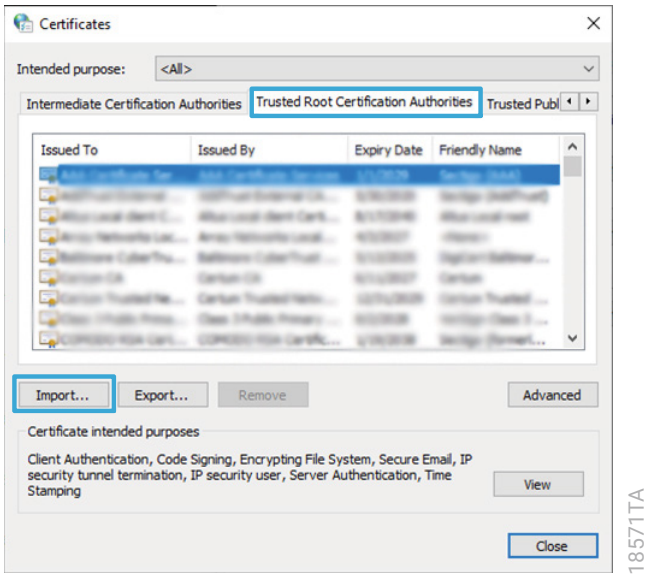

Figure 4. 'Certificates' window.

4. The Certificate Export Wizard starts. Follow the wizard to import the exported certificate file.

In the “Certificate store:” section displayed on the wizard, select “Trusted Root Certification Authorities”.

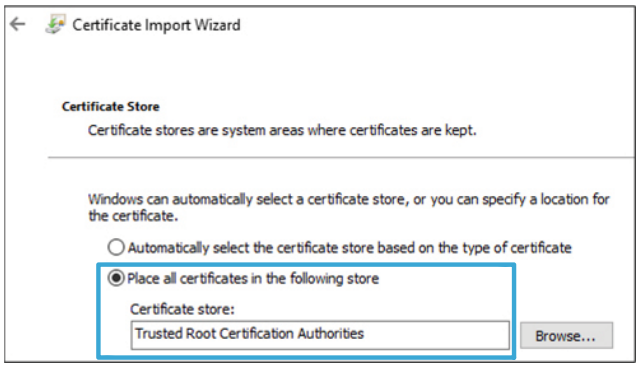

Figure 5. Certificate Import Wizard.

1.5.3 Checking the Installed Certificate

1. Close the web browser if it is running.
2. Open the web browser and type the following URL:

   https://IP address of the instrument/CCERemoteAccess

3. Check that the Login screen is displayed, instead of a screen with the “Your connection is not private” message.

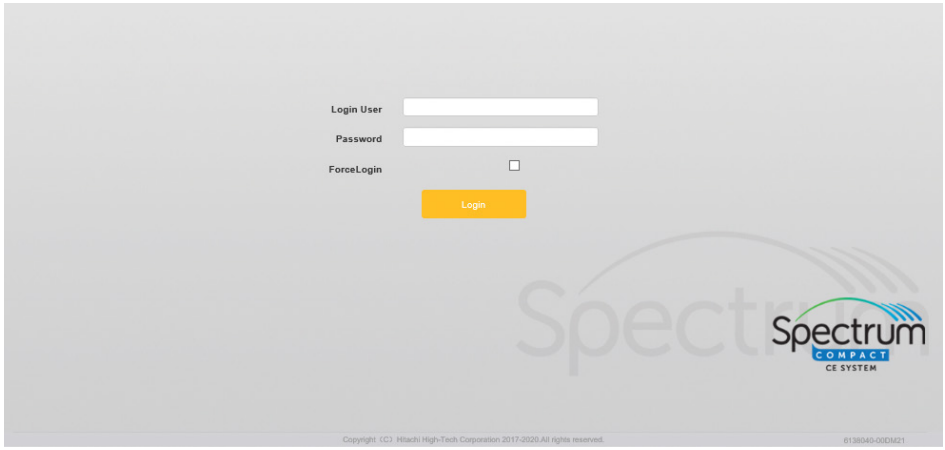

Figure 6. Login screen.

If you see the screen with the “Your connection is not private” message, reboot the instrument with the network cable kept connected, and retry importing the certificate.

If you still see the screen with the “Your connection is not private” message, contact Promega Technical Services.

Even if the certificate fails to be properly installed and you get the “Your connection is not private” message, you can still use Remote Access with the following method:

a. On the screen with the “Your connection is not private” message, choose **Advanced**.

b. Select **Proceed to (IP address) (unsafe)** in the displayed section.

c. The Login screen is displayed.

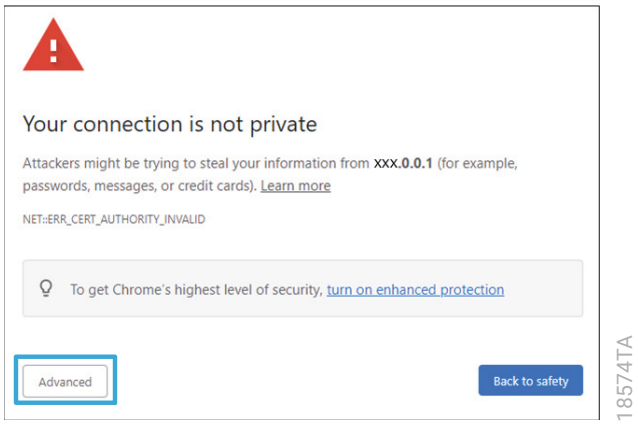

Figure 7. Screen with the “Your connection is not private” message shown in Google Chrome.

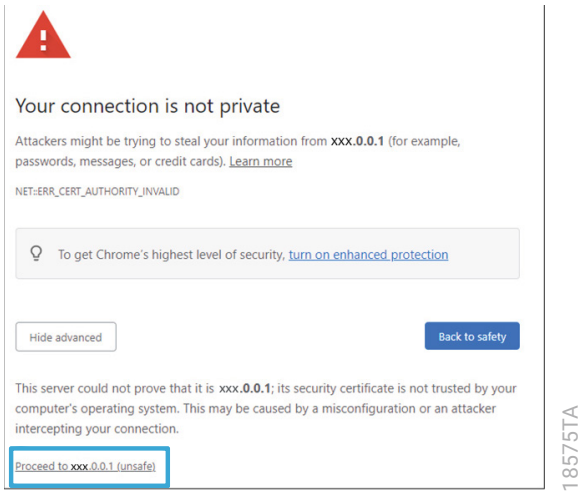

Figure 8. Screen with the “Your connection is not private” message.

System Connections 2

2.1 Network Connections

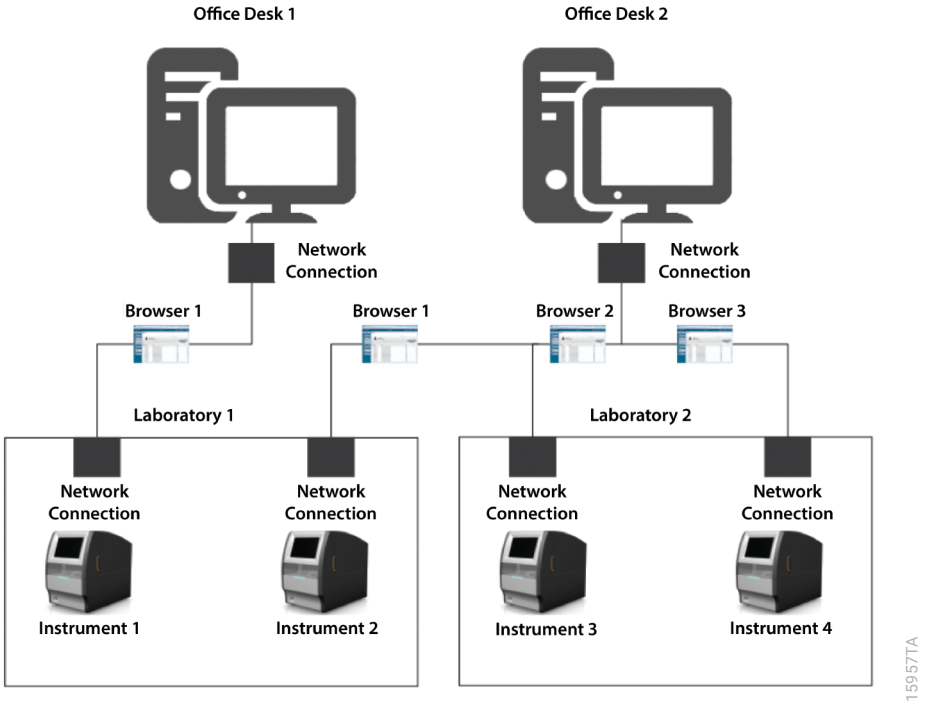

Figure 9. Example system connection diagram.

The Spectrum Compact Remote Access Software allows a user to connect to a Spectrum Compact CE System from a PC on the same network (Figure 9). Up to five separate user remote access connections per instrument are allowed at a given time. The same PC can connect to multiple instruments.

Notes:

1. When one PC is used to connect to multiple Spectrum Compact CE Systems, different browser windows within the same browser can be used to connect to the different instruments. It is not necessary to have separate browsers applications for each Spectrum Compact CE System.

2. While up to five separate users may connect to one instrument, the same user account cannot be used to access the same instrument more than once. A duplicate remote access login of a user that is currently logged in via the Spectrum Compact Remote Access Software is not allowed. The first user is not kicked out of the system by the attempted log in of a second user with the same user ID.

2.2 Network Settings and User Accounts for the Spectrum Compact CE System

Instructions for connecting the Spectrum Compact CE System to an external computer (either directly or via a local network connection) are provided in Section 8.2 of the *Spectrum Compact CE System Operating Manual* #TMD058.

Instructions for creating user accounts for the Spectrum Compact CE System are provided in Section 8.4 of the *Spectrum Compact CE System Operating Manual* #TMD058. User's rights to use the Spectrum Compact Remote Access Software may be enabled or disabled as described in Section 8.4.1 of the *Spectrum Compact CE System Operating Manual* #TMD058.

Operating the Software 3

3.1 Navigating the Spectrum Compact CE System Remote Access Software

1. Enter the following URL into your web browser:
   https://Instrument IP address/CCERemoteAccess

   Notes:

   a. Contact your IT department or site Administrator to configure the Spectrum Compact CE System with an IP address, according to the IT procedures pertinent to your institution.

   b. Spectrum Compact CE System Remote Access Software is preloaded and located on Spectrum Compact CE System. The Spectrum Compact CE System must be turned on and connected to the same network as the external computer to connect with and use the Spectrum Compact CE System Remote Access Software.

   c. While connecting to the Spectrum Compact Remote Access Software using your internet browser, if you get a warning message indicating that the site is not secure, not private, or there is a potential security risk (warning will vary slightly depending on browser), select **Advanced** or **More information** (depending on browser) and then **Proceed to indicated IP address**, **Go on to webpage**, or **Accept risk and continue** (depending on browser) to access the 'Login' screen.

Browser	Warning	Icon to Select on Warning Screen	Icon to Select to Proceed to Login Screen
Internet Explorer 11	This site is not secure	More information	Go on to webpage (not recommended)
Google Chrome	Your connection is not private	Advanced	Proceed to XX.XX.XXX.XX (unsafe)

Browser	Warning	Icon to Select on Warning Screen	Icon to Select to Proceed to Login Screen
Mozilla Firefox	Warning: Potential Security Risk Ahead	Advanced	Accept the Risk and Continue
Microsoft Edge	Your connection isn't private	Advanced	Continue to XX.XX.XXX.XX (unsafe)

2. Confirm that the 'Login' screen is displayed (Figure 10) and enter User Name and Password.

   Notes:

   a. The 'Login' screen requiring User Name and Password is displayed under both Normal and High security settings on the Spectrum Compact CE System (see Section 8.3 of *Spectrum Compact CE System Operating Manual* #TMD058). Once logged in to a Spectrum Compact CE System under Normal security settings, all users are treated as administrators in the same way as if working on the Spectrum Compact CE System Software at the instrument.

   b. User Name and Passwords are established in the instrument user accounts (see Section 8.4 of the *Spectrum Compact CE System Operating Manual* #TMD058). The following table lists rules for characters that can be used on the Spectrum Compact CE System and Spectrum Compact CE System Remote Access Software for user names, passwords, strip IDs, sample names, protocol IDs and assays.

Acceptable Characters	1 to 30 characters for user names and Strip IDs
	1 to 40 characters for passwords, protocol IDs and assays
	1 to 50 characters for sample names
	Upper- and lowercase alphabetic characters
	Numbers
	Symbols unless listed below
Unacceptable Characters	#%&{}\<>*?/$!'":@+`|= and space

3. Select **Login** on the 'Spectrum Compact CE System Remote Access Software Login' screen (Figure 10).

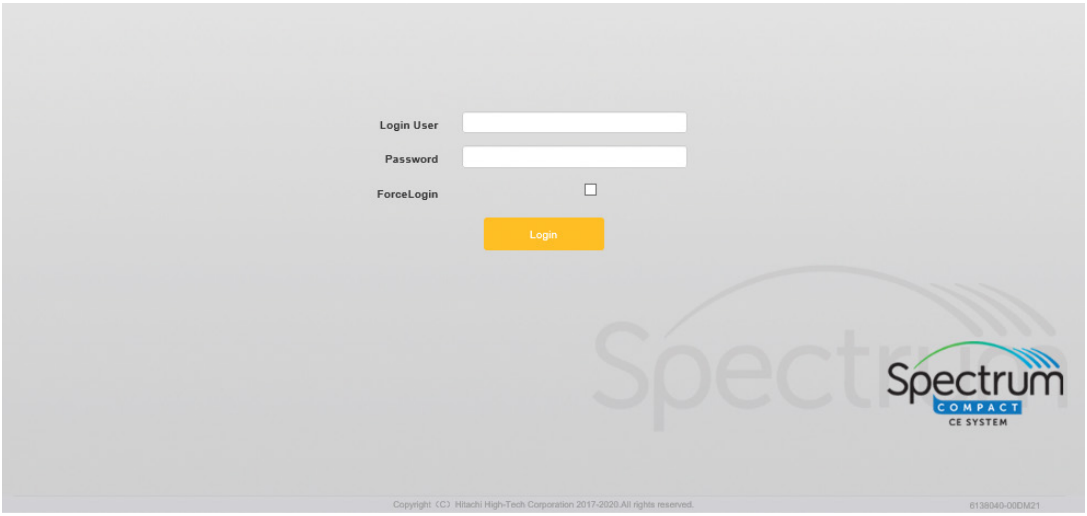

Figure 10. 'Spectrum Compact CE System Remote Access Software Login' screen.

Note: If the Spectrum Compact CE System Remote Access Software was not properly closed from a prior login session, the following error will occur when attempting to login again: "Access is denied. Entered User ID has been logged in by another computer." (Figure 11). Check the **ForceLogin** box and repeat login procedure with Login User and Password. See Section 10 for logging out instructions when closing the Spectrum Compact CE System Remote Access Software.

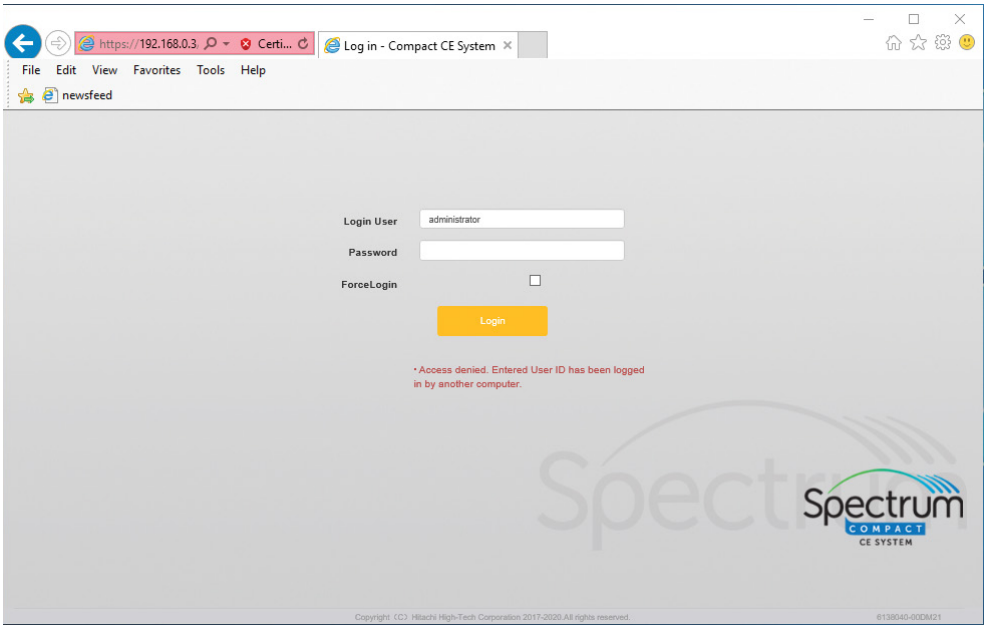

Figure 11. 'Access is denied. This account already logged in' error screen.

4. The ‘HOME’ screen is composed of the Header, Run List and Main Menu (left side of ‘HOME’ screen; Figure 12).

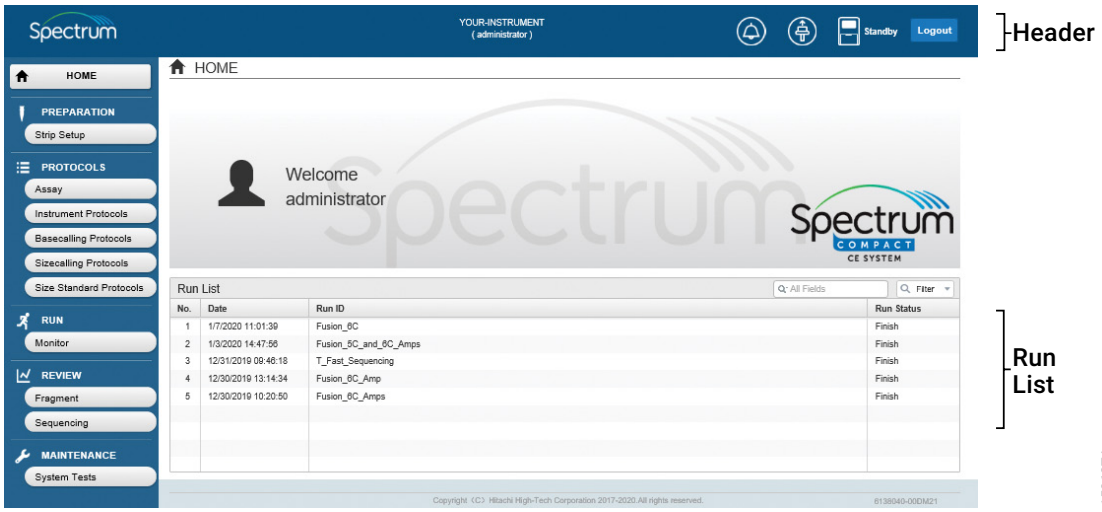

Figure 12. Spectrum Compact Remote Access Software ‘HOME’ screen.

5. The Spectrum Compact CE System Remote Access Software contains several navigation and informational icons in the header. Each icon provides information about a specific function or component.

Icon	Name	Description
	Alarm	Displayed when an alarm has been triggered on the connected Spectrum Compact CE System (Section 9.1). This indicator also acts as a shortcut to the 'Alarm List' screen, which shows details of the alarm (see Section 9.2 of the *Spectrum Compact CE System Operating Manual* #TMD058).
	Consumables	Select this icon to open the 'Consumables' screen (Section 9.2), which shows detailed information and status of each installed consumable. Replacement of consumables must be performed at the instrument using the integrated touch screen (see Section 3 of the *Spectrum Compact CE System Operating Manual* #TMD058).
	Instrument Status	Displays the instrument status. **Standby:** System is idle, but ready to start a run. **Run:** Run is in process. **Stop:** Instrument is in the process of finishing a run, but is not idle (not the same as stopping due to an error). **Open:** Front door or oven-unit door is open. **Recovery:** Initialization after closing door. **Error:** an error is detected and the run has stopped. **Critical:** instrument trouble.
	Unit Name (Login User)	**Unit name:** The Spectrum Compact CE System unique ID is shown. The Remote Access User Name is shown in parentheses.
	Logout	Select **Logout** to log off the current user. **Note:** Do not close the browser before logging out, as this will keep the user logged into the instrument.

6. The 'Run List' (a list of all of the runs stored on the Spectrum Compact CE System) on the 'HOME' screen shows the following information:
   - Run Number (No.)
   - Date
   - Run ID
   - Run Status

3.2 Main Menu

The ‘Main Menu’ portion of the ‘HOME’ screen is divided into five main sections:

Main Menu Item	Name/Button	Contents
		Strip Setup allows the user to assign sample details such as Sample Name and Sample Type (Unused, Positive Control, Negative Control, Sample and Allelic Ladder) to a Strip ID.

Main Menu Item	Name/Button	Contents
		An assay is comprised of application type (sequencing or fragment), instrument protocol, polymer type, dye set, and an analysis protocol required for data collection. The analysis protocol used depends on the application: • Fragment: Sizecalling Protocol • Sequencing: Basecalling Protocol
		Defines the instrument settings to be applied during a run. These include: • Application Type (Sequencing or Fragment) • Polymer Type • Electrophoresis Conditions
		The initial analysis protocol required for sequencing applications. Defines the parameters for assigning base calls to data peaks.
		The initial analysis protocol required for fragment applications. Defines the parameters for assigning size calls to data peaks.
		Defines size of DNA fragments of known lengths. Used to generate a sizing curve by which unknown fragments are sized.
		Shows real-time data of the current injection.

Main Menu Item	Name/Button	Contents
		Shows results of primary analysis for completed fragment analysis runs.
		Shows results of primary analysis for completed sequencing analysis runs.
		Shows the result of the system test.

Note: System Tests can only be performed by Promega-qualified service engineers.

Preparation 4

4.1 Preparing the Strip Cartridge

Sample setup in the sample cartridge is the same for fragment and sequencing analysis. Samples prepared in 8-well strip tubes are assembled into the strip base and retainer to form the sample cartridge that is then loaded onto the instrument (see Section 2.4 of the *Spectrum Compact CE System Operating Manual* #TMD058).

4.2 Assigning Sample Details to a Strip ID

There are two methods available to assign strip information with the Spectrum Compact CE System Remote Access Software. The two methods are the same for sequencing and fragment analysis:

- Creating new strip information
- Editing an existing strip

Note: If the Spectrum Compact CE System is currently running, other users who are logged in via remote access can create new strip IDs, but cannot edit or delete an existing strip ID even if that strip ID is not being currently run.

4.2.1 Creating New Strip Information

1. Select **Strip Setup** under PREPARATION from the 'Main Menu' of the 'HOME' screen (Figure 12), and then select **Create** (Figure 13).

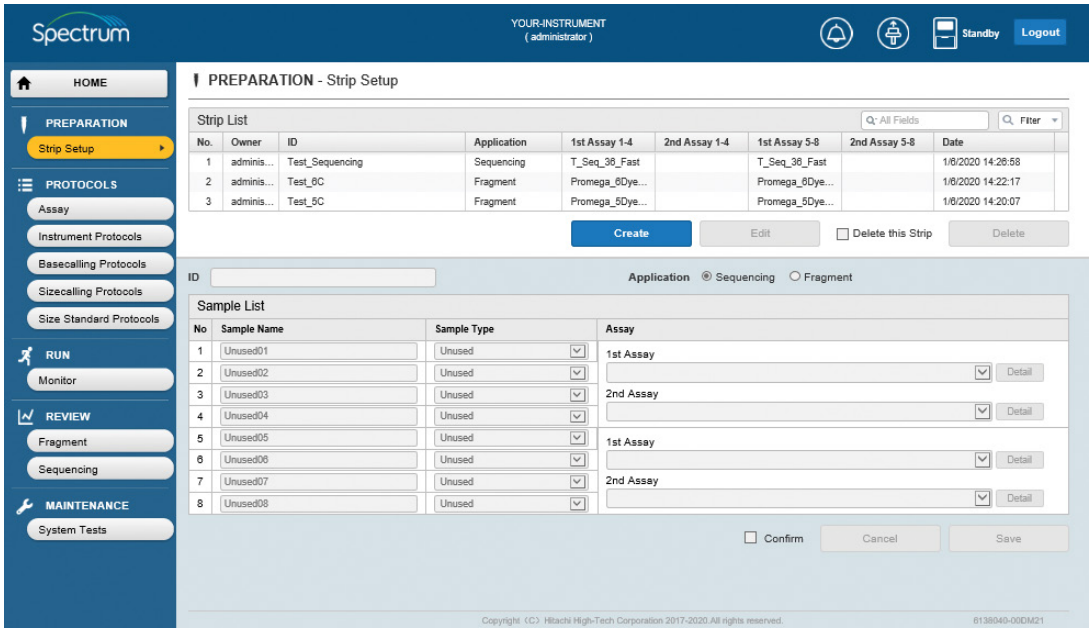

Figure 13. 'Strip Setup' screen.

2. Enter a Strip ID for the new strip by selecting the **ID** field to activate the cursor (Figure 14).
3. Select the application using the appropriate radio button (Sequencing or Fragment) (Figure 14).
4. Select Sample Type (Sample, Positive Control, Negative Control, Allelic Ladder, or Unused) (Figure 14).

   Notes:

   a. The Allelic Ladder sample type is only available for Fragment Analysis.

   b. The Sample Name fields do not become active until a Sample Type has been selected.

   c. A sample type other than "Unused" must be assigned to at least one well in each injection set. If all of the four wells in an injection set are assigned as "Unused", the injection set will not be run. If all eight wells in a strip are assigned as "Unused", a warning message will be displayed on the Spectrum Compact CE System when trying to Link that strip.

5. Input the Sample Names by selecting the **Sample Name** for each well field to activate the cursor (Figure 14).
6. Select the **1st Assay** which will be used for the initial injection using the pulldown menu (Figure 14). Assays are assigned for each set of 4 wells separately (wells 1–4 and wells 5–8).

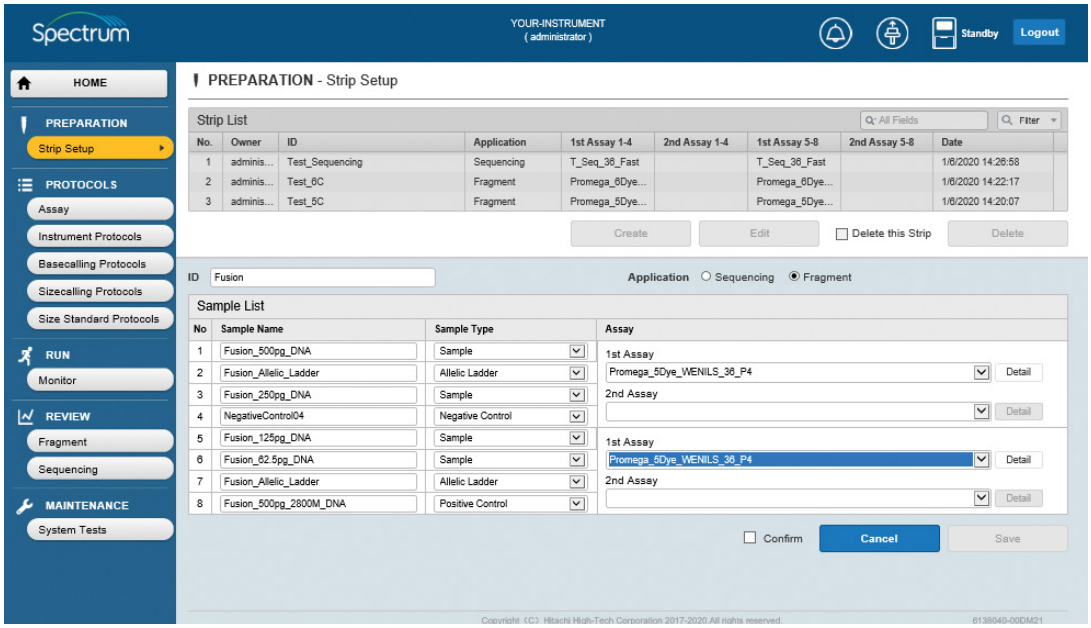

Figure 14. 'Strip Setup' screen: Selecting 1st Assay.

7. You can verify the settings of the assay chosen by selecting **Detail** to the right of the chosen assay (Figure 14). This will display a window showing these settings but will not allow you to edit them (Figure 15). To edit the assay, see Section 5.5.2.

   Note: Detail only becomes active after an assay has been selected.

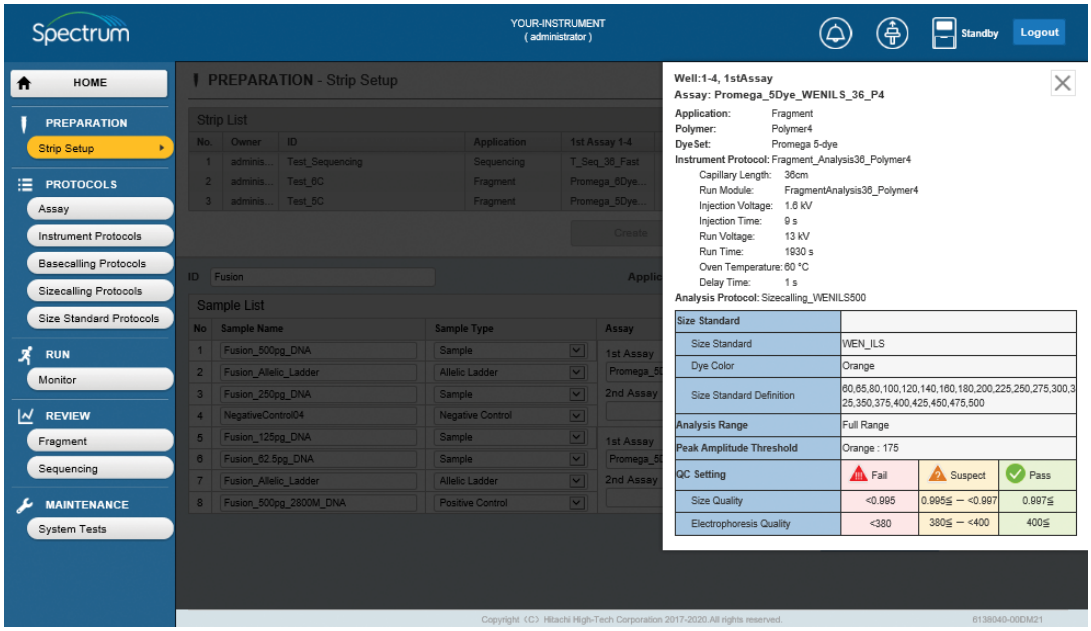

Figure 15. 'Assay Detail' screen.

8. If desired, select the **2nd Assay** which will be used to reinject the same sample using the pull-down menu. Alternatively, the **2nd Assay** can be left blank.

   Note: The assays available in the **2nd Assay** field are filtered based on the dye set in the assay selected in the **1st Assay** field. For example, if a 'Promega_5-dye' dye set based assay is chosen in the **1st Assay** field, then only assays using that same dye set are available as an option in the **2nd Assay** field. In this way, it is possible to duplicate injections with the same assay conditions by choosing the same assay in the **2nd Assay** field as that used in the **1st Assay** field. It is also possible to run duplicate injections of the same assay conditions by using the **Duplicate** function of the 'Edit Injection List' screen when setting up a run on the Spectrum Compact CE System (see Section 5.6 of the *Spectrum Compact CE System Operating Manual* #TMD058).

9. Check the **Confirm** box and select **Save** (Figure 16). If no errors are detected, "Normal End" in a green horizontal box will appear on the screen. If errors are detected, either "Invalid data entered" or "The value is out of range" will appear in a red horizontal box and the software will indicate where the error is occurring.

   Notes:

   a. The **Confirm** check box must be selected to enable **Save**.

   b. **Cancel** does not require checking the **Confirm** box to become active and is always available. Select **Cancel** at any time during creation of a new Strip ID to exit out of the Strip ID creation process without saving any information.

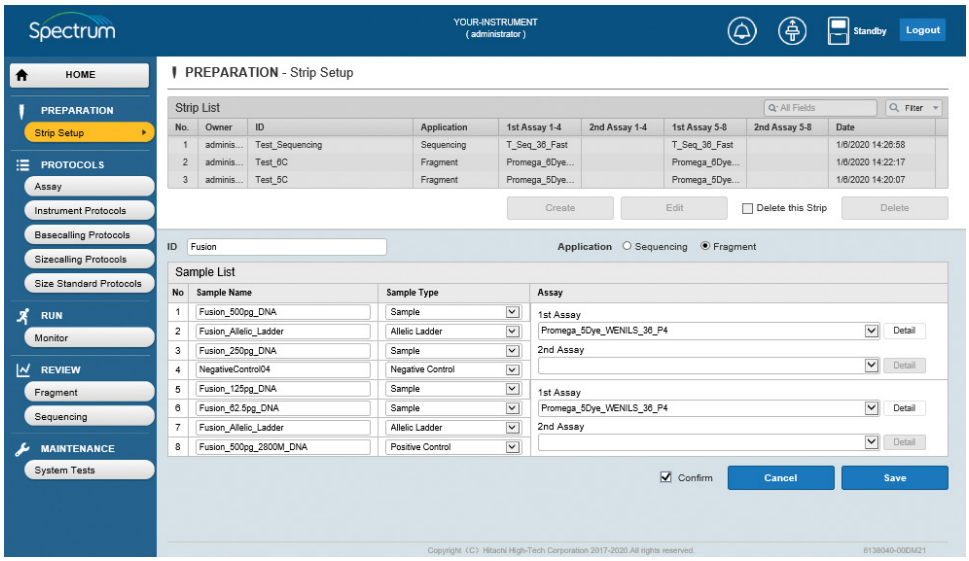

Figure 16. Saving a new strip setup.

10. The saved strip information is now available on the Spectrum Compact Control Software touch screen as well as on the Spectrum Compact CE System Remote Access Software and can be loaded into a run created on the Spectrum Compact Control Software touch screen (see Section 5.3.3 of the *Spectrum Compact CE System Operating Manual* #TMD058).

    Note: Instrument runs cannot be created or started from the Spectrum Compact CE System Remote Access Software. Runs must be created and started on the Spectrum Compact CE System.

4.2.2 Editing an Existing Strip

1. Select **Strip Setup** under PREPARATION from the Main Menu of the 'HOME' screen (Figure 12).
2. Data in the 'Strip List' may be searched and filtered (i.e., searched for based on specific values and then filtered such that only strips that meet the criteria are displayed in the 'Strip List'). Select the magnifying glass icon on the **Select Search Field** box to display a window with radio button selections that allows you to search by All Fields, Owner, ID, Application, 1st Assay 1–4, 2nd Assay 1–4, 1st Assay 5–8, 2nd Assay 5–8, or Date (Figure 17).

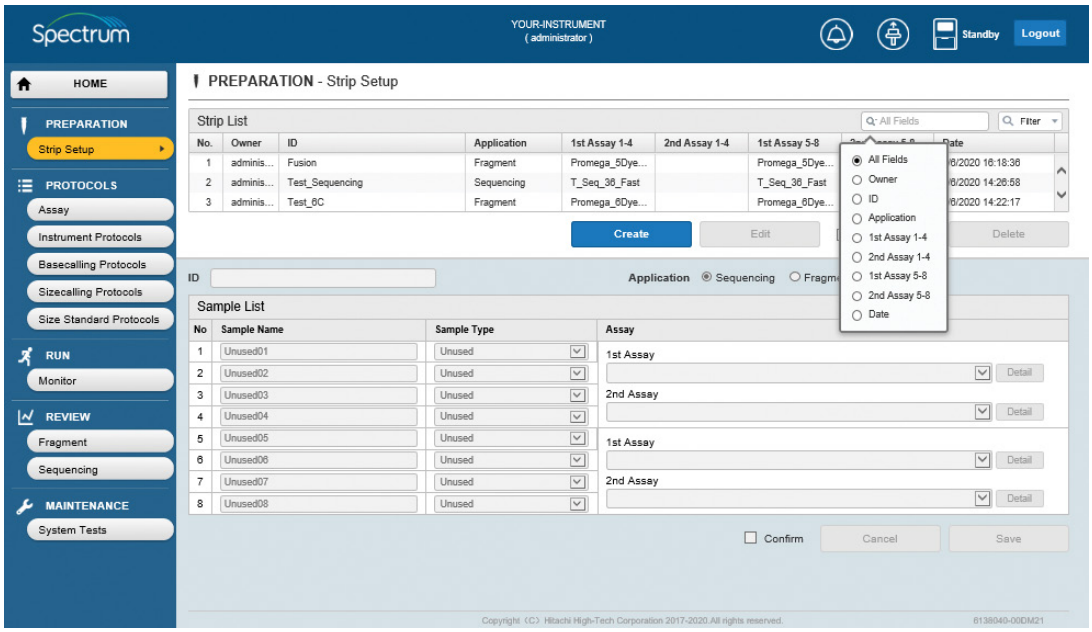

Figure 17. 'Strip List' select search field radio button window.

3. After selecting the appropriate search field, select the magnifying glass or down arrow icon in the **Filter** box to display filtering options by the different fields (Figure 18).
4. Search terms can be filtered by:
   - is
   - begins
   - contains
   - ends

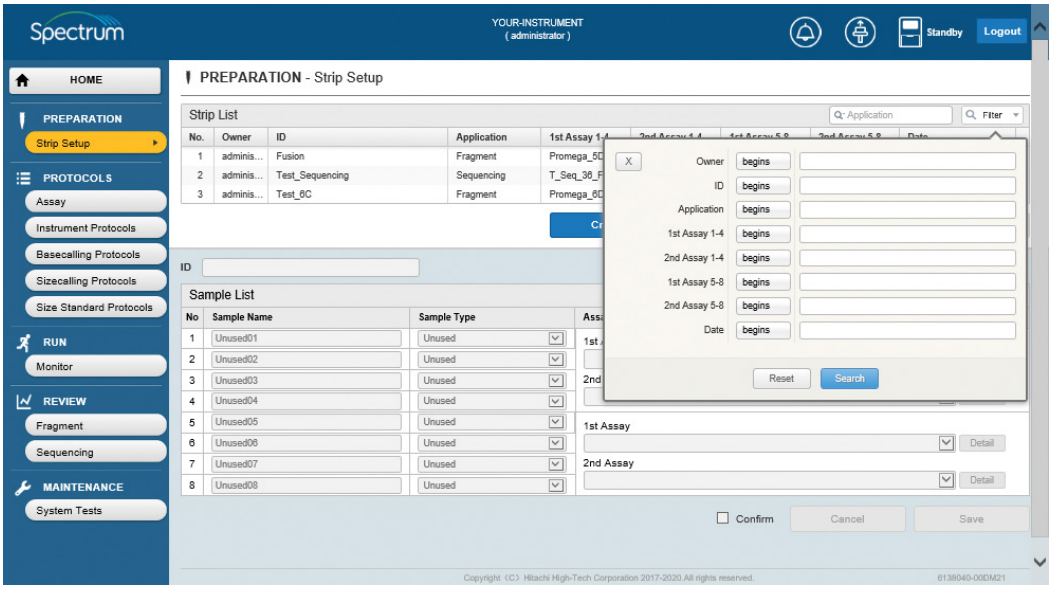

Figure 18. 'Strip List' search filter option selection.

5. After selecting the appropriate filter for the search term in the field being searched (i.e., Owner, ID, Application, 1st Assay 1–4, 2nd Assay 1–4, 1st Assay 5–8, 2nd Assay 5–8 or Date), type the desired search term in the adjacent box and select **Search** (Figure 19). For example, for the Applications search field, select **contains** for the filter category and type "fragment" in the adjacent box. Alternatively, select **Reset** to exit.

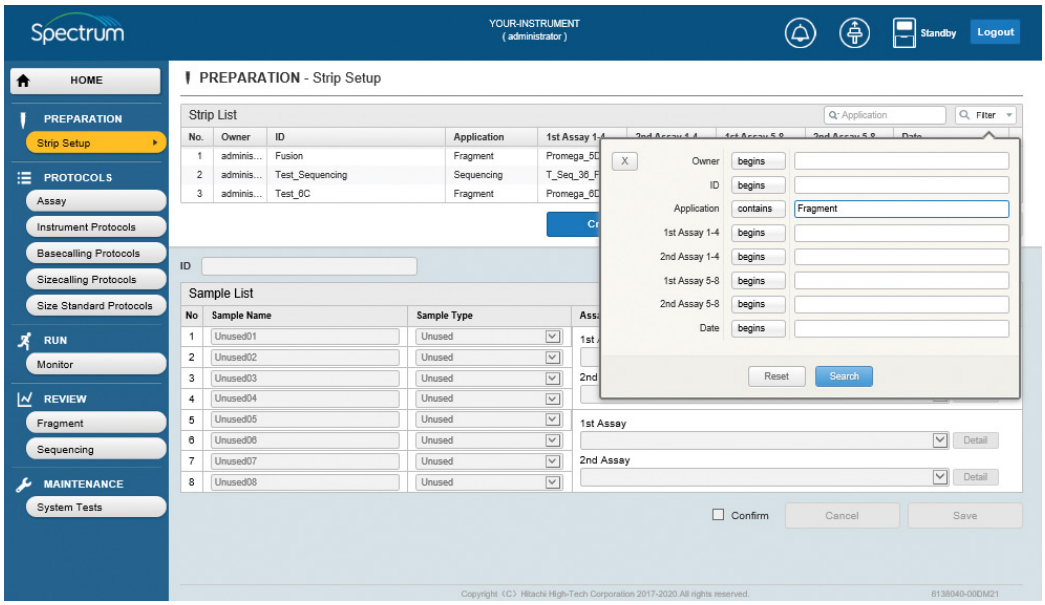

Figure 19. 'Strip List' search filter option selection.

6. The strips that meet the desired search and filter parameters are displayed at the top of the 'Strip List' (Figure 20).

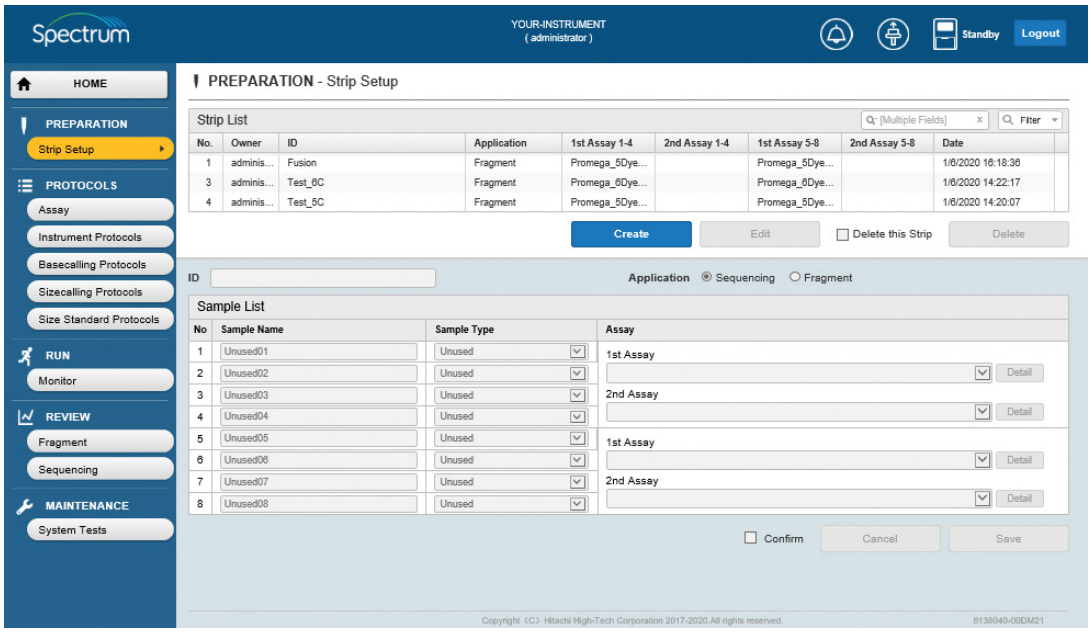

Figure 20. Searched and filtered strips.

7. Select the Strip ID in the Strip List that you want to edit. This will activate **Edit** (Figure 21).

   Note: Before selecting **Edit**, the information in the Sample List portion of the screen is grayed-out and noneditable.

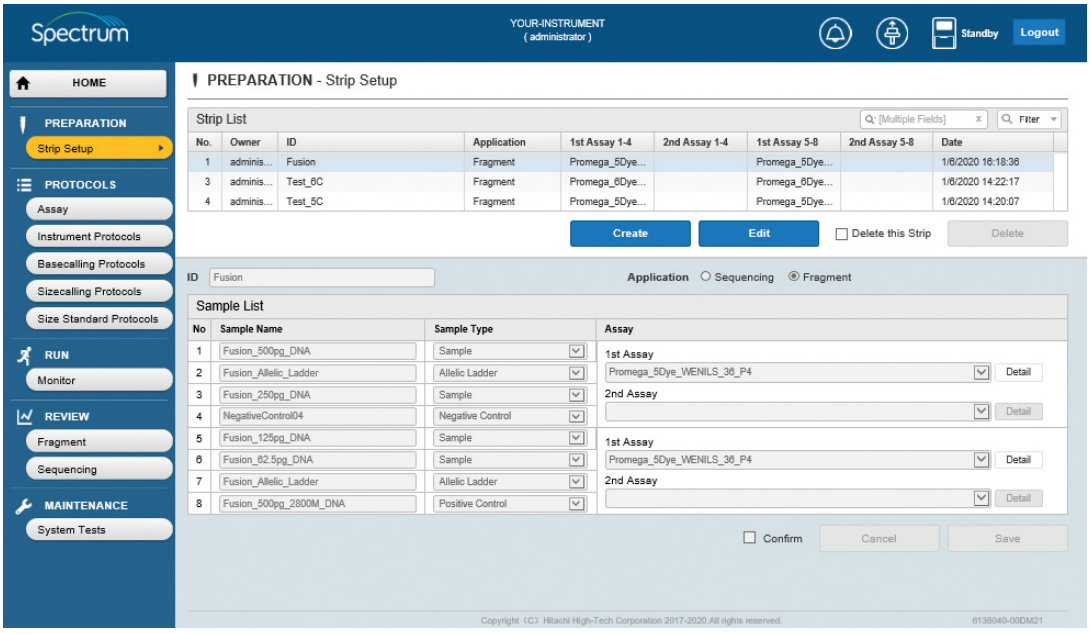

Figure 21. 'Strip Setup' screen with active Edit button.

8. Select **Edit**. This will enable the information in the Sample List part of the screen to be edited (Figure 22).

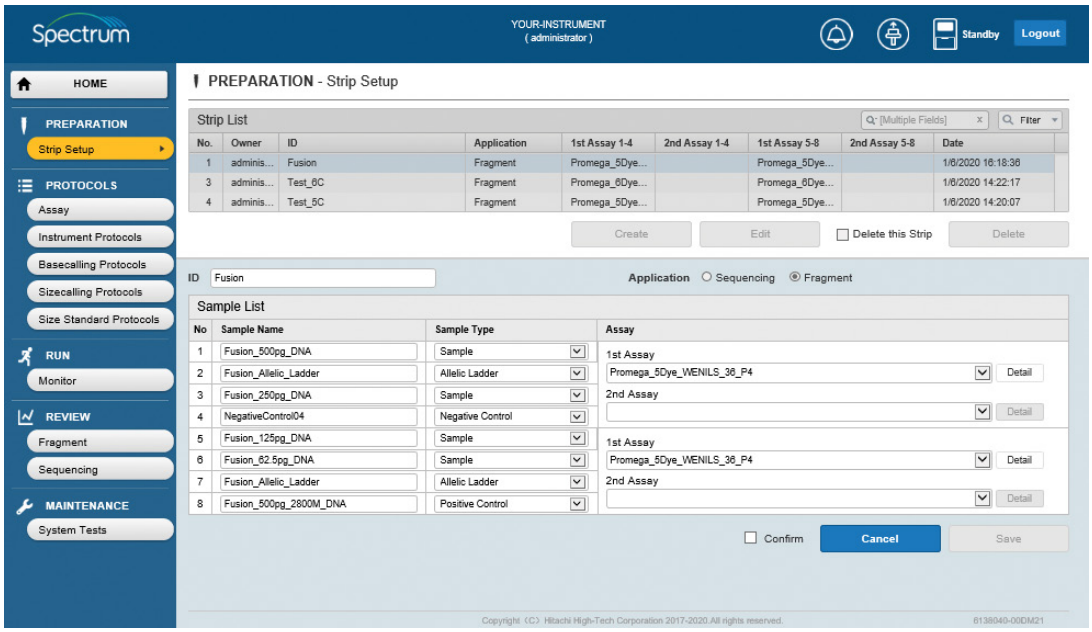

Figure 22. 'Strip Setup' screen with editable Sample List.

9. Enter a Strip ID for the new strip by selecting the **ID** field to activate the cursor or leave the current Strip ID to overwrite the information for that Strip ID.

   Note: There is no **Save As** function available after editing an existing Strip ID. Therefore, a new strip name must be entered into the Strip ID field if you do not want to overwrite the existing Strip ID.

10. Select Sample Type (Sample, Positive Control, Negative Control, Allelic Ladder or Unused).

    Notes:

    a. The Allelic Ladder sample type is only available for Fragment Analysis.

    b. A sample type other than "Unused" must be assigned to at least one well in each injection set. If all of the four wells in an injection set are assigned as "Unused", the injection set will not be run.

    c. Application type (Sequencing or Fragment) is preselected based on the Strip ID being edited and cannot be changed when editing an existing Strip ID.

11. Input the Sample Names by selecting the **Sample Name** field for each well to activate the cursor (Figure 14).

12. Select the **1st Assay** which will be used for the initial injection using the pull-down menu (Figure 14).

13. You can verify the settings of the assay by selecting **Detail** next to the chosen assay (Figure 14). This will display a window showing these settings but will not allow you to edit them (Figure 15). To edit the assay, see Section 5.5.2.
14. If desired, select the **2nd Assay** which will be used to reinject the same sample using the pull-down menu. Alternatively, the **2nd Assay** field can be left blank.

    Note: The assays available in the **2nd Assay** field are filtered based on the dye set in the assay selected in the **1st Assay** field. For example, if a 'Promega_5-dye' dye set based assay is chosen in the **1st Assay** field, then only assays using that same dye set are available as an option in the **2nd Assay** field. In this way, it is possible to duplicate injections with the same assay conditions by choosing the same assay in the **2nd Assay** field as that used in the **1st Assay** field. It is also possible to run duplicate injections of the same assay conditions by using the **Duplicate** function of the 'Edit Injection List' screen when setting up a run on the Spectrum Compact CE System (see Section 5.6 of the *Spectrum Compact CE System Operating Manual* #TMD058).
15. Check the **Confirm** box and select **Save** (Figure 21). If no errors are detected, "Normal End" in a green horizontal box will appear on the screen. If errors are detected, either "Invalid data entered" or "The value is out of range" will appear in a red horizontal box and the software will indicate where the error is occurring.

    Notes:

    a. The **Confirm** check box must be selected to enable **Save**.

    b. **Cancel** does not require selecting the **Confirm** box to become active and is always available. Select **Cancel** at any time during editing of a Strip ID to exit out of the Strip ID editing process without saving any information and leave the Strip ID in its original unedited state.
16. The saved strip information is now available on the Spectrum Compact CE System Control Software touch screen as well as on the Spectrum Compact CE System Remote Access Software and can be loaded into a run created on the Spectrum Compact Control Software touch screen (see Section 5.3.3 of the *Spectrum Compact CE System Operating Manual* #TMD058).

    Note: Instrument runs cannot be created or started from within the Spectrum Compact CE System Remote Access Software. Runs must be created and initiated on the Spectrum Compact CE System.

4.3 Deleting an Existing Strip

1. Select **Setup Strip** from the Main Menu of the 'HOME' screen (Figure 12), and then select the Strip ID in the Strip List that you want to delete (Figure 21).

   Note: Data in the Strip List may be searched and filtered as described in Section 4.2.2.

2. Check the "Delete this Strip" box and select **Delete** (Figure 23).

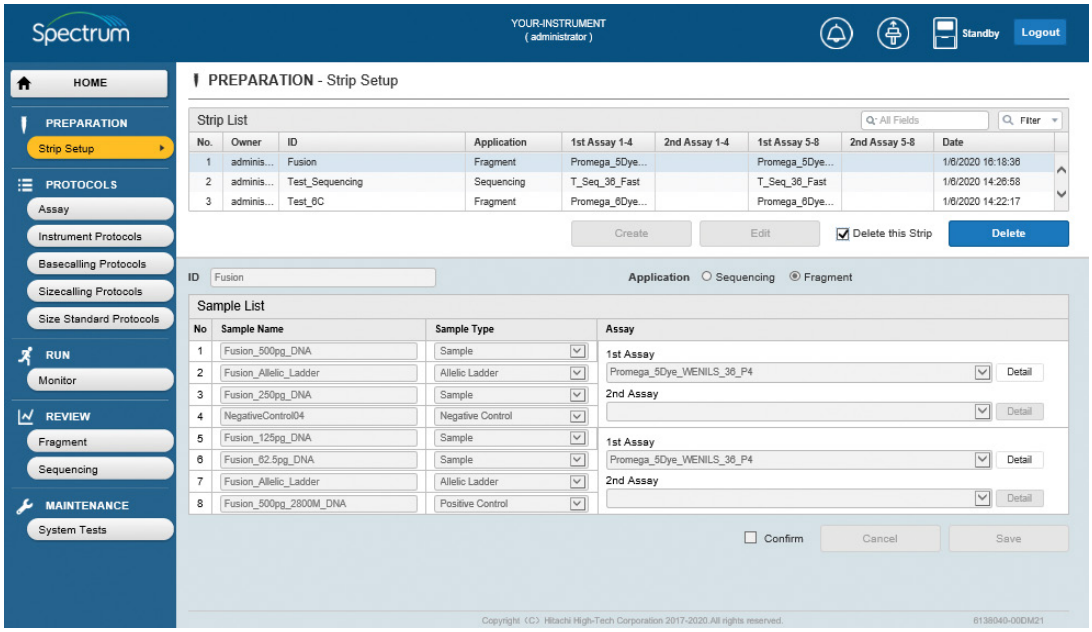

Figure 23. 'Strip Setup' screen with active Delete button.

Protocols 5

Protocols can be created and edited from the Spectrum Compact CE System Remote Access Software for use on the connected Spectrum Compact CE System. Five types of assays and protocols may be accessed from the Main Menu of the Spectrum Compact CE System Remote Access Software.

Note: If the Spectrum Compact CE System is currently running, other users who are logged in via remote access can create new assays and protocols, but cannot edit and overwrite an existing assay or protocol or delete it, even if that assay or protocol is not being currently run. However, an existing assay and protocol can be edited and saved with a new name.

Type	Description
Assay[1]	An assay is comprised of application type (sequencing or fragment), instrument protocol, polymer type, dye set and analysis protocol required for data collection. The analysis protocol used depends on the application. • Fragment: Sizecalling Protocol • Sequencing: Basecalling Protocol
Instrument Protocol	Defines the instrument settings to be applied during a run. This includes: application type (sequencing or fragment), polymer type, injection and electrophoresis conditions.
Basecalling Protocol	The analysis protocol required for sequencing applications. Defines parameters for assigning base calls to data peaks.
Sizecalling Protocol	The analysis protocol required for fragment applications. Defines the parameters for assigning size calls to data peaks.
Size Standard Protocol	Defines size of DNA fragments of known lengths. Used to generate a sizing curve by which unknown fragments are sized.

[1]Assays are created by associating a specific instrument protocol with a specific analysis protocol. If the instrument and analysis protocols are added from the library, a copy of these protocols is added to the assay such that they can be modified within the created assay independently from the original items stored in the library (i.e., changes made to the instrument and analysis protocol within the newly created assay do not affect the instrument and analysis protocols stored in the library).

The Spectrum Compact CE System comes with a series of preloaded assays and protocols. Pre-loaded assays and protocols are locked and cannot be edited or deleted, but these can serve as templates for creation of new assays or protocols via the edit function, if a new Protocol ID is used. Under high security settings (see Section 8.3 of *Spectrum Compact CE System Operating Manual* #TMD058) administrators can create, edit, or delete all user-defined assays and protocols. Users have the ability to create their own assays and protocols under high security settings (if User Rights allow, as described in Section 8.3.1 of the *Spectrum Compact CE System Operating Manual* #TMD058) which can be edited or deleted by the user who created them. Assays and protocols created under high-security settings by a user are locked from other users but not from administrators. Under Normal security settings, all users are treated as administrators (see Section 8.3 of the *Spectrum Compact CE System Operating Manual* #TMD058).

5.1 Instrument Protocol

Electrophoresis parameters such as injection voltage and time, run voltage and time, oven temperature, and data delay (time after injection before data collection starts) can be set once the application type, polymer and run module are selected.

5.1.1 Creating a New Instrument Protocol

1. Select **Instrument Protocols** under PROTOCOLS from the Main Menu of the 'HOME' screen (Figure 12) and then select **Create** (Figure 24). This activates the ID, Application, Polymer and Run Module fields (Figure 25).

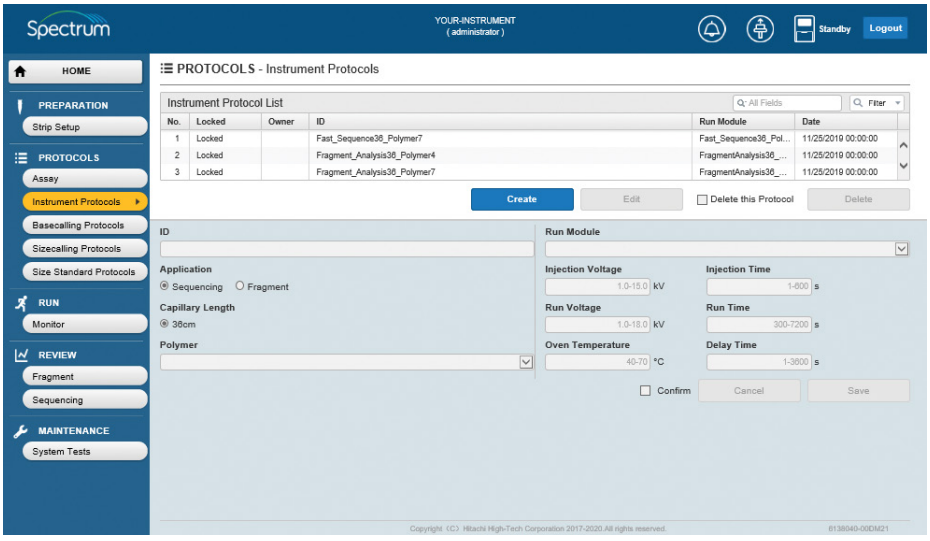

Figure 24. 'Instrument Protocols' screen.

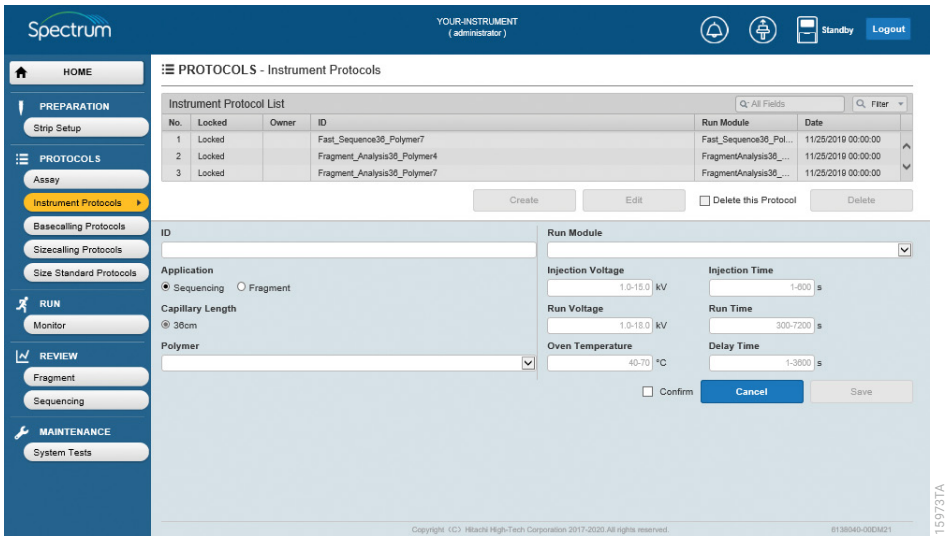

Figure 25. 'Instrument Protocols' screen with active fields.

2. Enter an Instrument Protocol ID for the new instrument protocol by selecting the ID field to activate the cursor (see Section 3.1 for information on acceptable and unacceptable characters).
3. Select the Application using the appropriate radio button (**Sequencing** or **Fragment**).
4. Select the Polymer (**Polymer4** or **Polymer7**) using the pull-down menu.

   Note: Polymer type must be selected prior to selecting a run module. If you select Run Module first and then Polymer type, the act of selecting Polymer type erases your Run Module selection.
5. Select the **Run Module** using the pull-down menu. The following run module parameters may be adjusted as desired.

Parameter	Information	Minimum Value Allowed	Maximum Value Allowed
Injection Voltage (kV)	Defines the injection voltage.	1	15
Run Voltage (kV)	Defines the voltage applied during electrophoresis.	1	18
Oven temperature (°C)	Defines the target oven temperature setting for the protocol.	40	70
Injection Time (sec)	Defines the injection duration.	1	600
Run Time (sec)	Defines the time needed to complete the run and collect data from all labeled fragments.	300	7200

Parameter	Information	Minimum Value Allowed	Maximum Value Allowed
Delay Time (sec)	Defines the time to delay data collection while fragments travel from the capillary tips to the detection window.	1	3600

6. Check the **Confirm** box and select **Save** (Figure 26). If no errors are detected, "Normal End" in a green horizontal box will appear on the screen. If errors are detected, either "Invalid data entered" or "The value is out of range" will appear in a red horizontal box and the software will indicate where the error is occurring.

Notes:

a. The **Confirm** check box must be selected to enable **Save**.

b. The **Cancel** button does not require selecting the **Confirm** box to become active and is always available. Select **Cancel** at any time during creation of a new Instrument Protocol to exit out of the instrument protocol creation process without saving any information.

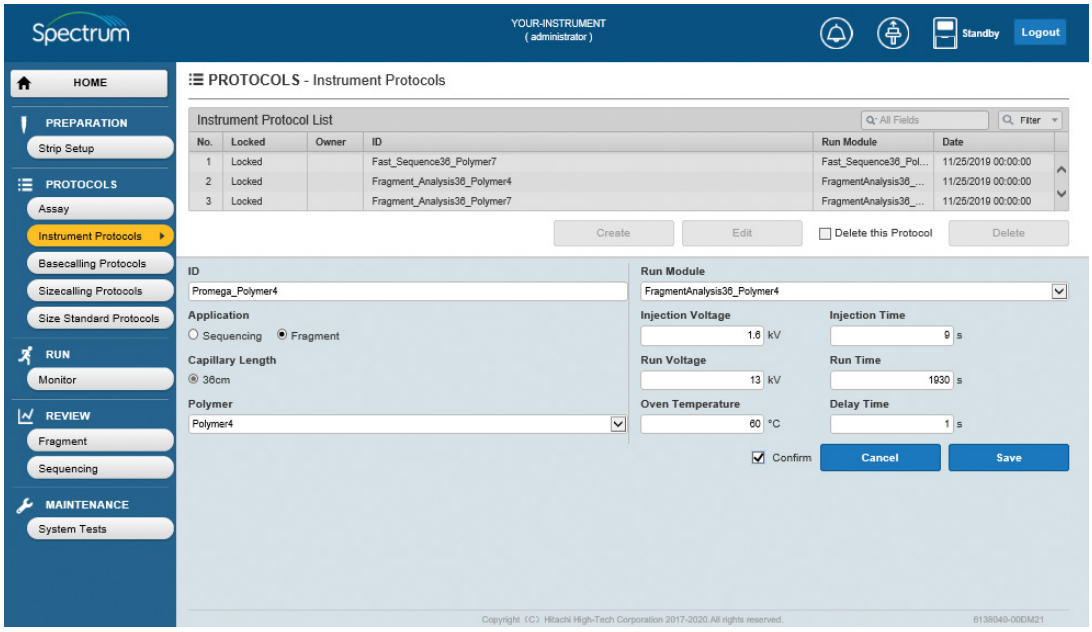

Figure 26. Saving a new instrument protocol.

7. The instrument protocol is now available on the Spectrum Compact CE System instrument touch screen as well as on the Spectrum Compact CE System Remote Access Software and can be used to create an assay in both locations (see Section 5.5 for creation of assays with the Spectrum Compact CE System Remote Access Software and Section 7.2.4 of the *Spectrum Compact CE System Operating Manual* #TMD058 for creating assays on the Spectrum Compact CE System Control Software).

5.1.2 Editing an Existing Instrument Protocol

1. Select **Instrument Protocols** under PROTOCOLS from the Main Menu of the 'HOME' screen (Figure 12).
2. Data in the Instrument Protocol List may be searched and filtered (i.e., searched for based on specific values and filtered such that only instrument protocols that meet those criteria are displayed in the Instrument Protocol List). Select the magnifying glass icon on the Select Search Field box to display a window with radio button selections that allows you to search by All Fields, Locked, Owner, ID, Run Module or Date (Figure 27).

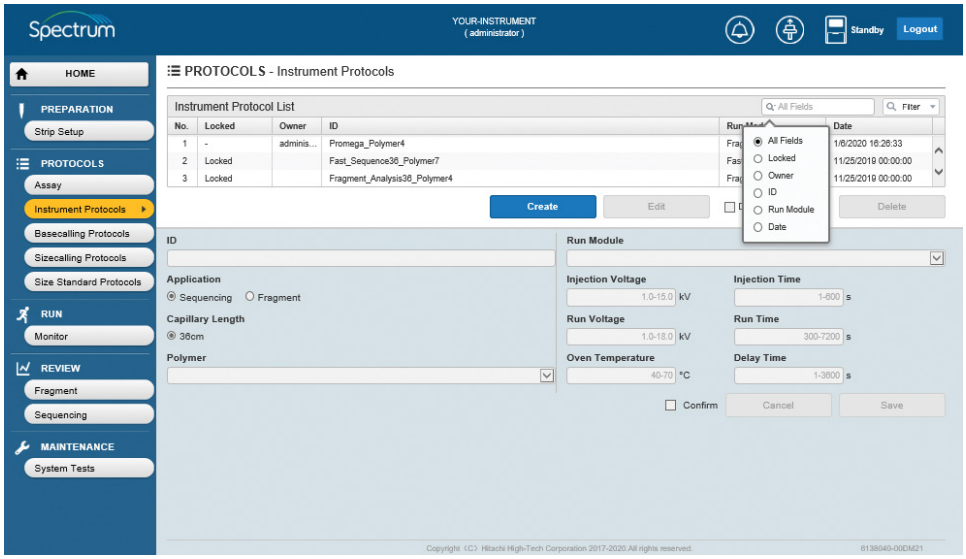

Figure 27. Instrument Protocol List select search field radio button window.

3. After selecting the appropriate search field, select the magnifying glass or down arrow icon in the Filter box to display filtering options by the different fields (Figure 28).
4. Search terms can be filtered by:
   - is
   - begins
   - contains
   - ends

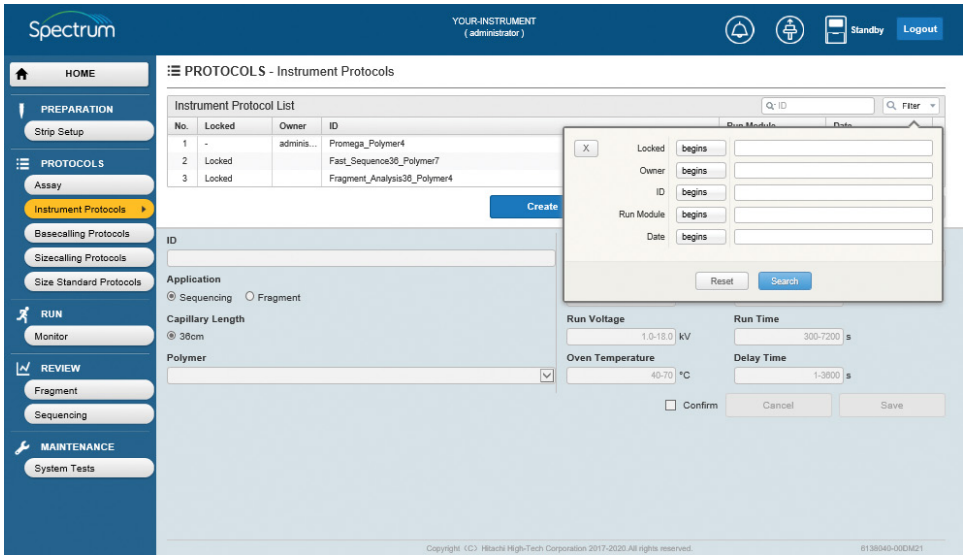

Figure 28. Instrument Protocol List search filter option selection.

5. After selecting the appropriate filter for search terms in the field being search (i.e., Locked, Owner, ID, Run Module or Date), type the desired search term in the adjacent box and select **Search** (Figure 29). Alternatively, select **Reset** to exit.

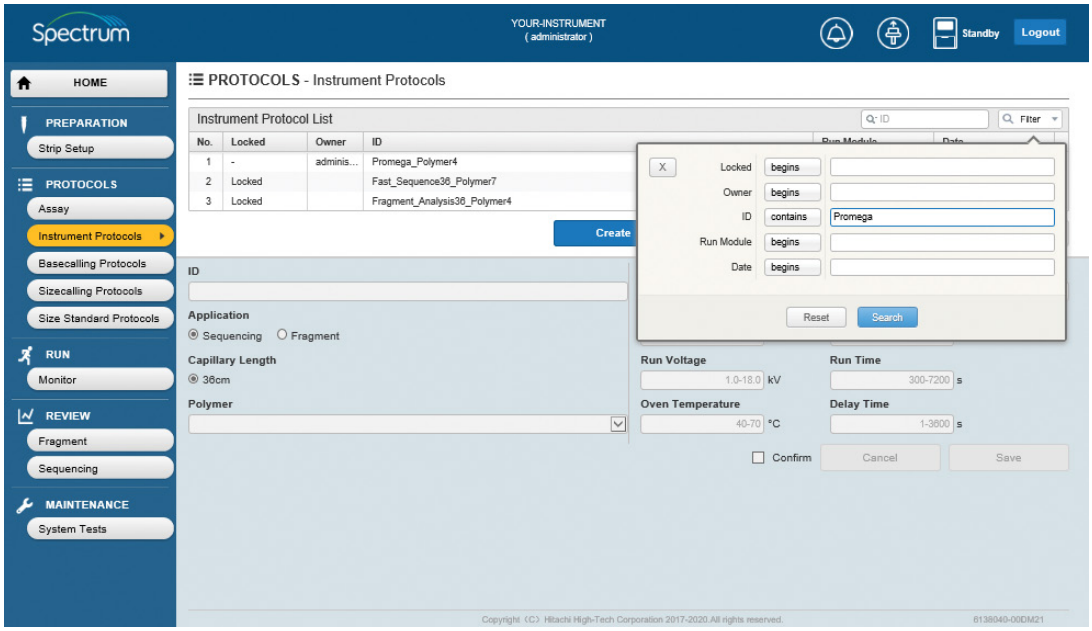

Figure 29. Instrument Protocol List search filter option selection.

6. The instrument protocols that meet the desired search and filter parameters are displayed at the top of the Instrument Protocol List.

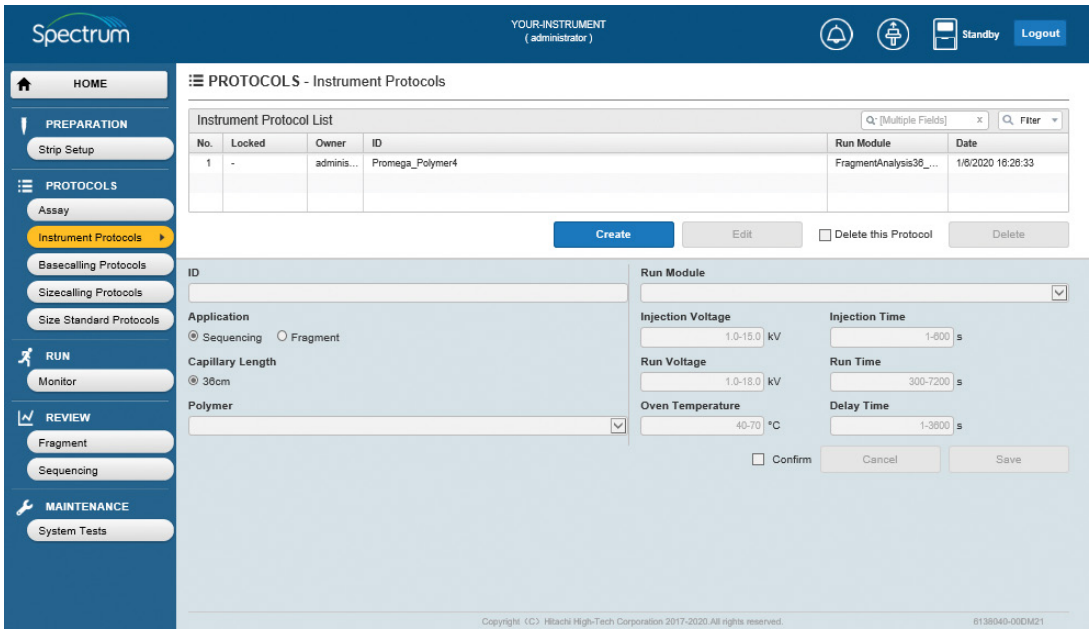

Figure 30. Search and filtered instrument protocols.

7. Select the Instrument Protocol ID in the Instrument Protocol List to edit. This will activate **Edit** (Figure 31).

   Note: Before selecting **Edit**, the editable portion of the screen is grayed out and is not editable.

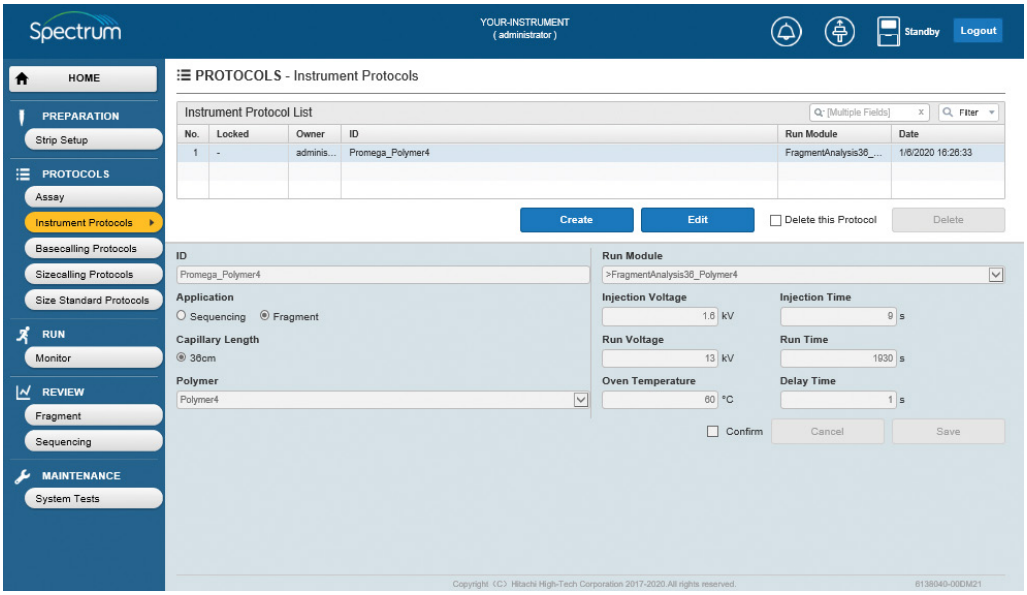

Figure 31. 'Instrument Protocols' screen with active Edit button.

8. Select **Edit**. This will enable the ID and Run Module fields (Figure 32).

   Note: When editing an existing protocol, it is not possible to change the application or polymer type. Only parameters within the Run Module may be edited.

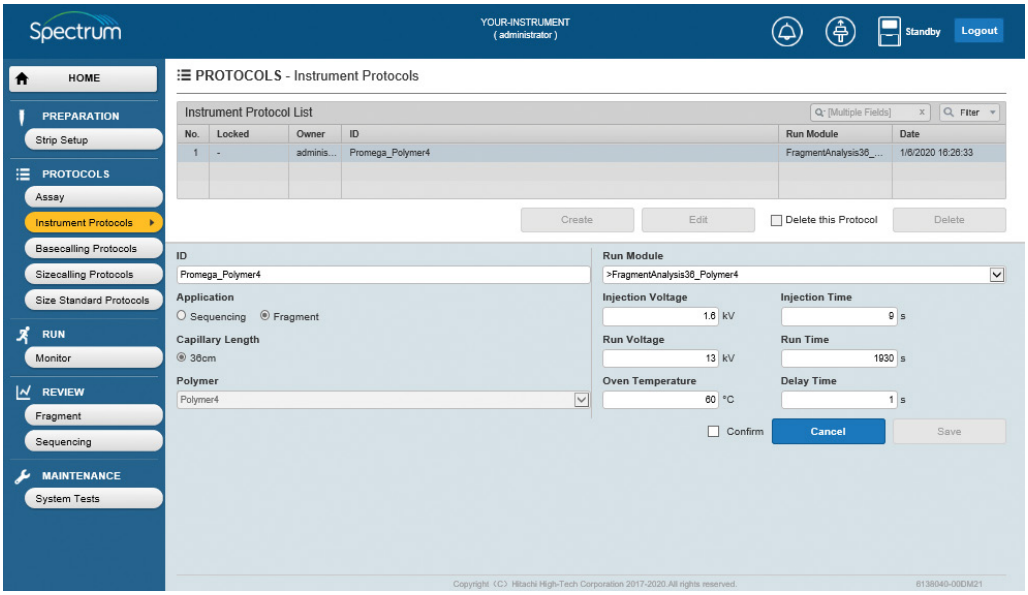

Figure 32. 'Instrument Protocols' edit screen with active fields.

9. Follow Steps 2–7 of Section 5.1.1.

   Note: Preloaded protocols cannot be overwritten. A new Instrument Protocol ID must be assigned. For user-defined protocols, you can choose to either overwrite the existing protocol or save with a new Instrument Protocol ID.

5.1.3 Deleting an Existing Instrument Protocol

1. Select **Instrument Protocols** under PROTOCOLS from the Main Menu of the 'HOME' screen (Figure 12) and then select the Instrument Protocol ID in the Instrument Protocol List that you want to delete (Figure 31).

   Note: Data in the Instrument Protocol List may be searched and filtered as described in Section 5.1.2.

2. Check the "Delete this Protocol" box and select **Delete** (Figure 31).

   Note: The "Delete this Protocol" check box must be selected to enable **Delete**.

5.2 Basecalling Protocol

The following settings and parameters for analyzing and evaluating sequence data are incorporated into basecalling protocols.

Setting	Description
Mixed Bases Setting	When this function is enabled in the basecalling protocol, if there are two peaks at the same position and the smaller intensity peak is greater than the Secondary Peak Height Threshold (height as a percentage of the major peak at the same position) set in the basecalling protocol, then the software will identify this peak as a mixed base. Minimum and maximum values allowed for the Secondary Peak Height Threshold are 1% and 99%, respectively.
Clear Range First bp–Last bp	When using the 'Clear Range First bp–Last bp' method in the basecalling protocol, the first base pair position to be considered for analysis is set by entering the 5′ bp position in the 'First bp' field. There are two methods for setting the 3′ end point (last bp position to be considered for analysis) of the clear range: • 'Last bp': Enter the final base in the sequence to be considered for analysis (enter 3′ bp position in 'Last bp' field). • 'Bases to trim from 3′ end': Trims the specified number of bases from the 3′ end of the sequence run to determine the last bp to consider for analysis (enter number of bases to trim in 'Bases to trim from 3′ end' field). Minimum and maximum values allowed by software for 'First bp', 'Last bp' and 'Bases to trim from 3′ end' fields are 1bp and 1200bp, respectively. **Note:** When creating a new Basecalling Protocol, the default setting for Clear Range First bp-Last bp is disabled (box unchecked).

Setting	Description
Clear Range Quality Value	The software creates a clear range by removing bases from the 5′ and 3′ end of the read based on QV values. In the resulting clear range, no sliding window of 'bases out of' **Z** (e.g., 30) will contain more than the specified number of bases (e.g., 4) in the 'fewer than' field **X**, with a QV value below that set in the 'have QVs less than' field **Y** (e.g., 20). Any sliding 30 base window in the first or last part of the sequence that does not meet these parameters is trimmed from these ends. Minimum and maximum values allowed by software for 'fewer than' and 'bases out of' fields are 1bp and 1200bp, respectively. The value entered in the 'fewer than' field must always be less than the 'bases out of' field. Minimum and maximum values allowed by software in the 'have QVs less than' field are 1 and 60, respectively. **Note:** When creating a new Basecalling Protocol, the default setting for Clear Range Quality Value is disabled (box unchecked).
Sequencing Quality	Defines the Contiguous Read Length (CRL), QV20+ and Trace Score values (parameters described below) for passing and failing data. Data which fall between these values will be flagged as suspect. Minimum and maximum values allowed by software for CRL are 1bp and 800bp, respectively. The value entered in the fail field must always be less than the pass field. Minimum and maximum values allowed by software for QV20+ are 1bp and 800bp, respectively. The value entered in the fail field must always be less than the pass field. Minimum and maximum values allowed by software for Trace Score are 1 and 60, respectively. The value entered in the fail field must always be less than the pass field.

Parameter	Description
CRL	Number of contiguous bases in the sequence that have an average quality value (QV) score ≥20 over a 21 base sliding window.
QV20+	Total number of bases with a QV score from the basecaller of at least 20 (i.e., base call accuracy of at least 99%).
Trace Score	Average QV score across bases in clear range (as defined in basecalling protocol), or across entire range if clear range is disabled.

5.2.1 Creating a New Basecalling Protocol

1. Select **Basecalling Protocols** under PROTOCOLS from the Main Menu of the 'HOME' screen (Figure 12), and then select **Create** Figure 33). This activates the ID field (Figure 34) and the **Mixed-bases Setting**, **Clear Range First bp–Last bp**, **Clear Range Quality Value** and **Sequencing Quality** pull-down menus.

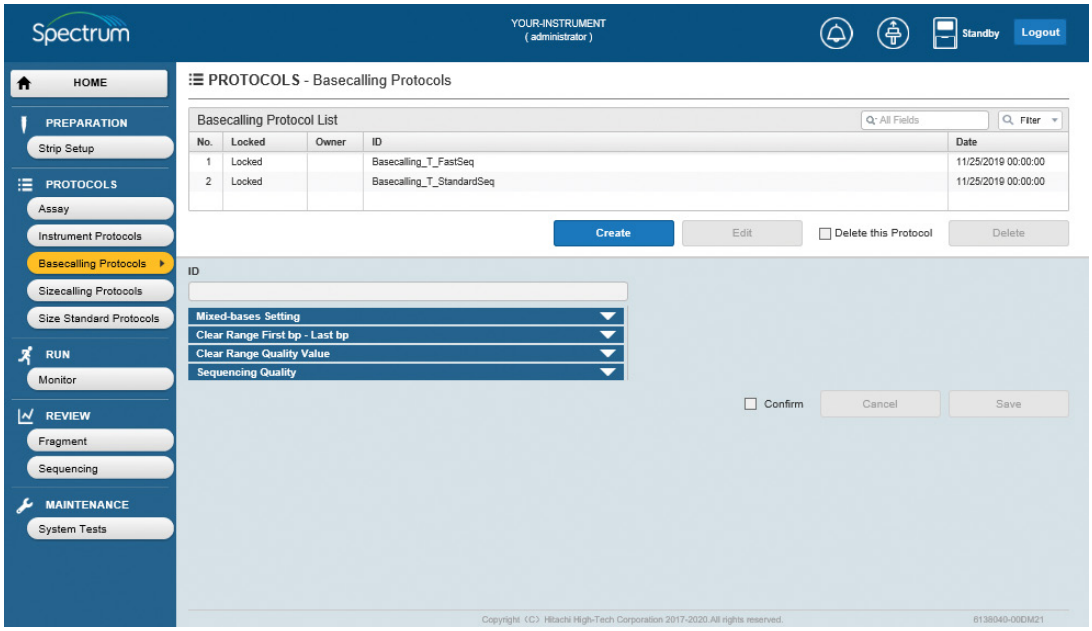

Figure 33. 'Basecalling Protocols' screen.

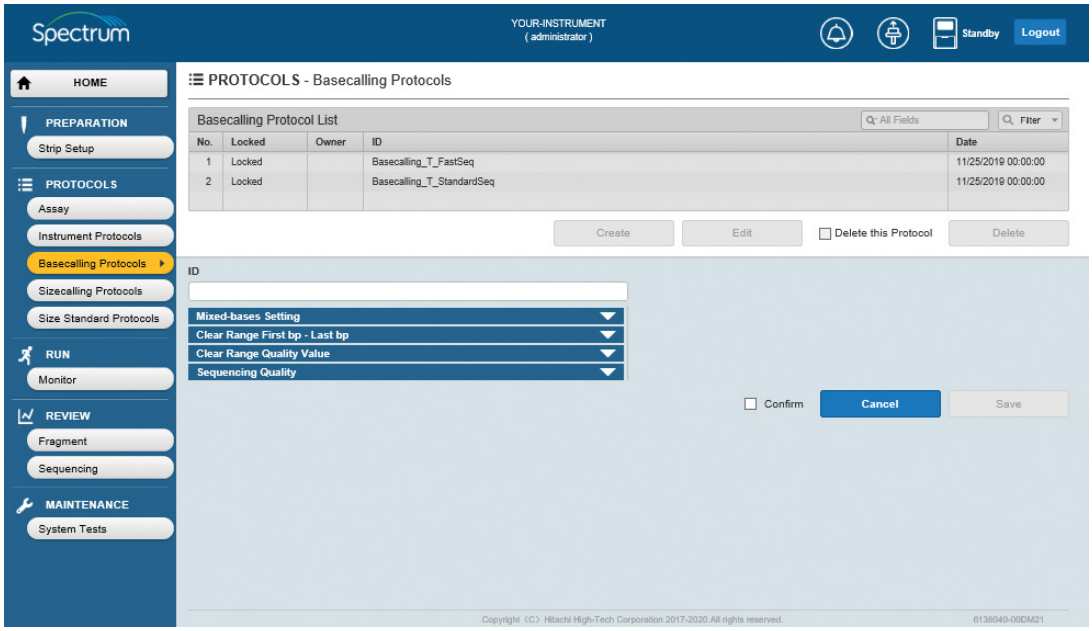

Figure 34. 'Basecalling Protocols' screen with active fields.

2. Enter a Basecalling Protocol ID for the new basecalling protocol by selecting the **ID** field to activate the cursor (see Section 3.1 for information on acceptable and unacceptable characters). Select the **Mixed-bases Setting** pull-down menu and select the **Enable** radio button if desired, followed by the Secondary Peak Height Threshold value (Figure 35).

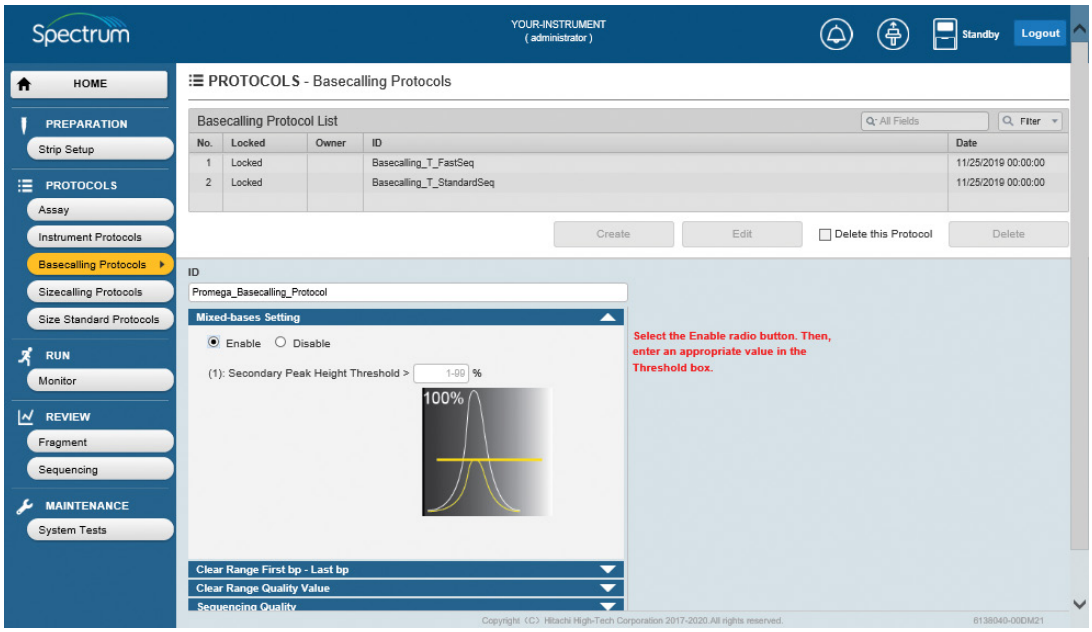

Figure 35. 'Mixed-bases Setting' pull-down screen.

3. Select the **Clear Range First bp–Last bp** pull-down menu and select the **Enable** radio button if desired, to reveal the options for setting the first and last base to consider in the sequence (Figure 36). When this is enabled, the first bp position to be considered for analysis is set by entering the 5′ bp position in the **First bp** field. The default 3′ bp setting is the **Last bp** radio button which specifies the last bp in the sequence to consider (e.g., if set to 700bp, any base after the base-pair number 700 will not be analyzed). Enter the desired values to specify the first and last bases of the sequence to consider for analysis.

   Note: When the **Disable** radio button is checked, the entire sequence will be considered for analysis (no base trimming will occur) unless the Clear Range Quality Value is enabled.

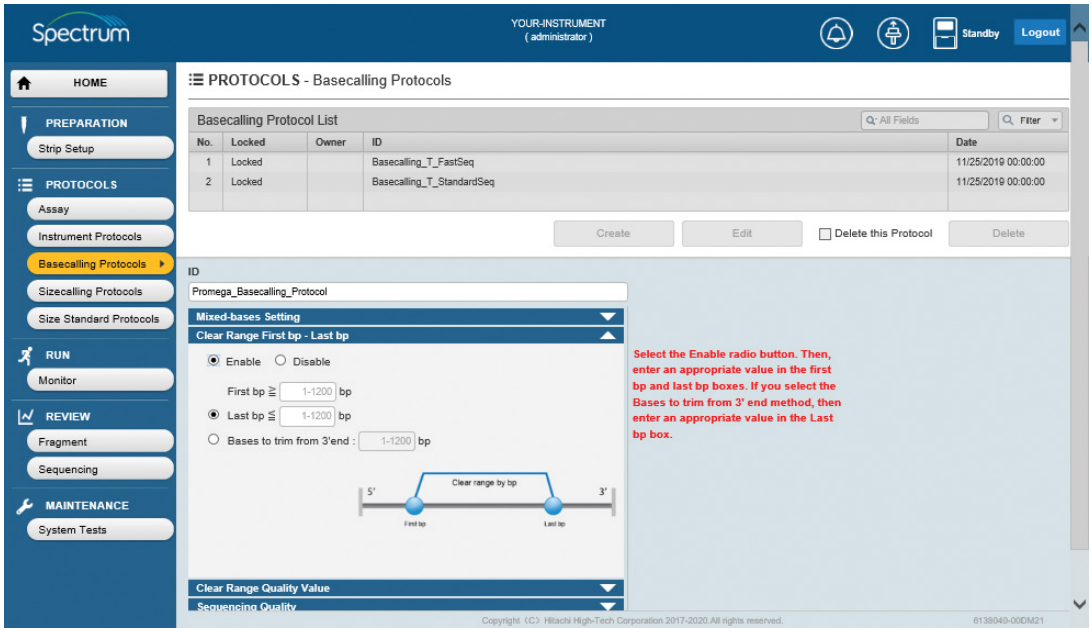

Figure 36. 'Clear Range First bp–Last bp' pull-down screen.

4. Alternatively, select the **Bases to trim from 3´ end** radio button. When this is enabled, the first bp position to be considered for analysis is set by entering the 5´ bp position in the First bp field. The software then trims the number of bases specified in the **Bases to trim from 3´ end** field from the 3´ end of the sequence to determine the last bp to consider for analysis (Figure 37). Under this setting, the last base considered will depend on the length of sequence obtained.

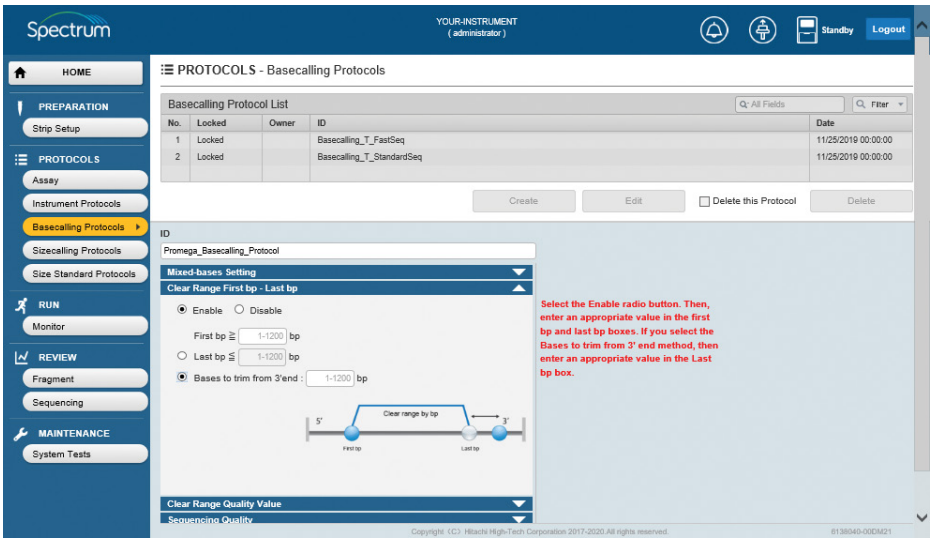

Figure 37. Clear Range First bp–Last bp: Bases to trim from 3´ end.

5. If desired, the clear range can be defined by a quality value instead of by entering defined start and stop base-pair locations for analysis. Select the **Clear Range Quality Value** pull-down menu and select the **Enable** radio button (Figure 38). In the **X** field, enter the number of bases that can have a QV lower than that specified in the **Y** field over a window size specified in the **Z** field. For example, “Remove bases from the ends until fewer than 4 bases (X) out of 30 (Z) have QVs less than 20 (Y)” is equivalent to no more than 4 bases over a window size of 30 bases can have a QV less than 20.

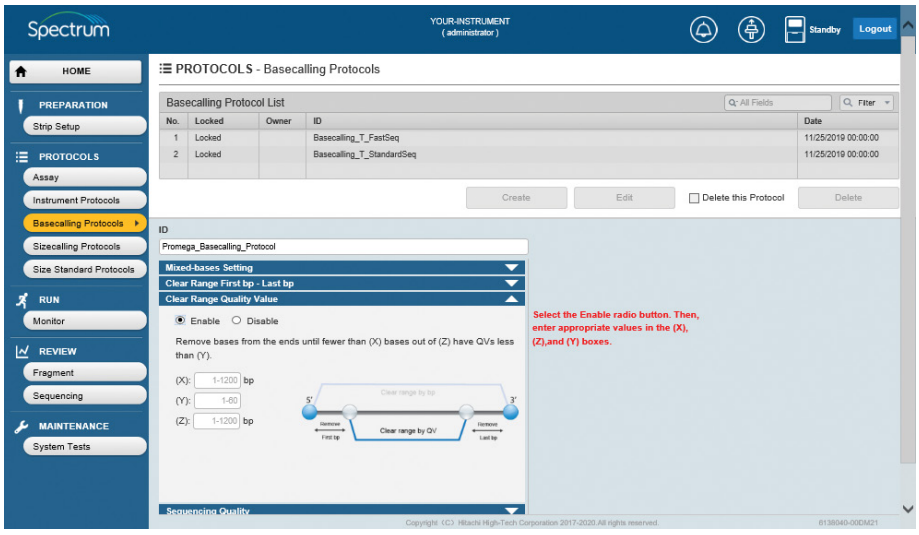

Figure 38. ‘Clear Range Quality Value’ pull-down screen.

6. Select the **Sequencing Quality** pull-down menu and check the boxes to the left of CRL, QV20+ and Trace Score to select which parameters to use for assessing sequencing quality. After checking these boxes, set the minimum passing and maximum failing CRL, QV20+ and Trace Score values (Figure 39).

   Notes:

   a. Selecting all three sequencing quality parameters is not required. Any one or two parameters may be selected as well as all three.

   b. Suspect CRL, QV20+ and Trace Score value ranges are defined by the minimum passing and maximum failing CRL, QV20+ and Trace Score values entered.

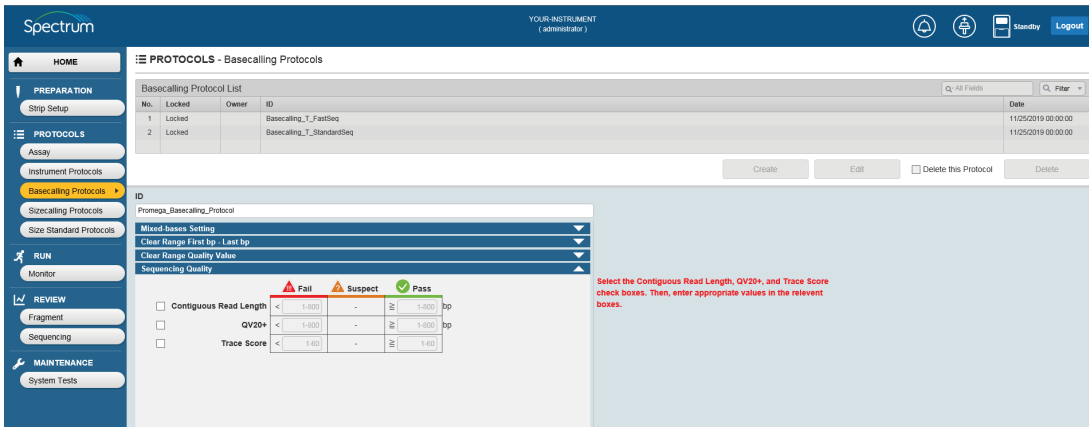

Figure 39. 'Sequencing Quality' pull-down screen.

7. Check the **Confirm** box and select **Save** (Figure 40). If no errors are detected, "Normal End" will appear on the screen in a green horizontal box. If errors are detected, either "Invalid data entered" or "The value is out of range" will appear in a red horizontal box and the software will indicate where the error is occurring.

   Notes:

   a. The **Confirm** check box must be selected to enable **Save**.

   b. The **Cancel** button does not require selecting the **Confirm** box to become active and is always available. Select **Cancel** at any time during creation of a new Basecalling Protocol to exit out of the basecalling protocol creation process without saving any information.

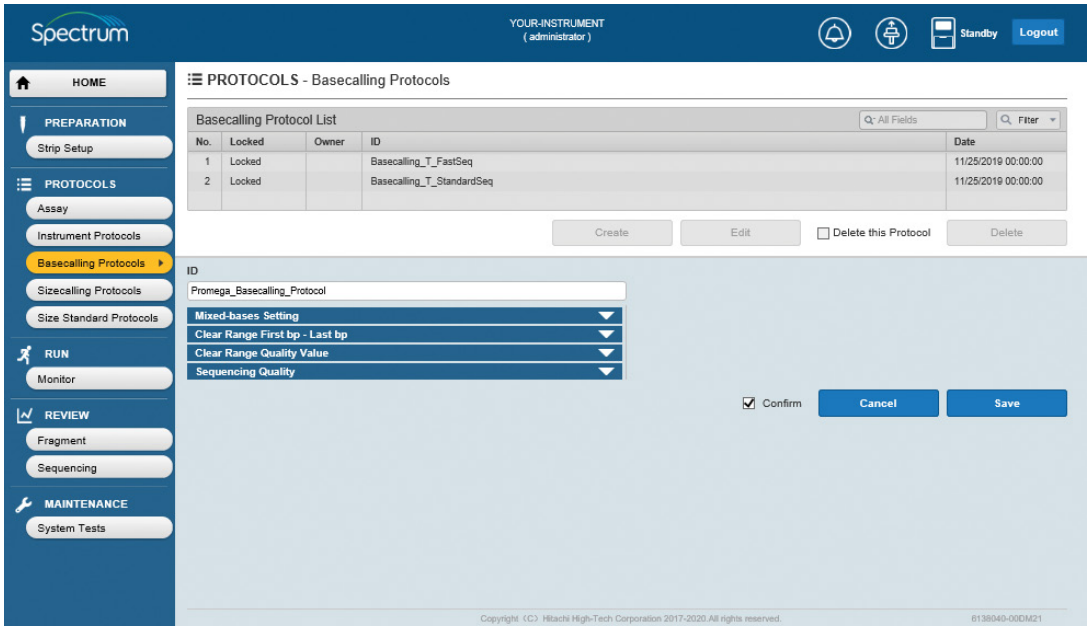

Figure 40. Saving a new Basecalling Protocol.

8. The basecalling protocol is now available on the Spectrum Compact Control Software touch screen as well as on the Spectrum Compact CE System Remote Access Software and can be used to create an assay in both locations (see Section 5.5 for creation of assays with the Spectrum Compact CE System Remote Access Software and Section 7.2.4 of the *Spectrum Compact CE System Operating Manual* #TMD058 for creation of assays on the Spectrum Compact Control Software touch screen).

5.2.2 Editing an Existing Basecalling Protocol

1. Select **Basecalling Protocols** under PROTOCOLS from the Main Menu of the 'HOME' screen (Figure 12).
2. Data in the Basecalling Protocol List may be searched and filtered (i.e., searched for based on specific values and filtered such that only basecalling protocols that meet those criteria are displayed in the Basecalling Protocol List). Select the magnifying glass icon on the Select Search Field box to display a window with radio button selections that allows you to search by All Fields, Locked, Owner, ID or Date (Figure 41).

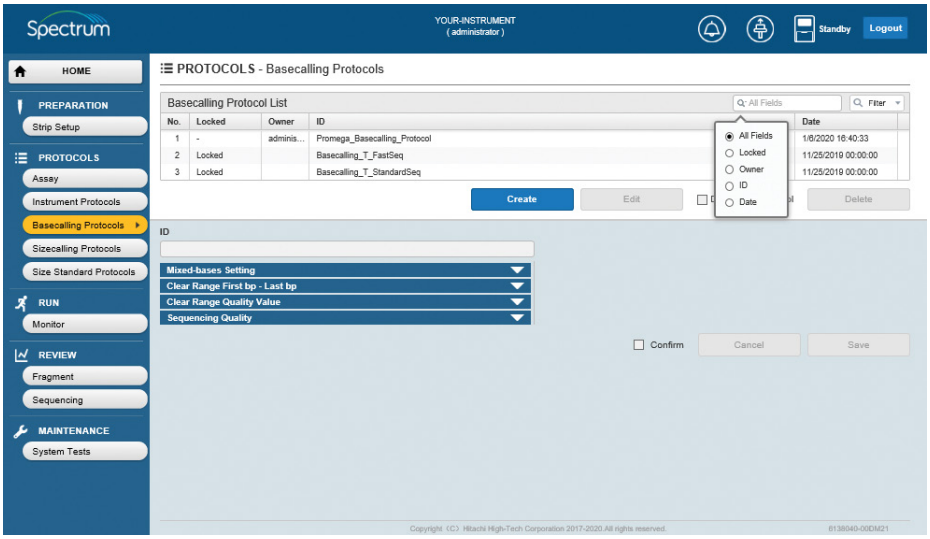

Figure 41. Basecalling Protocol List select search field radio button window.

3. After selecting the appropriate search field, select the magnifying glass or down arrow icon in the Filter box to display filtering options by the different fields (Figure 42).
4. Search terms can be filtered by:
   - is
   - begins
   - contains
   - ends

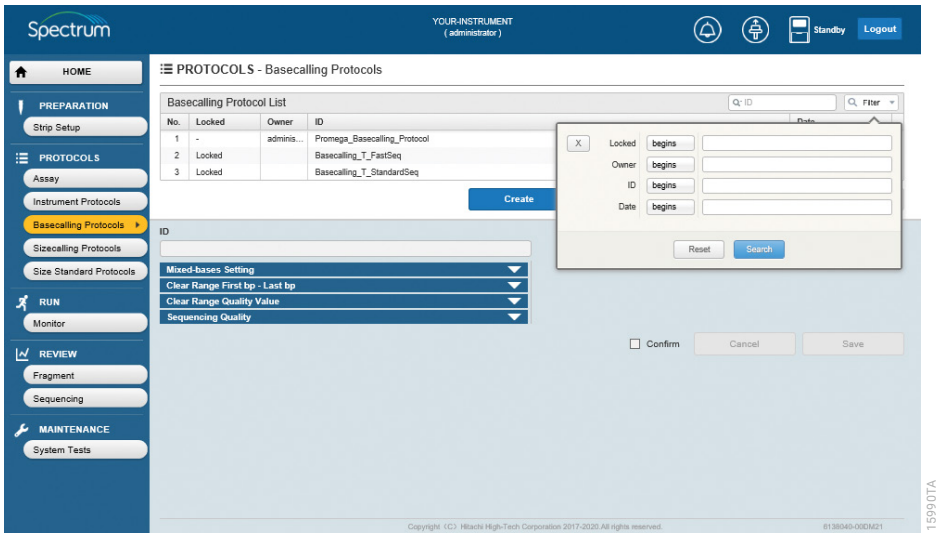

Figure 42. Basecalling Protocol List search filter option selection.

5. After selecting appropriate filters for search terms in the field being search (i.e., Locked, Owner, ID or Date), type the desired search term in the adjacent box and select **Search** (Figure 43). Alternatively, select **Reset** to exit.

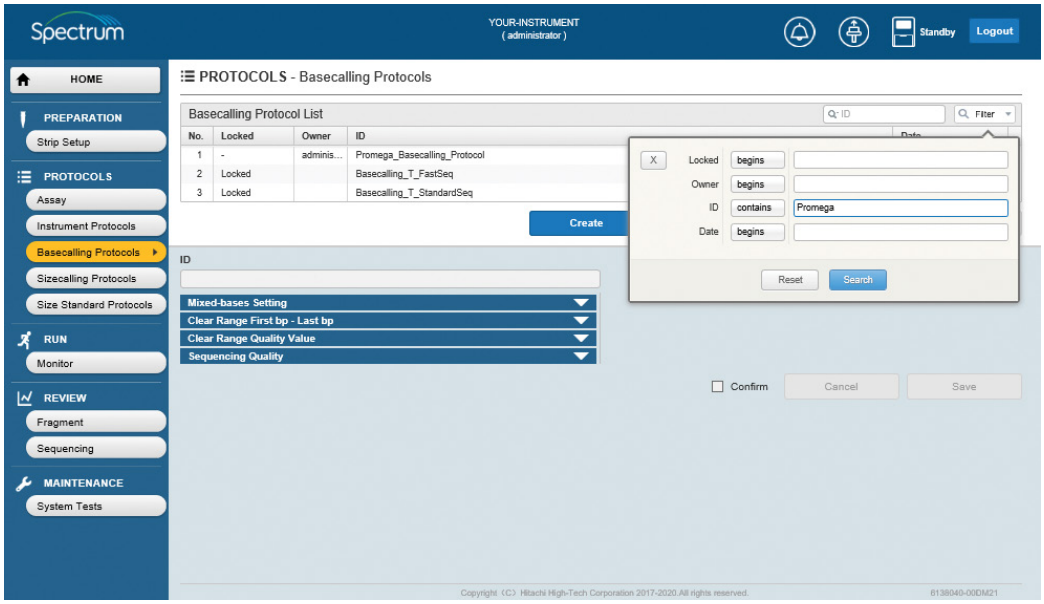

Figure 43. Basecalling Protocol List search filter option selection.

6. The basecalling protocols that meet the desired search and filter parameters are displayed at the top of the Basecalling Protocol List (Figure 44).

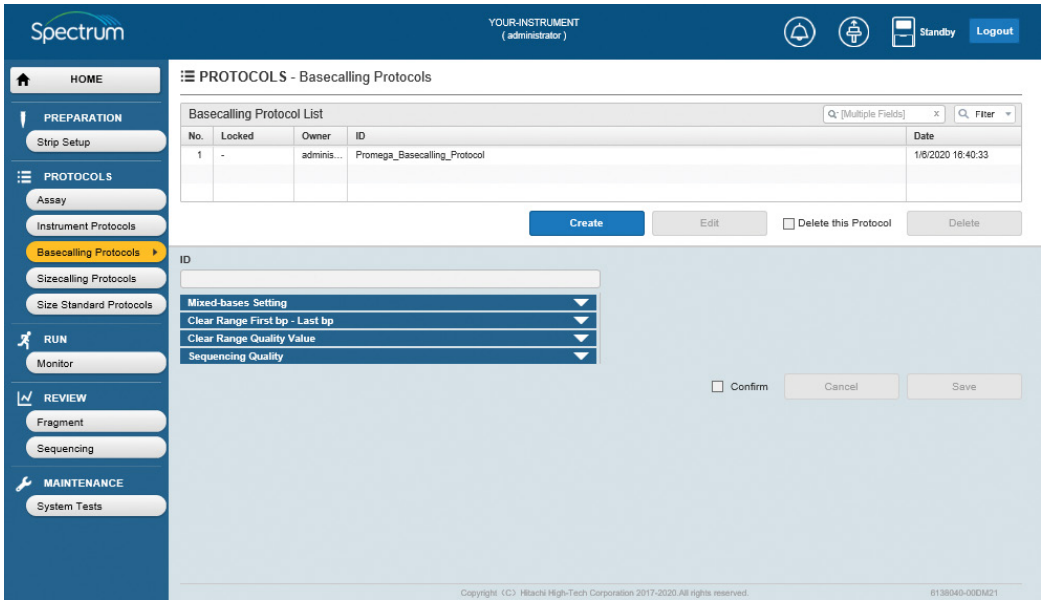

Figure 44. Searched and filtered basecalling protocols.

7. Select the Basecalling Protocol ID in the Basecalling Protocol List to edit. This will activate **Edit**.

   Note: Before selecting **Edit**, the editable portion of the screen is grayed out and is not editable.

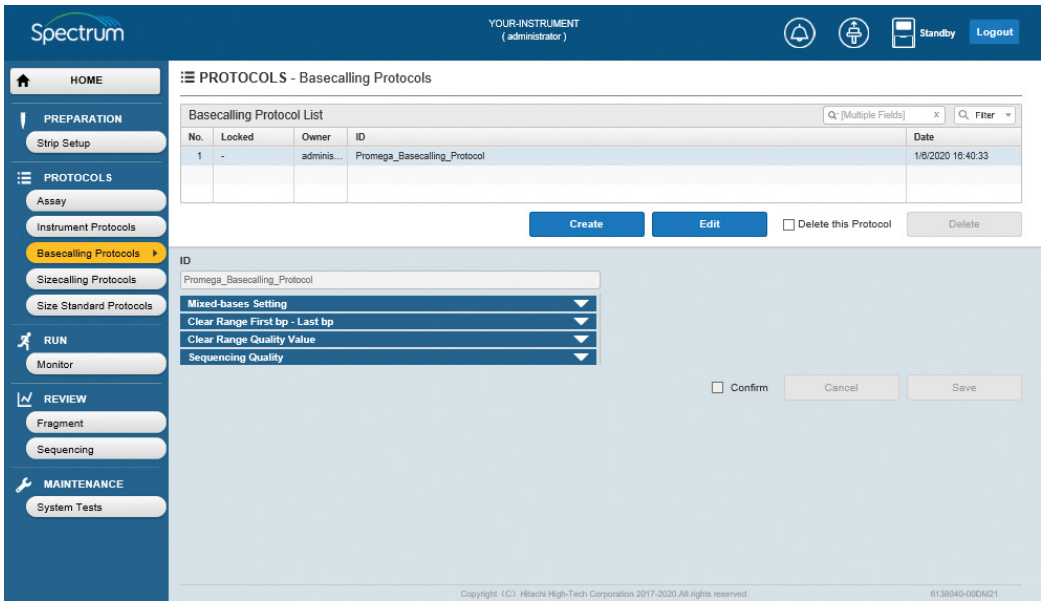

Figure 45. 'Basecalling Protocols' screen with active Edit button.

8. Select **Edit**. This will enable the ID field, **Mixed-bases Setting**, **Clear Range First bp–Last bp**, **Clear Range Quality Value** and **Sequencing Quality** pull-down menus (Figure 46).

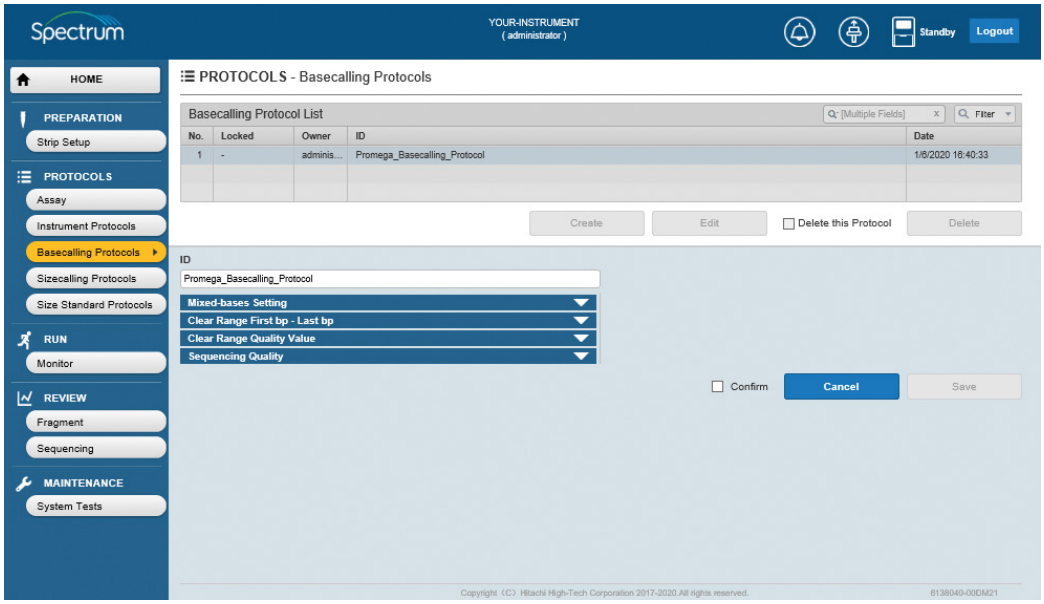

Figure 46. 'Basecalling Protocols Edit' screen with active fields.

9. Follow Steps 2–7 of Section 5.2.1.

   Note: Preloaded protocols cannot be overwritten. A new Basecalling Protocol ID must be assigned. For user-defined protocols, you can either overwrite the existing Basecalling Protocol ID or save with a new Basecalling Protocol ID.

5.2.3 Deleting an Existing Basecalling Protocol

1. Select **Basecalling Protocols** under PROTOCOLS from the Main Menu of the 'HOME' screen (Figure 12) and then select the Basecalling Protocol ID in the Basecalling Protocol List that you want to delete (Figure 45).

   Note: Data in the Basecalling Protocol List may be searched and filtered as described in Section 5.2.2.

2. Check the "Delete this Protocol" box and select **Delete** (Figure 45).

   Note: The "Delete this Protocol" check box must be selected to enable **Delete**.

5.3 Sizecalling Protocol

The following settings/parameters for analyzing and evaluating fragment data are incorporated into sizecalling protocols. The sizecalling protocol is intended as an initial analysis to assess data. It does not affect analysis in programs like GeneMapper® *ID*-X Software or GeneMarker®HID Software for Spectrum CE Systems.

Setting/Parameter	Description
Size Standard	Defines the size standard to use in sizecalling protocol and also to specify which peaks within the size standard are to be used by the sizecalling protocol when calculating sizing quality (SQ) and electrophoresis quality (EQ) (described below). **Note:** The size standard selected must match that used with samples.
Analysis Range	Defines the range in scan numbers/data points from which to process the data for peak detection. • Full: analyzes the entire range from beginning to end of the collection process, including the primer peak. • Partial: allows the user to define the start and stop points of the analysis range in scan number/data points using the fields in the Analysis Range pulldown menu. Data point range allowed by software for 'Start Point' and 'Stop Point' is 1 to 32767. The numerical value for 'Start Point' must always be lower than the numerical value entered for 'Stop Point'. **Note:** Data points outside of the specified analysis range are not analyzed. Therefore, all of the size standard peaks expected for the Sizecalling Protocol used must fall within the start and stop points selected when choosing partial range, otherwise a failing size quality will be obtained.

Setting/Parameter	Description
Peak Amplitude Threshold	Defines the minimum RFU value at which to size and call a peak. Peaks below this threshold will not be called, but peaks below the threshold will still be displayed. Checking the box adjacent to the dye channel color enables the user to enter a threshold for that dye channel (range allowed by software is 1RFU to 30,000RFU). A threshold must be set for the dye channel used for the size standard. Peaks in the size standard must exceed the peak amplitude threshold value set in the Sizecalling Protocol for that peak to be considered in the sizecalling algorithm. If a peak in the size standard fall below the peak amplitude threshold, it may result in a reduced SQ and EQ value for that sample. Thresholds are generally set the same as those used for secondary analysis.
Size Quality (SQ)	SQ is determined by comparing the fragment pattern observed for the size standard being used against that specified for that size standard in the sizecalling protocol. Defines the SQ values for passing and failing SQ data. Sizing data which fall between these values will be flagged as Suspect (data should be manually reviewed in the 'Results' tab of the Spectrum Compact Control Software touch screen to determine whether or not it is acceptable to the user or requires reinjection). **Note:** Numerical SQ range allowed by software is 0.001 to 1. The numerical value for "Fail" must always be lower than the numerical value entered for "Pass".
Electrophoresis Quality (EQ)	EQ is the size (in bp) at which the peak width at half maximal height is equal to the distance between two bases, as calculated from the size standard. Defines the EQ values (in bp) for passing and failing data. Sizing data which fall between these values will be flagged as suspect (data should be manually reviewed in the 'Results' tab of the Spectrum Compact Control Software touch screen to determine whether or not it is acceptable to the user or requires reinjection). **Notes:** a. The EQ range allowed by software is 1 to 1000. The numerical value for "Fail" must always be lower than the numerical value entered for "Pass". b. Accurate calculation of EQ by this method is dependent on using the same size standard in the sample that is specified in the assay used to run that sample. Failure to use the correct size standard can result in an erroneously failing EQ value.

5.3.1 Creating a New Sizecalling Protocol

1. Select **Sizecalling Protocols** under PROTOCOLS from the Main Menu of the 'HOME' screen (Figure 4) and then select **Create** (Figure 47). This activates the ID field (Figure 48) and the **Size Standard**, **Analysis Range**, **Peak Amplitude Threshold** and **Size Quality** pulldown menus.

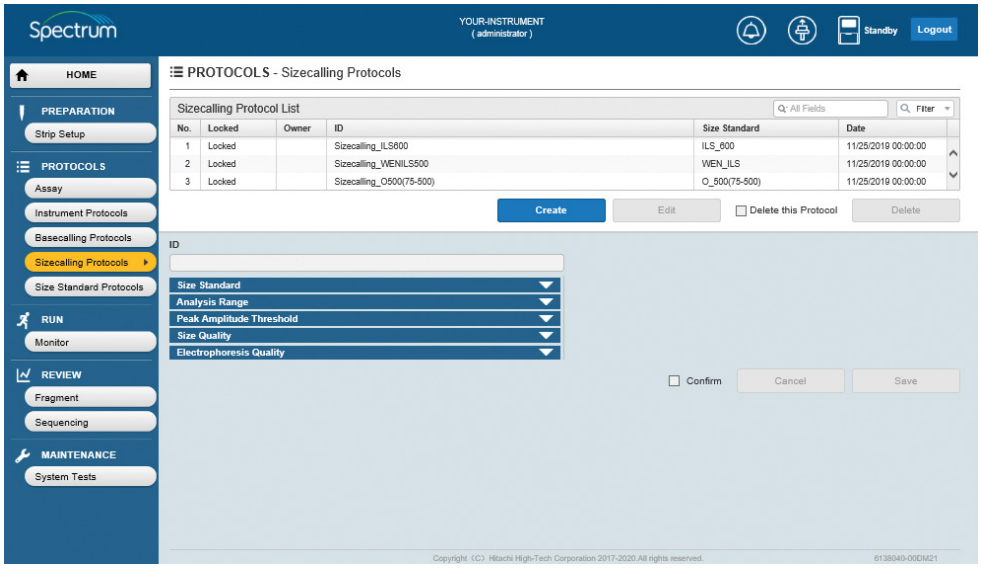

Figure 47. 'Sizecalling Protocols' screen.

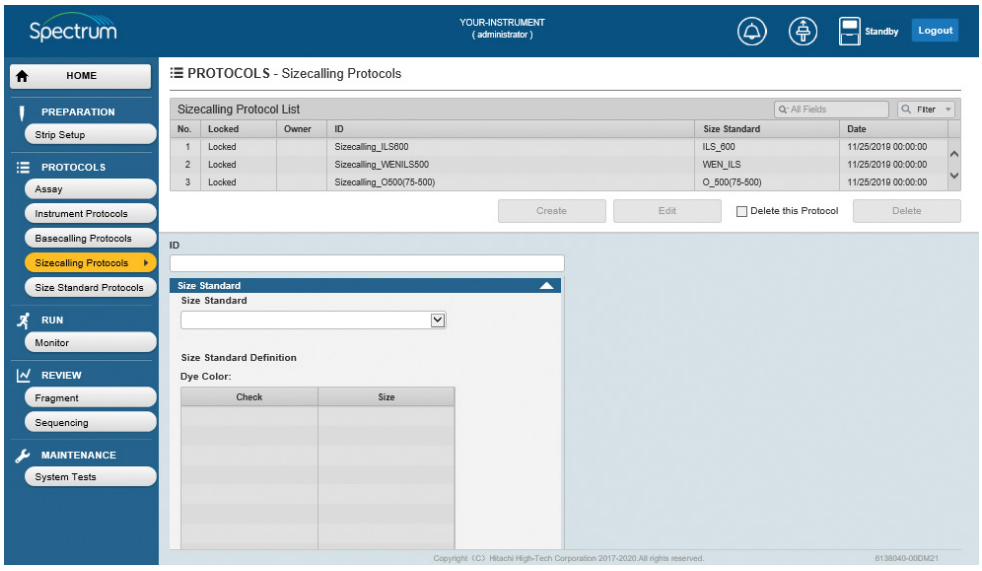

Figure 48. 'Sizecalling Protocols' screen with active fields.

2. Enter a Sizecalling Protocol ID for the new sizecalling protocol by selecting the ID field to activate the cursor (see Section 3.1 for information on acceptable and unacceptable characters). Select the **Size Standard** pull-down menu and select the desired Size Standard from the pull-down menu (Figure 49).

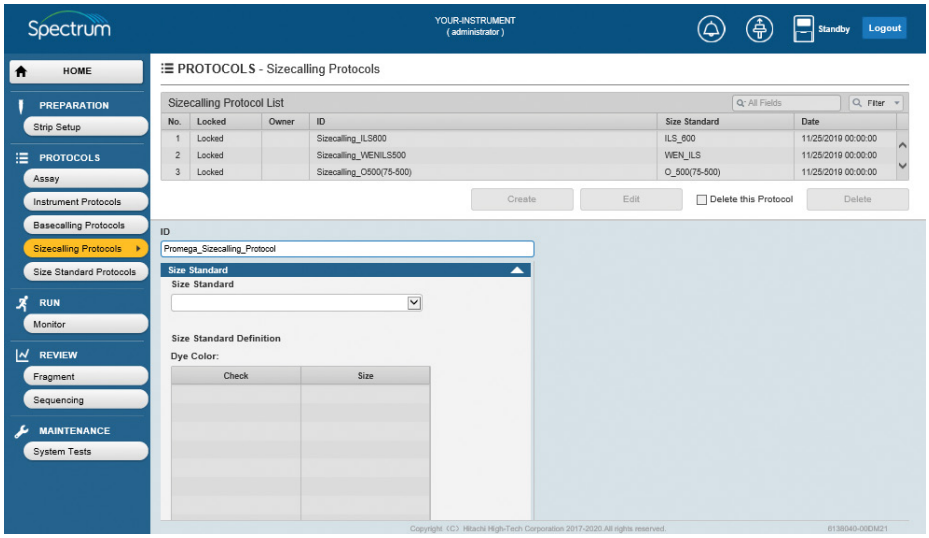

Figure 49. 'Size Standard' pull-down screen.

3. Once selected, the sizes of the individual fragments in the size standard are listed along with a check box adjacent to each one (Figure 50).

   Note: When creating or editing a sizecalling protocol, it is not possible to edit which fragments will be considered during fragment data analysis. This can only be done when editing a size standard protocol (See Section 5.4).

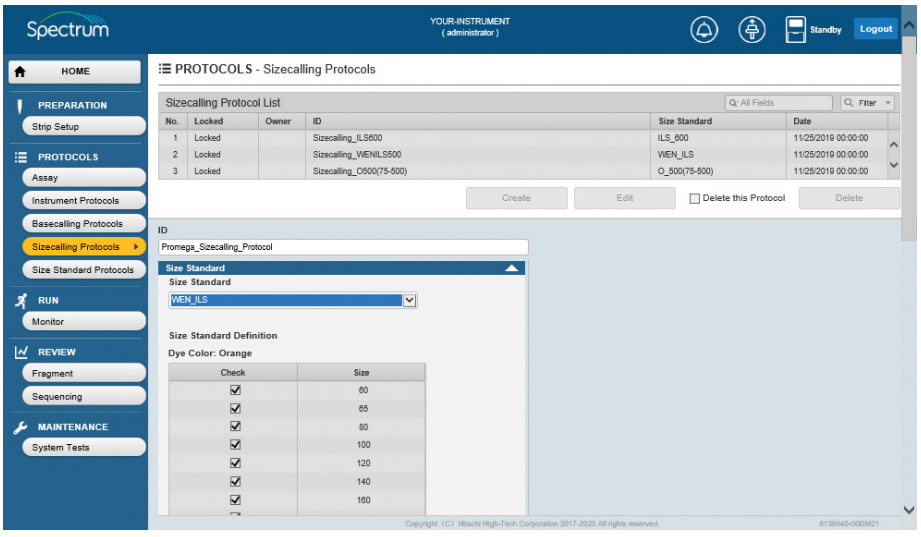

Figure 50. 'Size Standard' pull-down screen with selected size standard.

4. Select the **Analysis Range** pull-down menu. The default radio button setting is **Full** (Figure 51). If desired, select the **Partial** radio button to enable the start and stop point fields of the analysis range (Figure 52). Enter the desired scan number/data point values in these fields.

   Note: The numerical value for 'Start Point' must always be lower than the numerical value entered for 'Stop Point'.

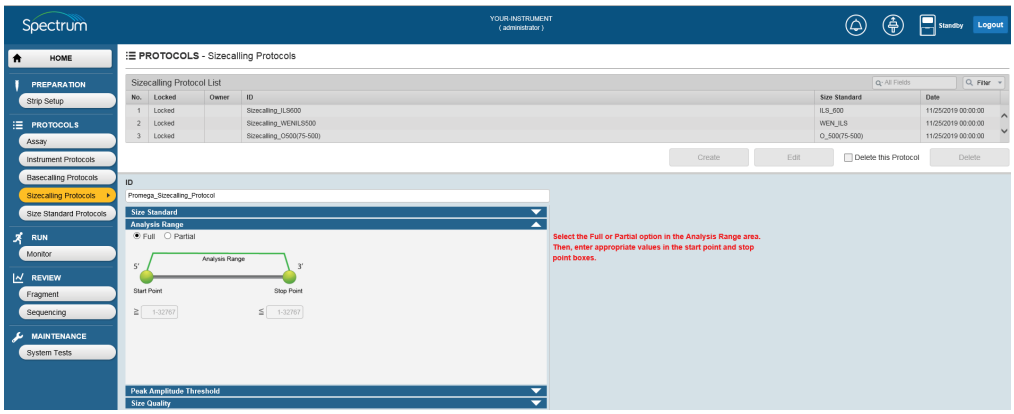

Figure 51. Full 'Analysis Range' pull-down screen.

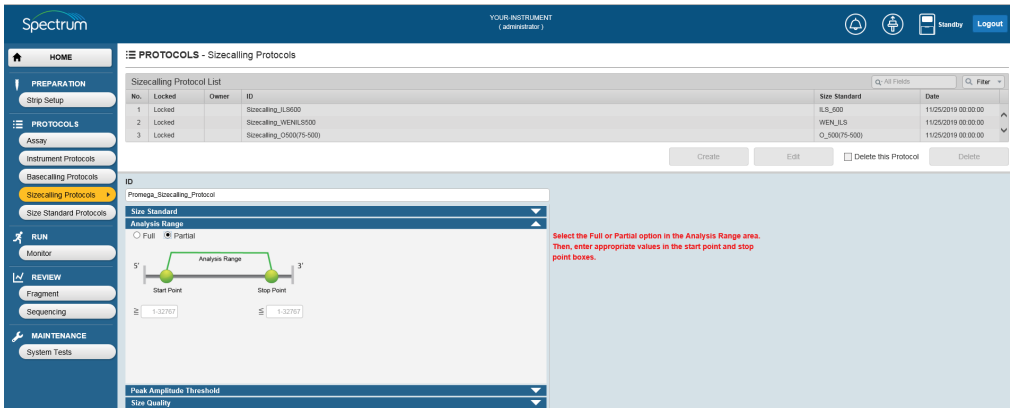

Figure 52. Partial 'Analysis Range' pull-down screen.

5. Select the **Peak Amplitude Threshold** pull-down menu to reveal the options for setting peak amplitude thresholds (Figure 53). Enter a Peak Amplitude Threshold value for the dye channel that contains the size standard. A Peak Amplitude Threshold value must be set for the dye channel that contains the size standard in order for sizing quality (SQ) and electrophoresis quality (EQ) to be determined.

   Note: Peaks that fall below the peak amplitude thresholds will still be present and available for analysis in secondary analysis software.

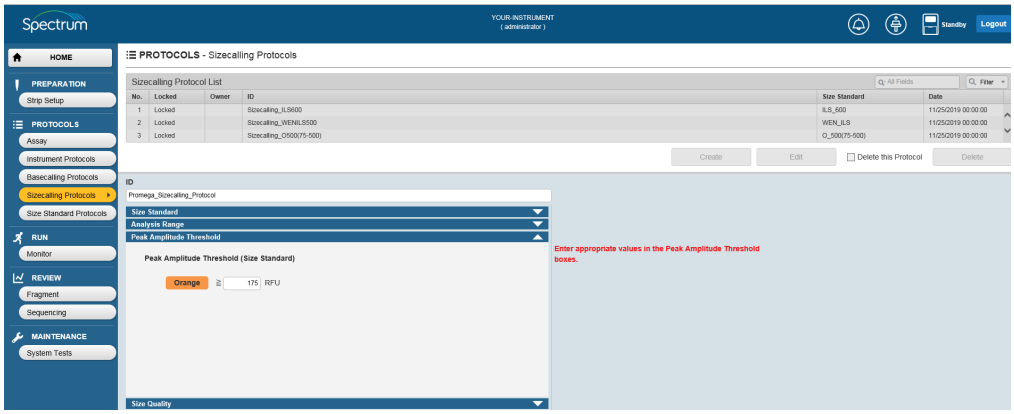

Figure 53. 'Peak Amplitude Threshold' pull-down screen.

6. Select the **Size Quality** pull-down menu and enter SQ values below which SQ data is considered failing and above which it is considered as passing (Figure 54).

   Note: Suspect SQ value ranges are defined by the minimum passing and maximum failing SQ values entered.

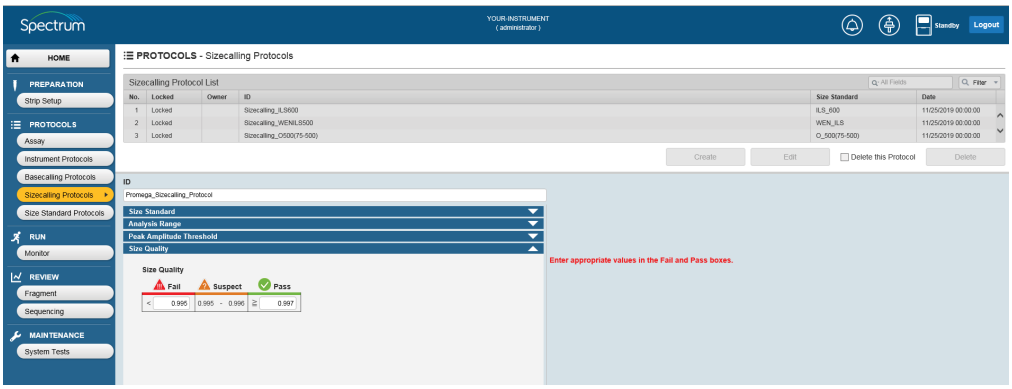

Figure 54. 'Sizing Quality' pull-down screen.

7. Select the **Electrophoresis Quality** pull-down menu and enter EQ values below which EQ data is considered failing and above which it is considered as passing (Figure 55).

   Note: Suspect EQ value ranges are defined by the minimum passing and maximum failing EQ values entered.

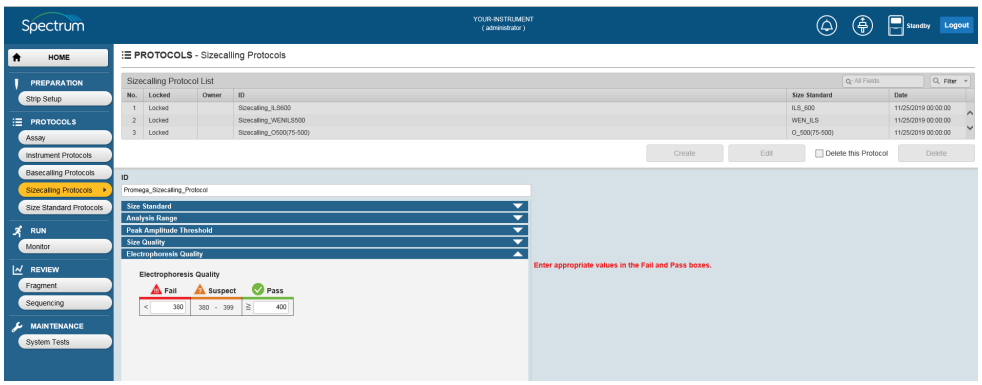

Figure 55. 'Electrophoresis Quality' pull-down screen.

8. Check the **Confirm** box and select **Save** (Figure 56). If no errors are detected, “Normal End” in a green horizontal box will appear on the screen. If errors are detected, either “Invalid data entered” or “The value is out of range” will appear in a red horizontal box and the software will indicate where the error is occurring.

Notes:

a. The **Confirm** check box must be selected to enable **Save**.

b. The **Cancel** button does not require selecting the **Confirm** box to become active and is always available. Select **Cancel** at any time during creation of a new Sizecalling Protocol to exit out of the sizecalling protocol creation process without saving any information.

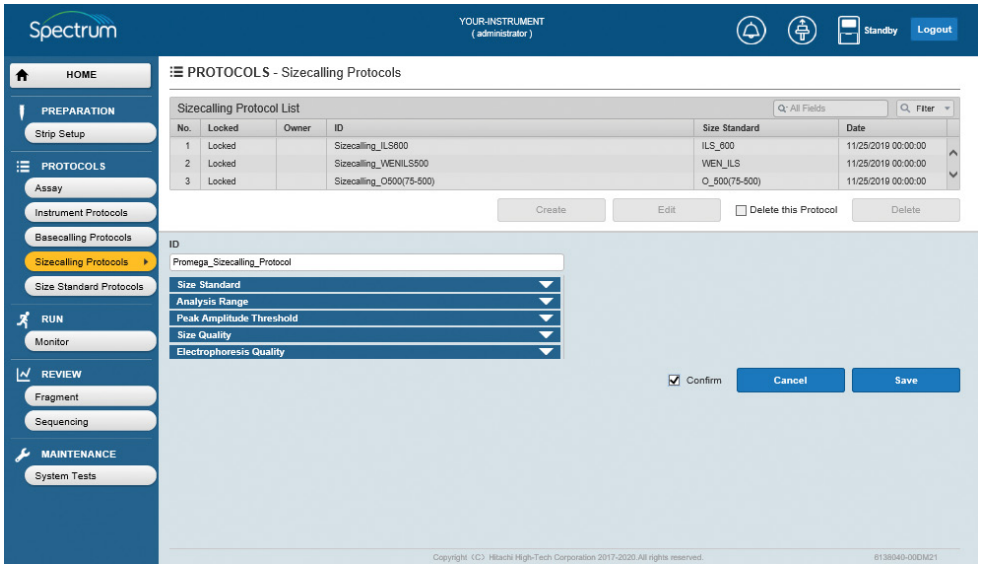

Figure 56. Saving a new Sizecalling Protocol.

9. The saved new sizecalling protocol is now available on the Spectrum Compact Control Software touch screen as well as on the Spectrum Compact CE System Remote Access Software and can be used to create an assay in both locations (see Section 5.5 for creating assays with the Spectrum Compact CE System Remote Access Software and Section 7.2.4 of the *Spectrum Compact CE System Operating Manual* #TMD058 for creating assays on the Spectrum Compact Control Software touch screen).

5.3.2 Editing an Existing Sizecalling Protocol

1. Select **Sizecalling Protocols** under PROTOCOLS from the Main Menu of the 'HOME' screen (Figure 12).
2. Data in the Sizecalling Protocol List may be searched and filtered (i.e., searched for based on specific values and filtered such that only sizecalling protocols that meet those criteria are displayed in the Sizecalling Protocol List). Select the magnifying glass icon on the Select Search Field box to display a window with radio button selections that allows you to search by All Fields, Locked, Owner, ID, Size Standard or Date (Figure 57).

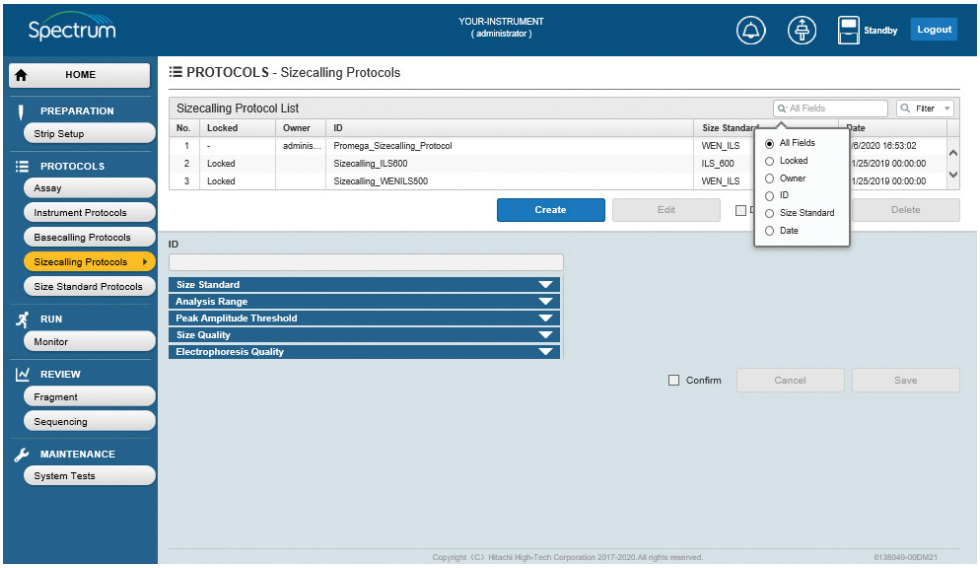

Figure 57. Sizecalling Protocol List select search field radio button window.

3. After selecting the appropriate search field, select the magnifying glass or down arrow icon in the Filter box to display filtering options by the different fields (Figure 58).
4. Search terms can be filtered by:
   - is
   - begins
   - contains
   - ends

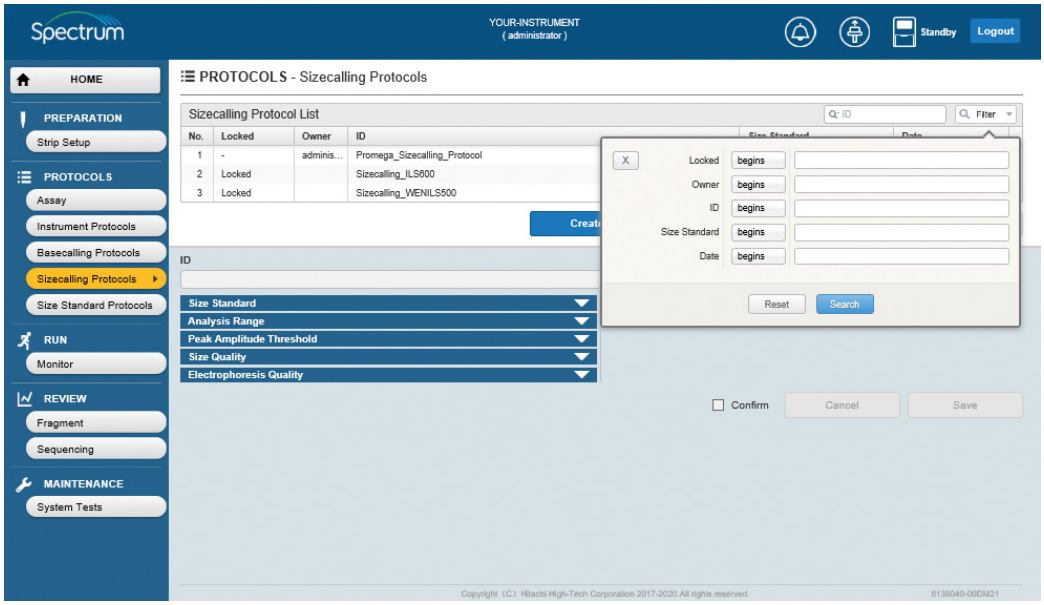

Figure 58. Sizecalling Protocol List search filter option selection.

5. After selecting the appropriate filter for search terms in the field being searched (i.e., Locked, Owner, ID, Size Standard or Date), type the desired search term in the adjacent box and select **Search** (Figure 59). Alternatively, select **Reset** to exit.

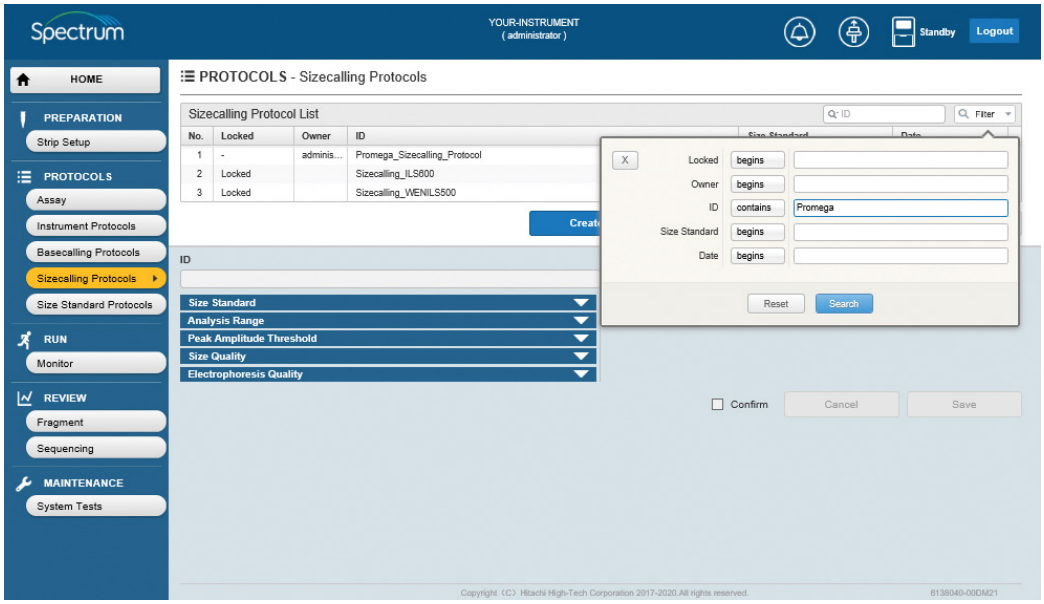

Figure 59. Sizecalling Protocol List search filter option selection.

6. The sizecalling protocols that meet the desired search and filter parameters will be displayed at the top of the Sizecalling Protocol List (Figure 60).

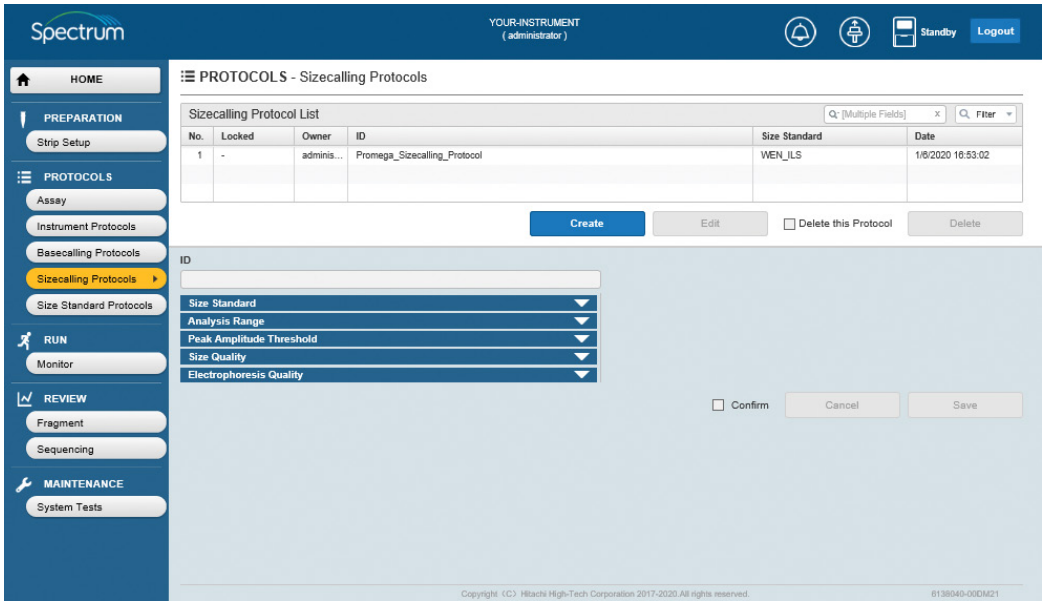

Figure 60. Searched and filtered sizecalling protocols.

7. Select the Sizecalling Protocol ID in the Sizecalling Protocol List to edit. This will activate **Edit** and the check boxes adjacent to the individual fragment sizes (Figure 61).

   Note: Before selecting **Edit**, the editable portion of the screen is grayed out and is not editable.

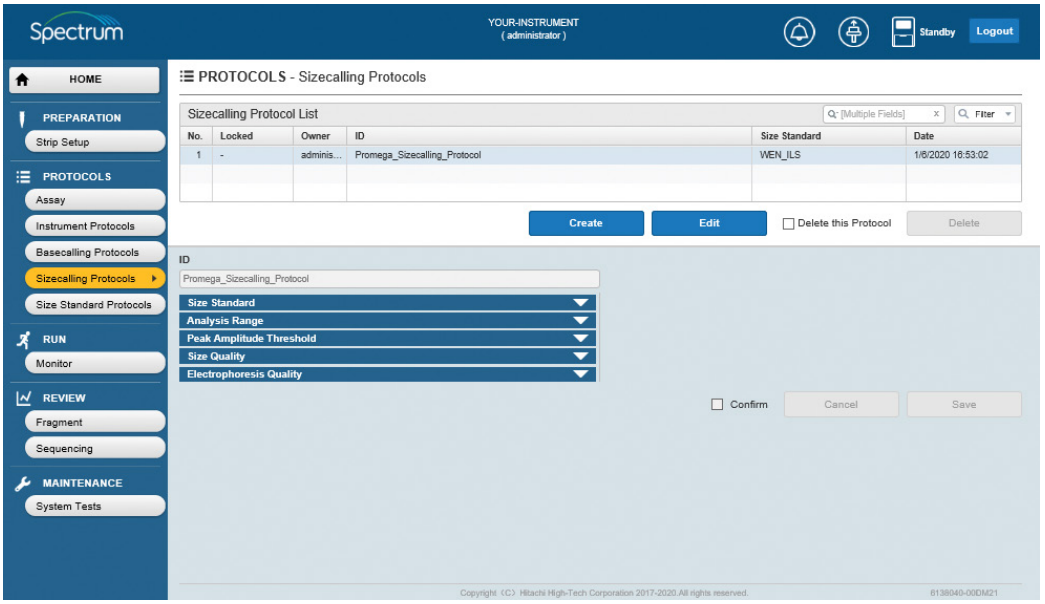

Figure 61. 'Sizecalling Protocols' screen with active Edit button.

8. Select **Edit**. This will enable the ID field as well as the **Size Standard, Analysis Range, Peak Amplitude Threshold, Size Quality** and **Electrophoresis Quality** pull-down menus (Figure 62).

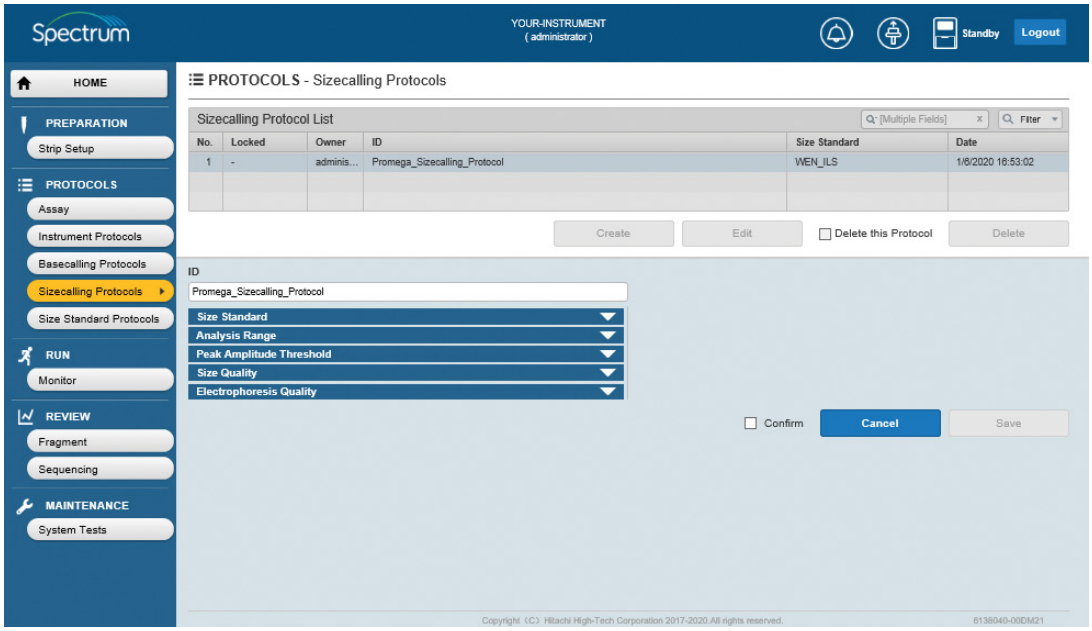

Figure 62. 'Sizecalling Protocols' edit screen with active fields.

9. Follow Steps 2–8 of Section 5.3.1.

   Note: Preloaded protocols cannot be overwritten. A new Sizecalling Protocol ID must be assigned. For user-defined protocols, you can either overwrite the existing Sizecalling Protocol ID or save with a new Sizecalling Protocol ID.

5.3.3 Deleting an Existing Sizecalling Protocol

1. Select **Sizecalling Protocols** under PROTOCOLS from the Main Menu of the 'HOME' screen (Figure 12), and then select the Sizecalling Protocol ID in the Sizecalling Protocol List that you want to delete (Figure 61).

   Note: Data in the Sizecalling Protocol List may be searched and filtered as described in Section 5.3.2.

2. Check the "Delete this Protocol" box and select **Delete** (Figure 61).

   Note: The "Delete this Protocol" check box must be selected to enable **Delete**.

5.4 Size Standard Protocol

Size standard protocols can only be edited and not created. The Spectrum Compact CE System comes with a series of preloaded size standard protocols for common commercially available size standards. These can be edited to create new variations on these preloaded size standards (i.e., versions that may not use all the fragments present). New size standard protocols can only be created using the preloaded versions. Preloaded protocols cannot be overwritten and must be saved with a new Size Standard Protocol ID.

5.4.1 Editing an Existing Size Standard Protocol

1. Select **Size Standard Protocols** under PROTOCOLS from the Main Menu of the 'HOME' screen (Figure 12).
2. Data in the Size Standard Protocol List may be searched and filtered (i.e., searched for based on specific values and filtered such that only size standard protocols that meet those criteria are displayed in the Size Standard Protocols List). Select the magnifying glass icon on the Select Search Field box to display a window with radio button selections that allows you to search by All Fields, Locked, Owner, ID, Size Standard or Date (Figure 63).

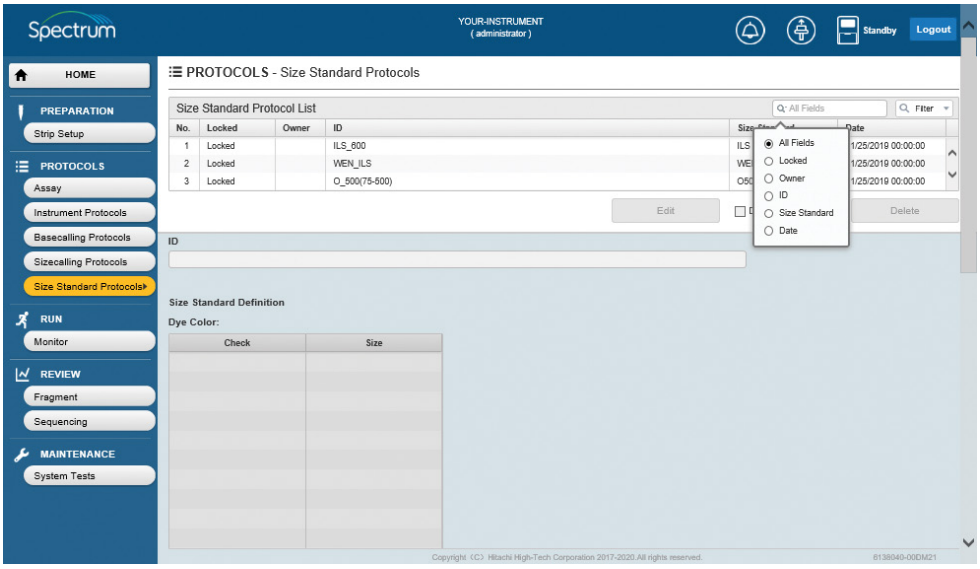

Figure 63. 'Size Standard Protocol List' select search field radio button window.

3. After selecting the appropriate search field, select the magnifying glass or down arrow icon in the Filter box to display filtering options by the different fields (Figure 64).
4. Search terms can be filtered by:
   - is
   - begins
   - contains
   - ends

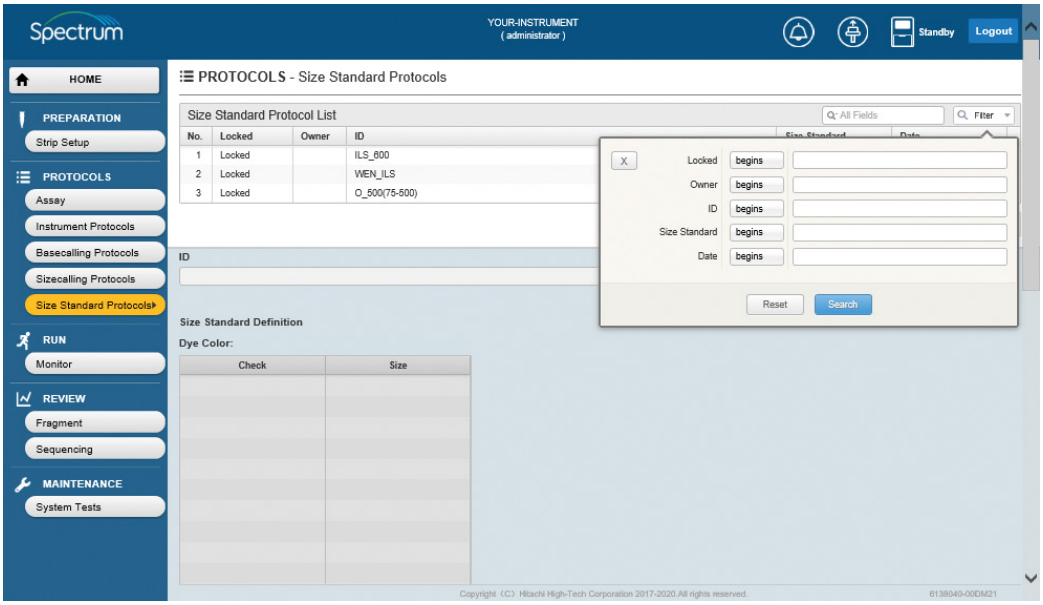

Figure 64. Size Standard Protocol List search filter option selection.

5. After selecting the appropriate filter for search terms in the field being search (i.e., Locked, Owner, ID, Size Standard or Date), type the desired search term in the adjacent box and select **Search** (Figure 65). Alternatively, select **Reset** to exit.

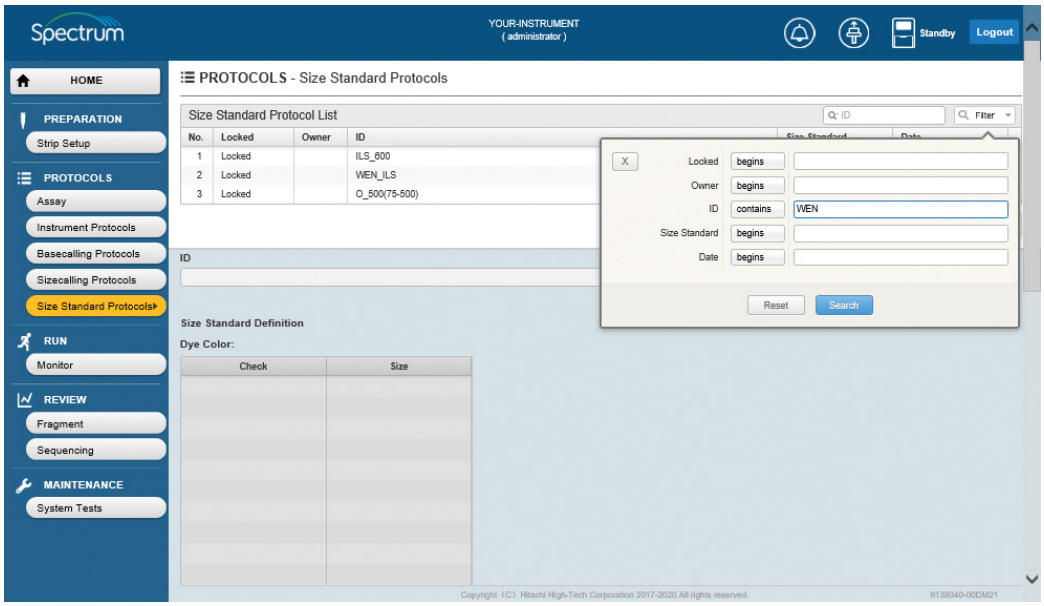

Figure 65. Size Standard Protocol List search filter option selection.

6. The size standard protocols that meet the desired search and filter parameters will be displayed at the top of the Size Standard Protocol List (Figure 66).

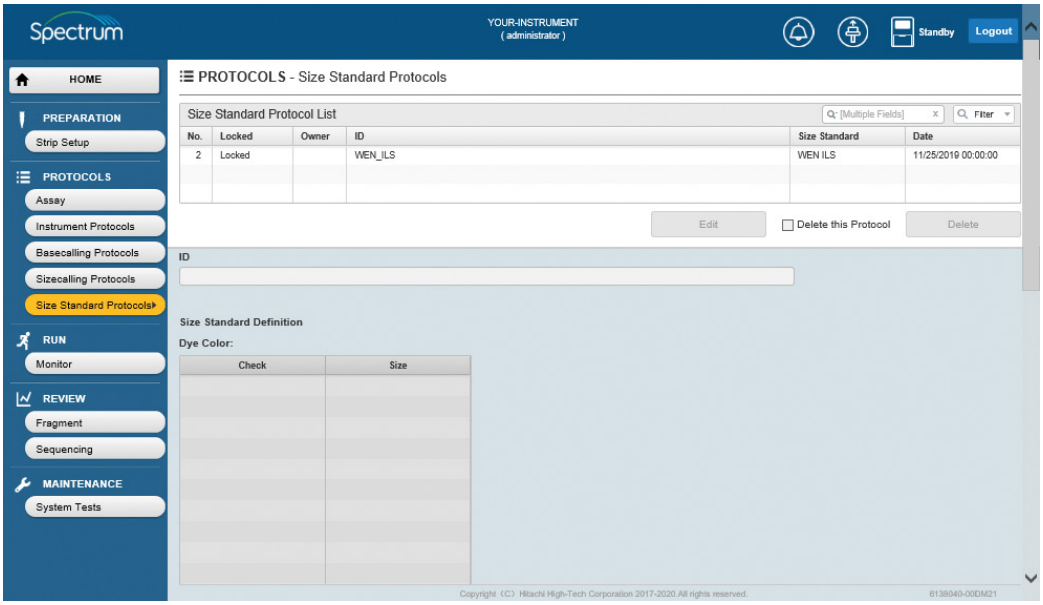

Figure 66. Searched and filtered size standard protocols.

7. Select the Size Standard Protocol ID in the Size Standard Protocol List to edit. This will activate **Edit** and the check boxes adjacent to the individual fragment sizes (Figure 67).

   Note: Before selecting **Edit**, the editable portion of the screen is grayed out and is not editable.

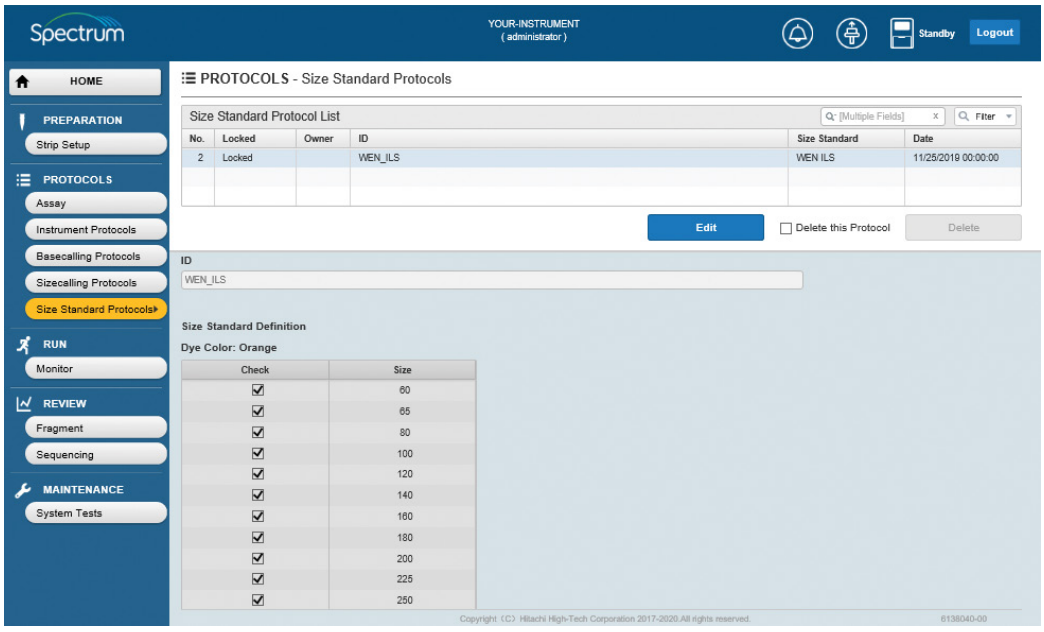

Figure 67. 'Size Standard Protocols' screen with active edit button.

8. Select **Edit**. This will enable the ID field (Figure 68).

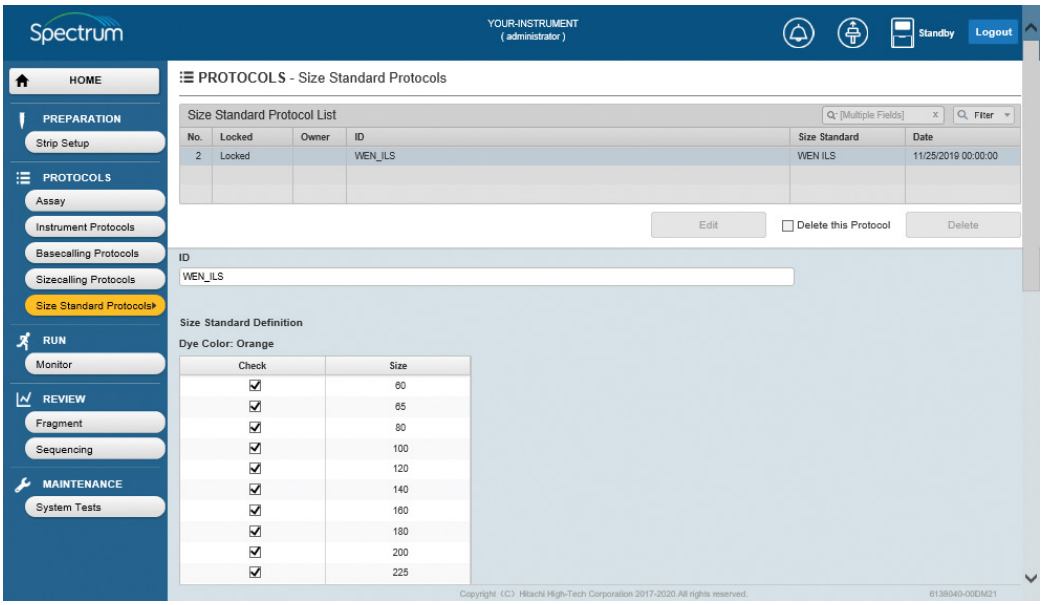

Figure 68. 'Size Standard Protocols' edit screen with active fields.

9. Enter a Size Standard Protocol ID for the new size standard protocol by selecting the ID field to activate the cursor (see Section 3.1 for information on acceptable and unacceptable characters). Select the desired fragments to include in the new size standard by ensuring that the box in the left column adjacent to the fragment size is checked. Uncheck boxes for those fragments that are not required in the new size standard protocol (Figure 69).

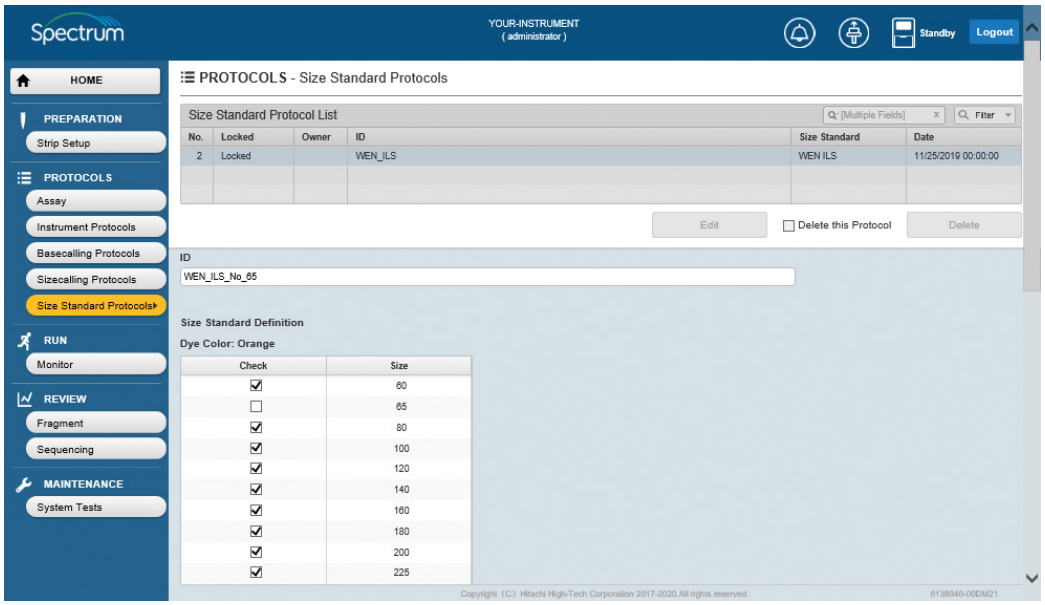

Figure 69. 'Size Standard Protocols' edit screen with edited size standard.

10. Scroll to the bottom of the screen and check the **Confirm** box and select **Save** (Figure 70). If no errors are detected, “Normal End” in a green horizontal box will appear on the screen. If errors are detected, either “Invalid data entered” or “The value is out of range” will appear in a red horizontal box and the software will indicate where the error is occurring.

    Notes:

    a. The **Confirm** check box must be selected to enable **Save**.

    b. The **Cancel** button does not require selecting the **Confirm** box to become active and is always available. Select **Cancel** at any time while editing a size standard protocol to exit out of the size standard protocol editing process without saving any information.

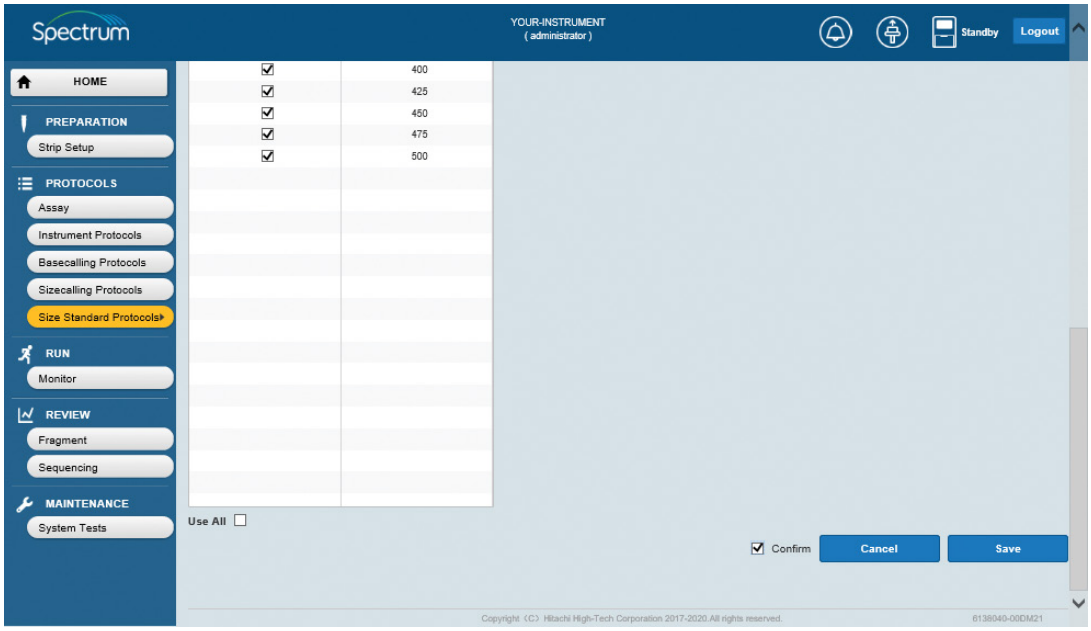

Figure 70. Saving an edited size standard protocol.

5.4.2 Deleting an Existing Size Standard Protocol

1. Select **Size Standard Protocols** under PROTOCOLS from the Main Menu of the ‘HOME’ screen (Figure 12) and then select the Size Standard Protocol ID in the Size Standard Protocol List that you want to delete (Figure 67).

    Note: Data in the Size Standard Protocol List may be searched and filtered as described in Section 5.4.1.

2. Check the “Delete this Protocol” box and select **Delete** (Figure 67).

    Note: The “Delete this Protocol” check box must be selected to enable **Delete**.

5.5 Assay

Assays are created by associating a specific instrument protocol with a specific analysis protocol (basecalling protocol for sequencing application or sizecalling protocol for fragment application). If the instrument and analysis protocols are added from the library, a copy of these protocols is added to the assay, such that they can be modified within the created assay independently from the original items stored in the library (i.e., changes made to the instrument and analysis protocol within the newly created assay will not be saved to the original instrument and analysis protocols stored in the library).

5.5.1 Creating a New Assay

1. Select **Assay** under PROTOCOLS from the Main Menu of the 'HOME' screen (Figure 12), and then select **Create** (Figure 71). This activates the ID field, Application radio button, and the **Polymer, Dye Set**, **Instrument Protocol**, and **Analysis Protocol** pull-down menus (Figure 72).

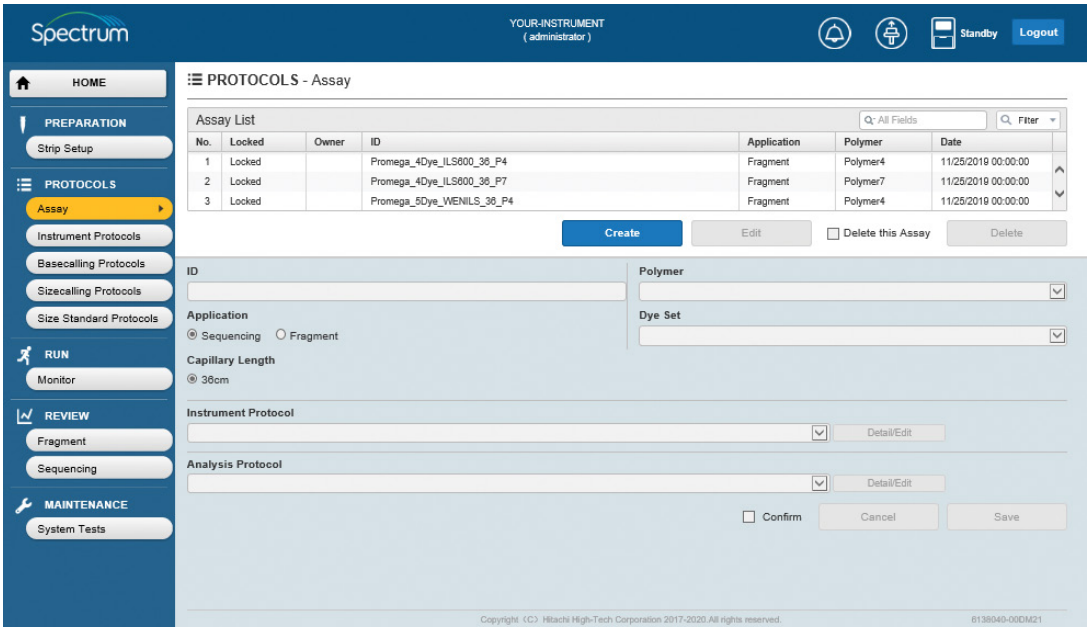

Figure 71. 'Assay' screen.

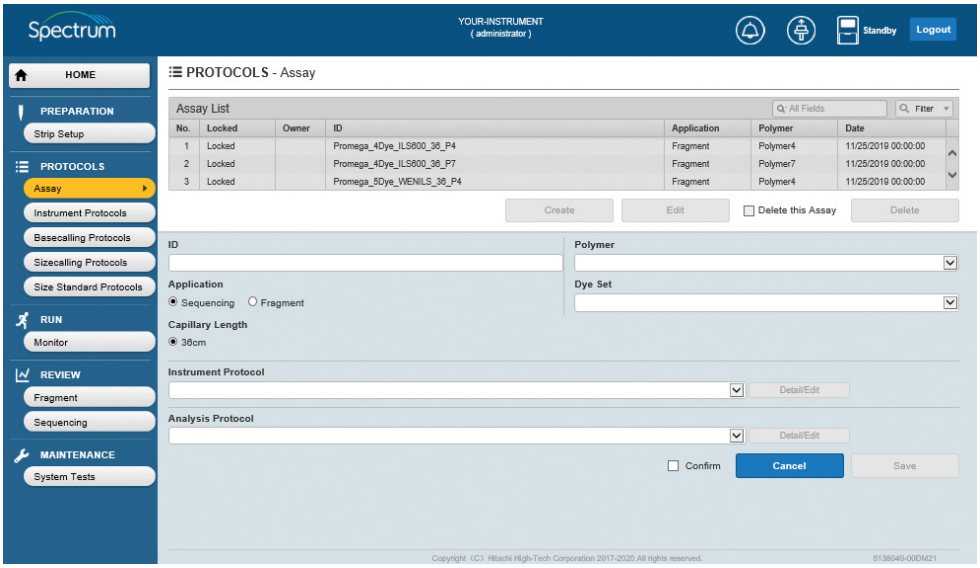

Figure 72. 'Assay' screen with active fields.

2. Enter an Assay ID for the new assay by selecting the ID field to activate the cursor (see Section 3.1 for information on acceptable and unacceptable characters).
3. Select the Application using the appropriate radio button (**Sequencing** or **Fragment**).
4. Select the Polymer (**Polymer4** or **Polymer7**) using the pull-down menu.
5. Select the **Dye Set** using the pull-down menu.
6. Select the **Instrument Protocol** using the pull-down menu. **Detail/Edit** becomes active. After selecting **Detail/Edit**, the run module parameters may be edited as desired (Figure 73; see Section 5.1.1 for minimum and maximum values that can be entered for these parameters).

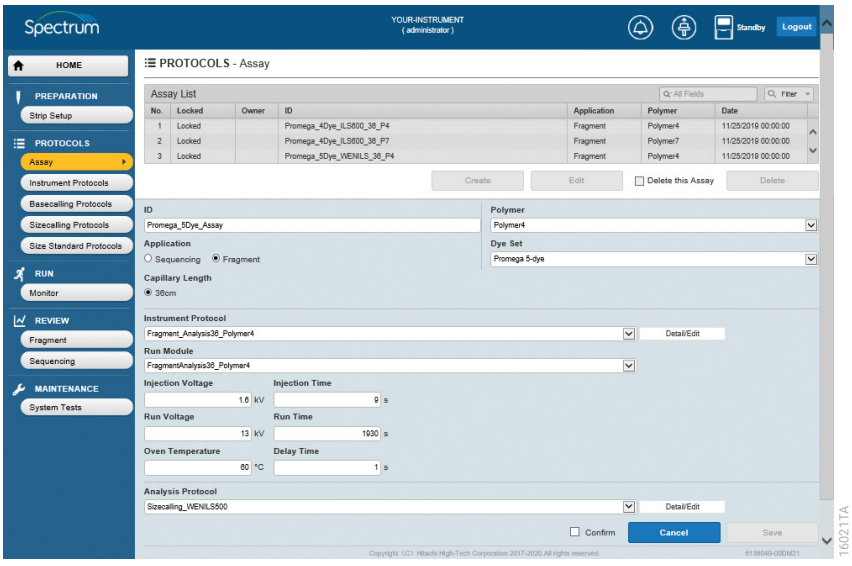

Figure 73. 'Assay' screen with editable instrument protocol fields.

7. Select **Analysis Protocol** using the pull-down menu.

   Note: Sizecalling protocols are shown in the **Analysis Protocol** pull-down menu when Fragment is chosen as the application type and basecalling protocols are shown when Sequencing is the application type.

8. **Detail/Edit** becomes active after selecting the desired Analysis Protocol. After selecting **Detail/Edit**, the parameters specific for basecalling (Figure 74) or sizecalling protocols (Figure 75) may be edited as described in Sections 5.2 and 5.3, respectively.

   Note: Edits made to the Instrument or Analysis Protocol when creating an assay do not change the parameters of those protocols stored in the library. Changes are only stored in this particular assay.

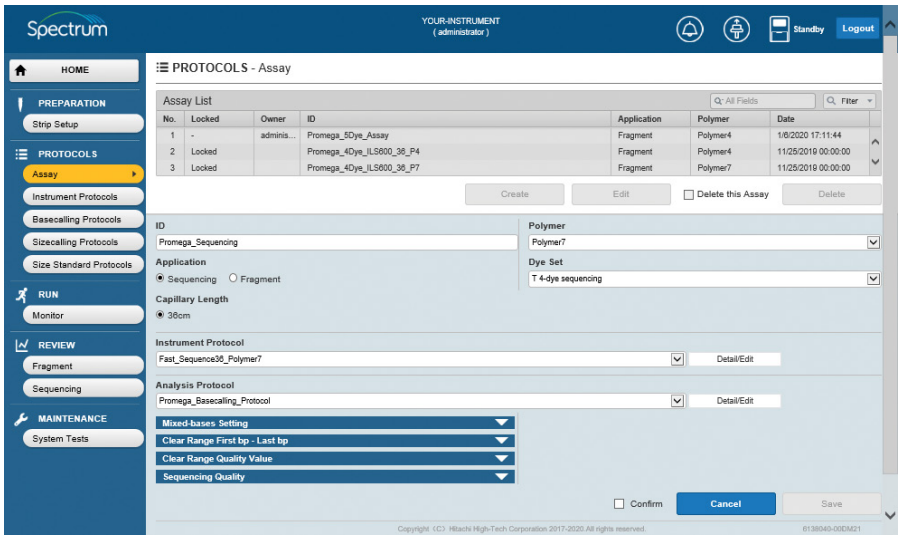

Figure 74. 'Assay' screen with editable basecalling protocol fields.

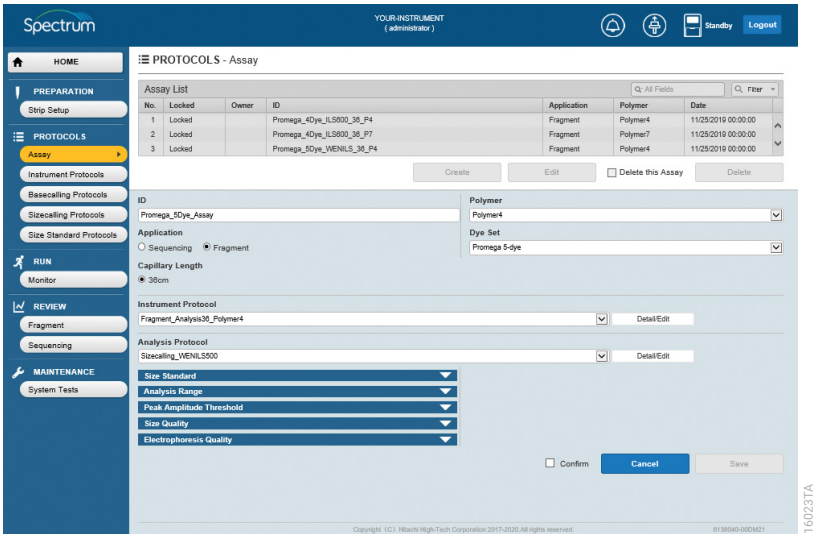

Figure 75. 'Assay' screen with editable sizecalling protocol fields.

9. Check the **Confirm** box, and then select **Save** (Figure 76). If no errors are detected "Normal End" in a green horizontal box will appear on the screen. If errors are detected, either "Invalid data entered" or "The value is out of range" will appear in a red horizontal box and the software will indicate where the error is occurring.

   Notes:

   a. The **Confirm** check box must be selected to enable **Save**.

   b. The **Cancel** button does not require selecting the **Confirm** box to become active and is always available. Select **Cancel** at any time during creation of a new assay to exit the assay creation process without saving any information.

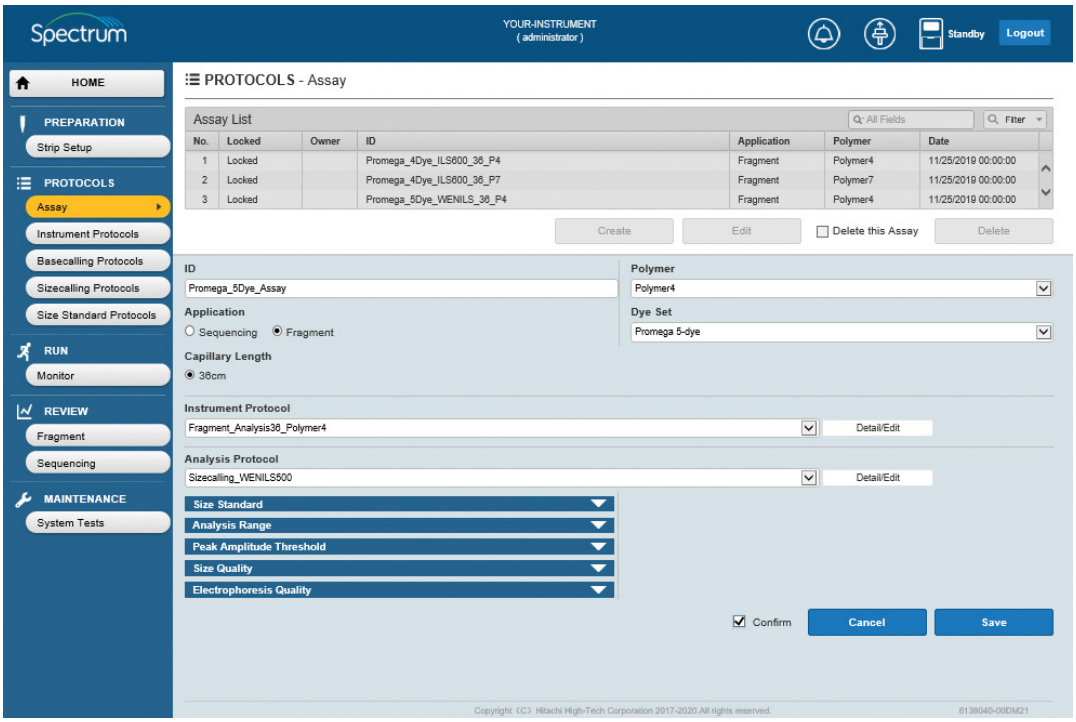

Figure 76. Saving a new assay.

10. The assay is now available on the Spectrum Compact Control Software touch screen as well as on the Spectrum Compact CE System Remote Access Software.

5.5.2 Editing an Existing Assay

1. Select **Assay** under PROTOCOLS from the Main Menu of the 'HOME' screen (Figure 12).
2. Data in the Assay List may be searched and filtered (i.e., searched for based on specific values and filtered such that only assays that meet those criteria are displayed in the Assay List). Select the magnifying glass icon on the Select Search Field box to display a window with radio button selections that allows you to search by All Fields, Locked, Owner, ID, Application, Polymer or Date (Figure 77).

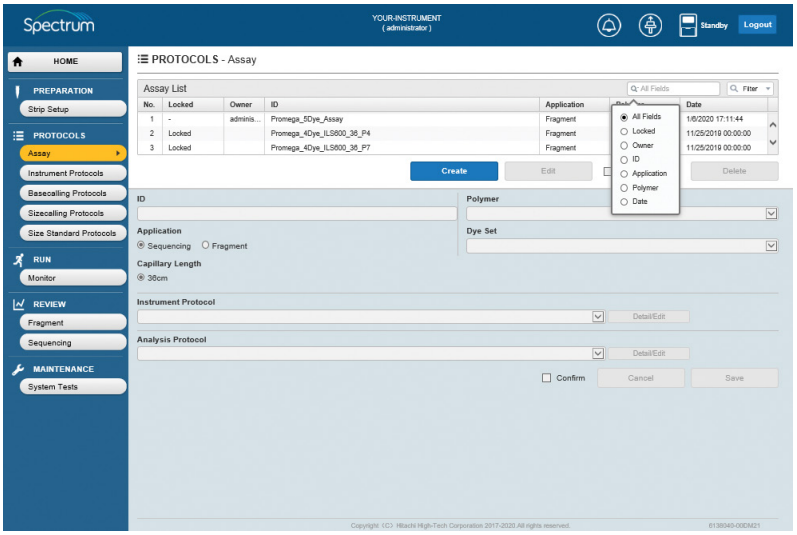

Figure 77. Assay List select search field radio button window.

3. After selecting the appropriate search field, select the magnifying glass or down arrow icon in the Filter box to display filtering options by the different fields (Figure 78).
4. Search terms can be filtered by:
   - is
   - begins
   - contains
   - ends

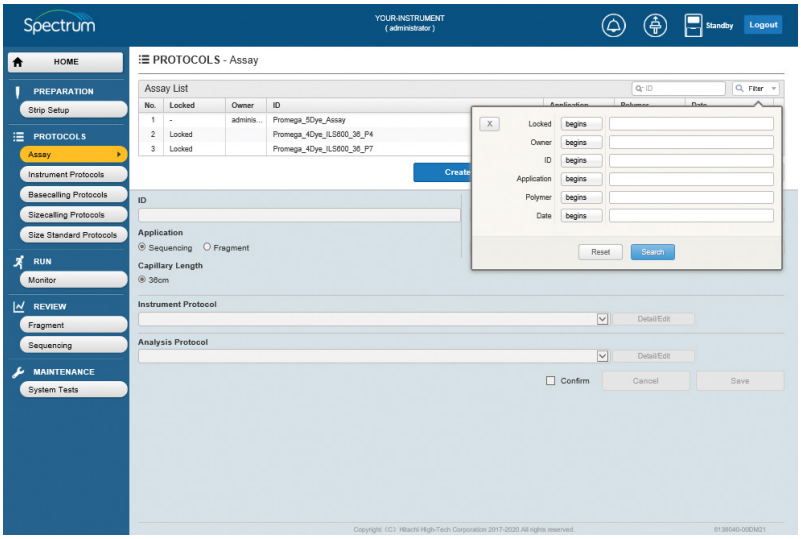

Figure 78. Assay List search filter option selection.

5. After selecting the appropriate filter for the search terms in the field being searched (i.e., Locked, Owner, ID, Application, Polymer or Date), type the desired search term in the adjacent box and select **Search** (Figure 79). Alternatively, select **Reset** to exit.

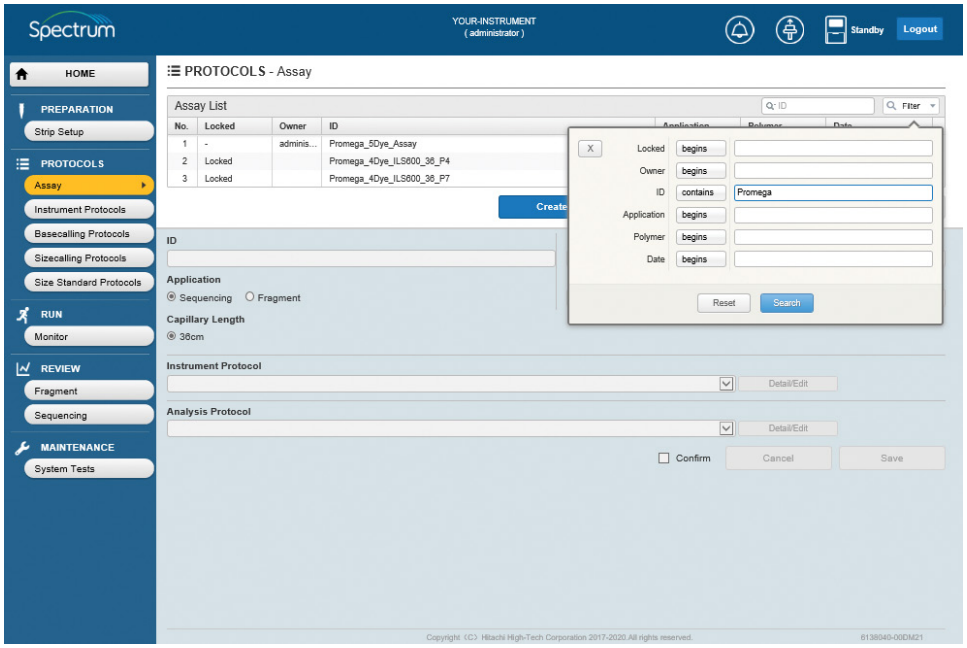

Figure 79. Assay List search filter option selection.

6. The assays that meet the desired search and filter parameters will be displayed at the top of the Assay List (Figure 80).

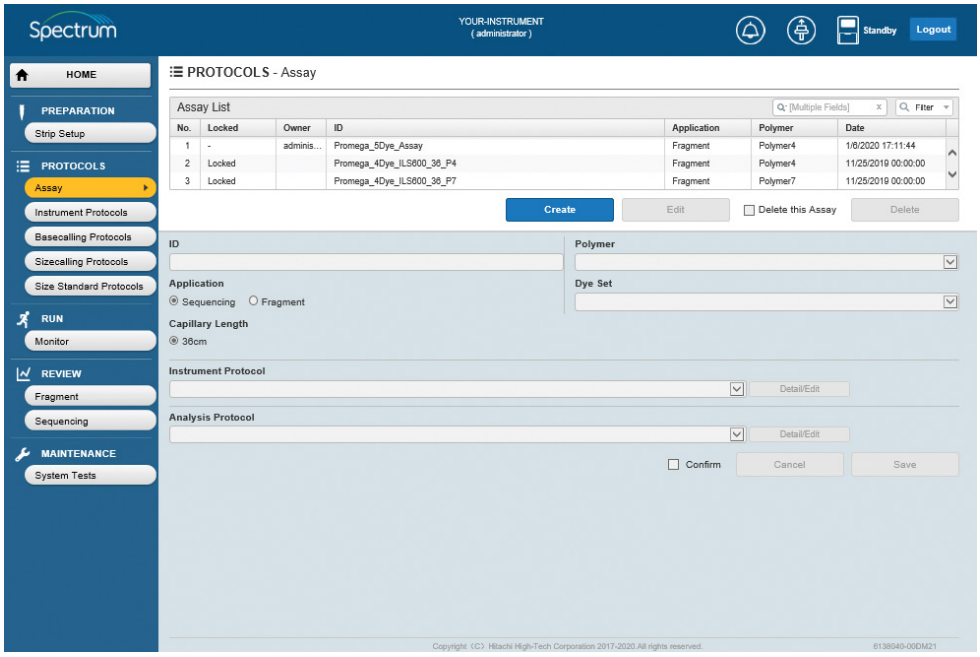

Figure 80. Searched and filtered assays.

7. Select the Assay ID in the Assay List to edit. This will activate **Edit** (Figure 81).

   Note: Before selecting **Edit**, the editable portion of the screen is grayed out and is not editable.

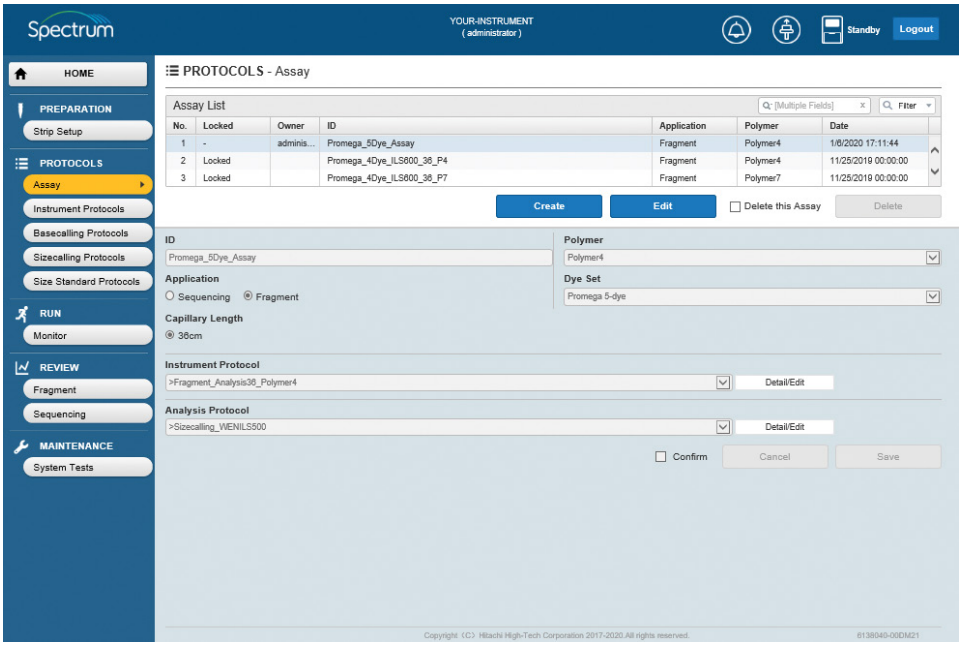

Figure 81. 'Assay' screen with active Edit button.

8. Select **Edit**. This will enable the ID field, as well as the **Instrument Protocol** and **Analysis Protocol** pull-down menus (Figure 82).

   Note: When editing an existing assay, it is not possible to change the application type, polymer type or dye set. Only parameters within the Instrument Protocol and Analysis Protocol may be edited.

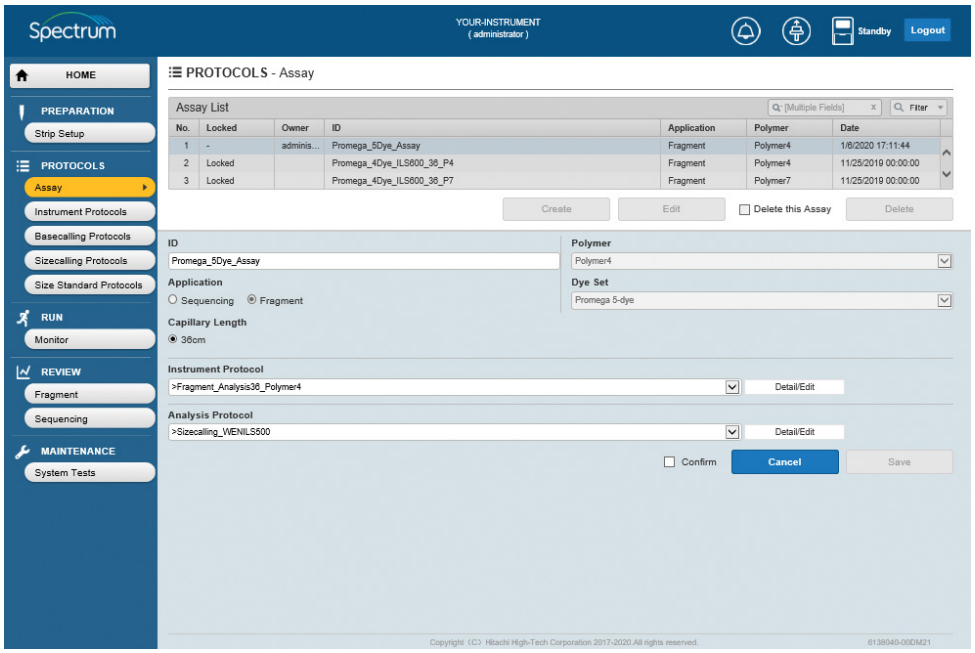

Figure 82. 'Assay' edit screen with active fields.

9. Follow Steps 2–10 of Section 5.5.1.

   Notes:

   a. Preloaded assays are locked and cannot be overwritten. A new Assay ID must be assigned. For user-defined assays, you can either overwrite the existing Assay ID or save with a new Assay ID.

   b. You cannot save changes to an existing user-defined assay (i.e., the assay cannot be overwritten) if that assay is currently be used to set up a run, or is part of an in-progress run on the Spectrum Compact CE System.

5.5.3 Deleting an Existing Assay

1. Select **Assay** under PROTOCOLS from the Main Menu of the 'HOME' screen (Figure 12) and then select the Assay ID in the Assay List that you want to delete (Figure 81).

   Note: Data in the Assay List may be searched and filtered as described in Section 5.5.2.

2. Check the "Delete this Assay" box and select **Delete** (Figure 81).

   Note: The "Delete this Assay" check box must be selected to enable **Delete**.

Run Monitor

6

Run Monitor allows users to view data coming off the Spectrum Compact CE System in real time using the Spectrum Compact CE System Remote Access Software.

1. Select **Monitor** under Run from the Main Menu of the 'HOME' screen (Figure 12) to reveal the 'RUN-Monitor' screen (Figure 83). The 'RUN-Monitor' screen is split into three sections from top to bottom as follows:
   - Injection List
   - Sample View
   - Data View

   Notes:

   1. To the right of the Injection List is the 'Assay Info' window. This displays the assay information for the injection selected in the Injection List. Since no injection is selected in Figure 83, there is no assay information displayed in the 'Assay Info' window. See Figure 84 for assay information in the 'Assay Info' window once an injection from the Injection List is selected.
   2. The injection currently running on the Spectrum Compact CE System is highlighted in orange on the Injection List.

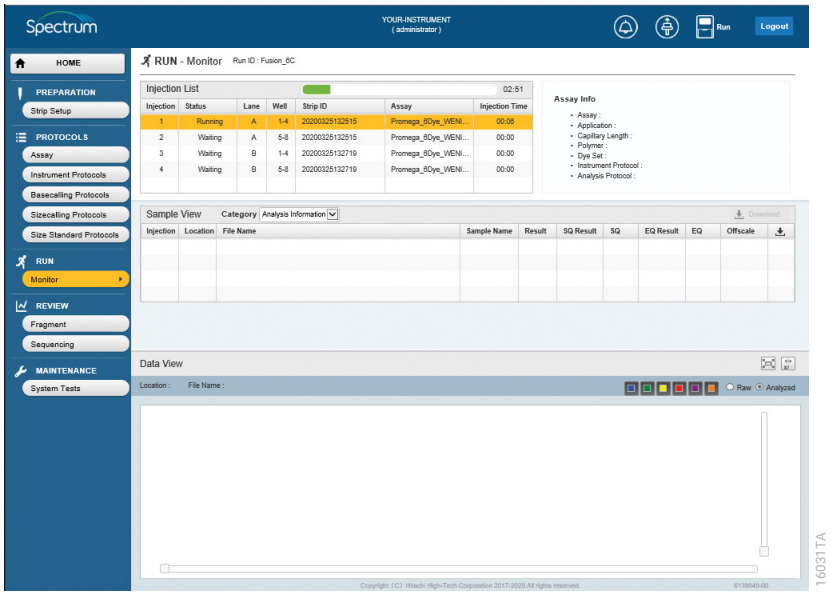

Figure 83. 'RUN-Monitor' screen.

2. The Injection List contains all the injections for the current run on the Spectrum Compact CE System, including the status of each injection (i.e., waiting, running or completed). A green horizontal timer bar is located at the top of the Injection List along with a numerical timer indicating the amount of time left before the run is completed.

   Notes:

   a. The injection currently running on the Spectrum Compact CE System is highlighted in orange on the Injection List.

   b. Only running and completed injections are viewable in the Sample View and Data View sections of the 'RUN-Monitor' screen.

3. The Injection List is split into seven columns.

Column Header	Description
Injection	Injection number in the run order set up.
Status	**Waiting:** Injections that have yet to be run. These cannot be viewed in the Data View section of the 'RUN-Monitor' screen. **Running:** The injection that is currently in process of being run. This may be viewed in the Data View section of the 'RUN-Monitor' screen. **Completed:** Injections that have been completed. These may still be viewed in the Data View section of the 'RUN-Monitor' screen.
Lane	Corresponds to lane position on the sample cartridge (see Section 2.4 of the *Spectrum Compact CE System Operating Manual* #TMD058).
Well	Corresponds to well positions on the sample cartridge (see Section 2.4 of the *Spectrum Compact CE System Operating Manual* #TMD058). Wells specified are either 1–4 or 5–8 per Lane.
Strip ID	Strip ID for 8-well strip tube.
Assay	Name of assay being used for that injection. Highlighting the injection displays the parameters for that assay to the right of the Injection List section of the 'RUN-Monitor' screen.
Injection Time	Time elapsed on a running injection. For a completed injection, the total time for that injection is displayed. For a waiting injection, zero time is displayed.

6.1 Monitoring Data for an In-Process Injection

1. Select the injection that is currently running (highlighted in orange) from the Injection List (Figure 84).

   Note: Assay information is displayed in the 'Assay Info' window for the injection selected in the Injection List.

2. This displays the list of samples in that injection in the Sample View section of the 'RUN-Monitor' screen. Select a specific sample to view the raw data as it is collected in real time (Figure 84).

   Notes:

   a. Only raw data from one sample at a time may be monitored as it is collected in real time. Select each sample separately to view the raw data being collected for each capillary.

   b. For injections that are still running, only the raw data is displayed. It is not possible to toggle between raw and analyzed data using the **Raw** and **Analyzed** radio buttons.

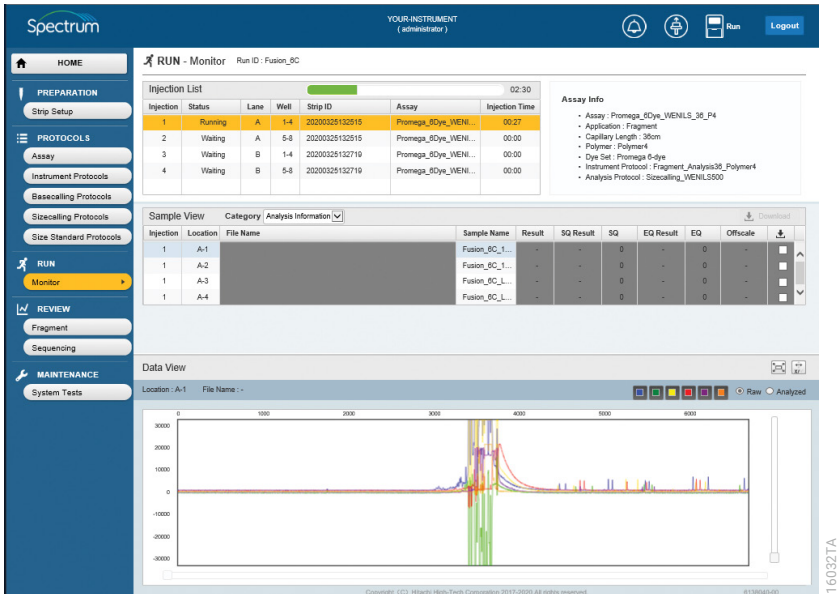

Figure 84. 'RUN-Monitor' screen with current injection and sample selected.

3. The 'Sample View' window has a **Category** pull-down menu that allows you to choose the following two options:

   a. Analysis Information

   b. Run Information

4. The Sample View section of the 'RUN-Monitor' screen will display the information for the selected category. When **Analysis Information** is selected with fragment data, the Sample View is split into eleven columns, as described in the following table.

Column Header	Description
Injection	Injection number in the run order set up.
Location	Specifies lane and well position of the injected sample (see Section 2.4 of the *Spectrum Compact CE System Operating Manual* #TMD058).
File Name	Name of the file for each sample and sample type (.fsa). **Note:** Not displayed for the in-process injection.
Sample Name	Name of sample as entered in Strip ID.
Result	Overall pass or fail based on SQ and EQ pass/fail values. **Note:** Not displayed for the in-process injection.
SQ Result	SQ pass, suspect, or fail result based on SQ settings in sizecalling protocol (see Section 5.3). **Note:** Not displayed for the in-process injection.
SQ	Calculated SQ value (upon which, the pass, suspect, or fail result is made based on SQ settings in sizecalling protocol). **Note:** Not displayed for the in-process injection.
EQ Result	EQ pass, suspect, or fail result based on EQ settings in sizecalling protocol (see Section 5.3). **Note:** Not displayed for the in-process injection.
EQ	Calculated EQ value (upon which, the pass, suspect, or fail result is made based on EQ settings in sizecalling protocol). **Note:** Not displayed for the in-process injection.
Offscale	Indicates whether any data in sample is offscale (fail) or below saturation (pass). **Note:** Not displayed for the in-process injection.
Download	Checking boxes in this column displays electropherogram images in Data View section of 'RUN-Monitor' screen and identifies which individual sample files in an injection can be downloaded. **Notes:** a. You can only download data from completed injections. b. **Download** only becomes active after at least one sample check box has been selected in the Download column.

5. When **Analysis Information** is selected with sequencing data, the Sample View is split into twelve columns, as described in the following table.

Column Header	Description
Injection	Injection number in the run order set up.
Location	Specifies lane and well position of the injected sample (see Section 2.4 of the *Spectrum Compact CE System Operating Manual* #TMD058).
File Name	Name of the file for each sample and sample type (.ab1). **Note:** Not displayed for the in-process injection.
Sample Name	Name of sample as entered in Strip ID.
Result	Overall pass or fail based on CRL, QV20+, and Trace Score pass/fail values. **Note:** Not displayed for the in-process injection.
CRL Result	CRL pass, suspect, or fail result based on CRL settings in basecalling protocol (see Section 5.2). **Note:** Not displayed for the in-process injection.
CRL	Calculated CRL value (upon which, the pass, suspect, or fail result is made based on CRL settings in basecalling protocol). **Note:** Not displayed for the in-process injection.
QV20+ Result	QV20+ pass, suspect, or fail result based on QV20+ settings in basecalling protocol (see Section 5.2). **Note:** Not displayed for the in-process injection.
QV20+	Calculated QV20+ value (upon which, the pass, suspect, or fail result is made based on QV20+ settings in basecalling protocol). **Note:** Not displayed for the in-process injection.
Trace Score Result	Trace Score pass, suspect, or fail result based on Trace Score settings in basecalling protocol (see Section 5.2). **Note:** Not displayed for the in-process injection.
Trace Score	Calculated Trace Score value (upon which pass, suspect, or fail result is made based on Trace Score settings in basecalling protocol). **Note:** Not displayed for the in-process injection.
Download	Checking boxes in this column displays electropherogram images in Data View section of 'RUN-Monitor' screen and identifies which individual sample files in an injection can be downloaded. **Notes:** a. You can only download data from completed injections. b. **Download** only becomes active after at least one sample check box has been selected in the Download column.

6. When **Run Information** is selected (for fragment or sequencing data), the Sample View is split into ten columns, as described in the following table.

Column Header	Description
Injection	Injection number in the run order set up.
Location	Lane and well position of the injected sample (see Section 2.4 of the *Spectrum Compact CE System Operating Manual* #TMD058).
File Name	Name of the file for each sample and sample type (.fsa or .ab1). **Note:** Not displayed for the in-process injection.
Run ID	Name of the Run.
Assay	Name of the Assay used for each injection during the run.
Instrument Protocol	Name of the Instrument Protocol used for each injection during the run.
Capillary	Capillary length being used.
Polymer	Polymer type used during run.
Capillary No.	Capillary number on which a particular sample was run.
Download	Checking boxes in this column displays electropherogram images in Data View section of 'RUN-Monitor' screen and identifies which individual sample files in an injection can be downloaded. **Note:** a. You can only download data from completed injections. b. **Download** only becomes active after at least one sample checkbox has been selected in the Download column.

Note: When either **Analysis Information** or **Run Information** is selected in the **Category** pull-down menu in the 'Sample View' screen, data are only viewable in all columns for completed injections. For injections in the process of running, the File Name column is blank in the Analysis Information or Run Information categories and the Results columns are blank in the Analysis Information category (Figure 84).

7. The Data View section of the 'RUN-Monitor' screen can be navigated using the icons on the screen.

Icon	Description
	Show/Hide Blue dye channel
	Show/Hide Green dye channel
	Show/Hide Yellow dye channel
	Show/Hide Red dye channel
	Show/Hide Purple dye channel
	Show/Hide Orange dye channel
	Show/Hide Aqua dye channel
	Show/Hide Brown dye channel
	Resets view after zooming (by mouse or using Y axis slider)
	Switch the zoom-in/zoom-out direction by mouse (X and Y axis together or X only)

Note: Purple and orange dye channel icons are not present when monitoring sequencing runs. The yellow dye channel is replaced by the black dye channel icon for sequencing runs.

8. Zoom in onto data by clicking on the mouse and drawing it across the region of the electropherogram of interest. Depending on the zoom selected (i.e., X and Y axis together or X axis alone) the image will be zoomed upon release of the mouse button.
9. Zoom in on the Y axis by moving the slider on the right hand side of the Data View section of the screen up (to increase peak heights) or down (to decrease peak heights).

6.2 Monitoring Data From a Completed Injection of an In-Process Run

1. Select a completed injection from the current in-process run from the Injection List (Figure 85).

   Note: Assay information is displayed in the 'Assay Info' window for the selected injection.

2. A list of samples in that injection is displayed in the Sample View section of the 'RUN-Monitor' screen. Select a specific sample in the Sample View to display the electropherogram for that sample in the Data View section of the 'RUN-Monitor' screen (Figure 85).

   Note: Only data from one sample at a time from a completed injection of an in-process run may be viewed in the Data View section. Select each sample separately to view the data for each capillary.

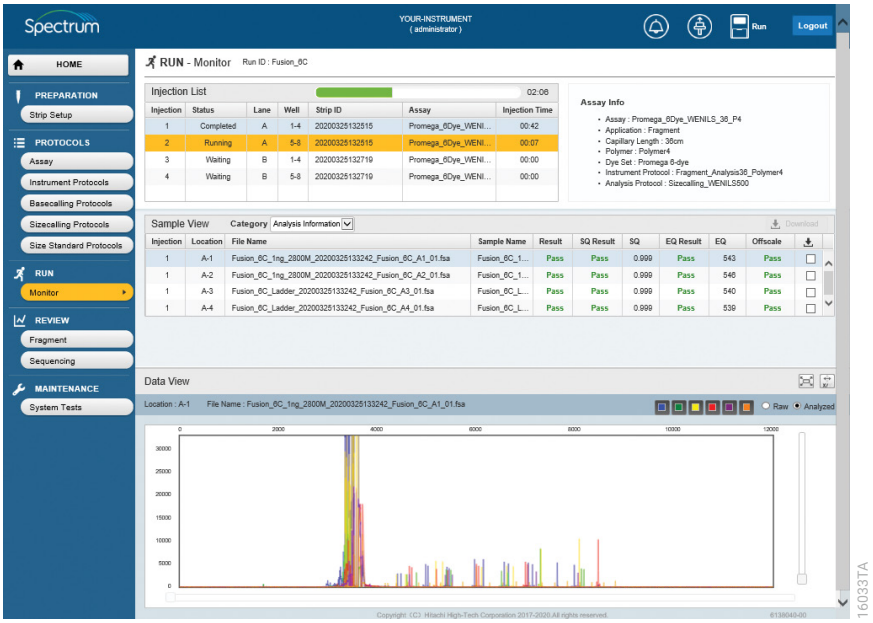

Figure 85. Electropherogram in Data View section of 'RUN-Monitor' screen.

3. The **Raw** and **Analyzed** radio buttons can be used to toggle between these two views of the data from completed injections. For injections that are in process (Section 6.1), only the raw data is displayed.

Application	Radio Button	Description
Fragment	Raw	Displays electropherogram peaks that have been spectrally separated, but the baselines have not been normalized.
	Analyzed	Primary analysis view displays electropherogram data with baseline normalization applied after the spectral separation.
Sequencing	Raw	Displays the electropherogram peaks prior to any mobility correction.
	Analyzed	Primary analysis view displays electropherogram data with mobility correction applied and after basecalling.

4. Navigating the Data View section for completed injections is the same as described above for reviewing in-process injections (see Section 6.1).

6.3 Downloading Data From a Completed Injection of an In-Process Run

1. To download a sample file or files from a completed injection of a run that is still in process, check the box adjacent to that sample in the Download column of the Sample View section of the 'RUN-Monitor' screen, then select **Download** above the column (Figure 86).

   Notes:

   a. Individual samples can be selected for download from either the Run Information or Analysis Information category of the Sample View section.

   b. For a run that is still in process, only individual samples from completed injections can be downloaded. Injections that are currently running cannot be downloaded.

   c. **Download** only becomes active after at least one sample check box has been selected in the Download column.

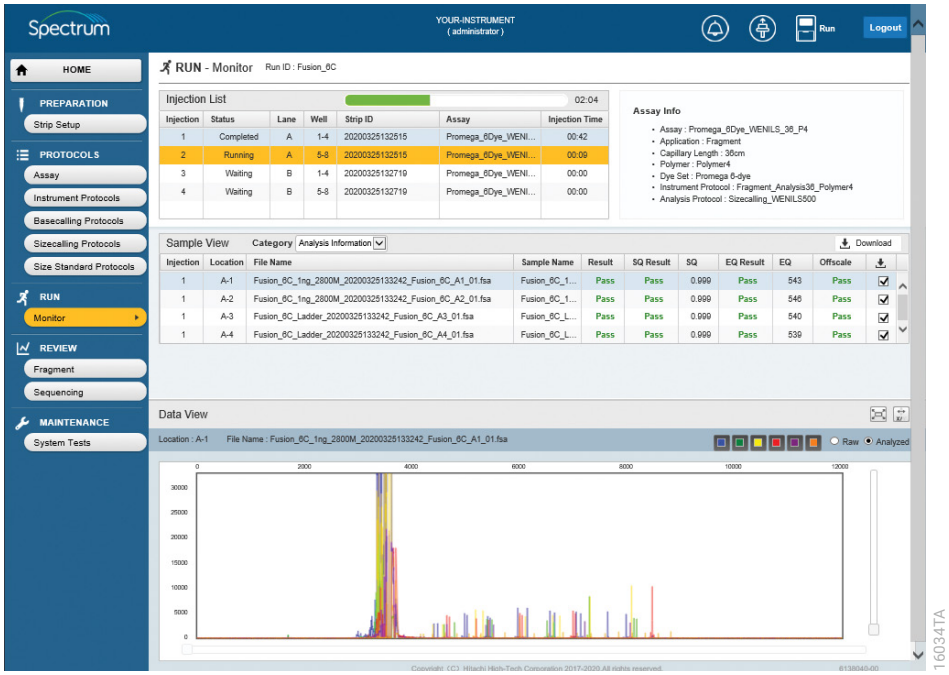

Figure 86. 'RUN-Monitor' screen with samples selected for download.

2. After selecting **Download**, a window appears at the bottom of the 'RUN-Monitor' screen asking if you want to **Open**, **Save** or **Cancel** the .zip file containing the run information for the selected samples (Figure 87). The .zip file is named with the date (Year/Month/Day) and time of export, followed by the Run ID.

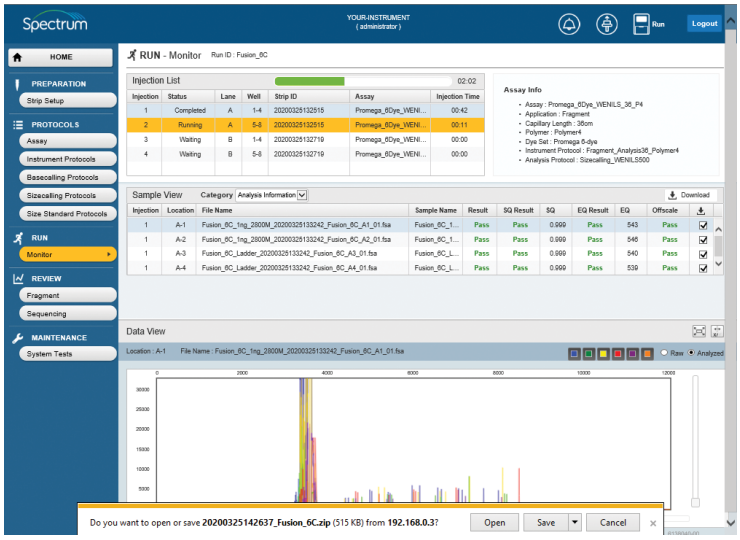

Figure 87. 'RUN-Monitor' screen with download window.

3. Selecting **Open** or **Save** opens a dialog box at the bottom of the 'RUN-Monitor' screen asking if you want to **Open**, **Open Folder** or **View Downloads** containing the run information for the selected samples (Figure 88). Selecting any one of these options allows you to access the downloaded run files for the selected samples. The files may be moved to another location on the PC or other network location. Selecting **Cancel** exits out of the download.

   Notes:

   a. Data are downloaded as a compressed .zip file which may be unzipped after download.

   b. Instead of downloading data from each injection as the run progresses, all the sample files can be downloaded from the completed run from the 'Review' screen (see Section 7).

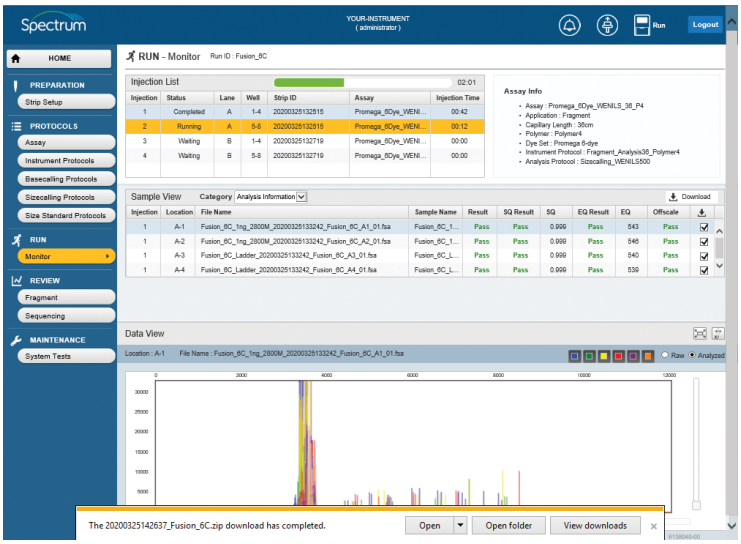

Figure 88. 'RUN-Monitor' screen with completed download window.

Review 7

Review allows for viewing results and downloading data previously generated on the connected Spectrum Compact CE System. Fragment or sequencing data can be reviewed and downloaded from the Main Menu of the 'HOME' screen (Figure 12).

7.1 Reviewing Fragment Data

1. Select **Fragment** under REVIEW from the Main Menu of the 'HOME' screen (Figure 12) to reveal the 'REVIEW-Fragment' screen (Figure 89). The 'REVIEW-Fragment' screen is split into three sections from top to bottom:
   - Run List
   - Sample View
   - Data View

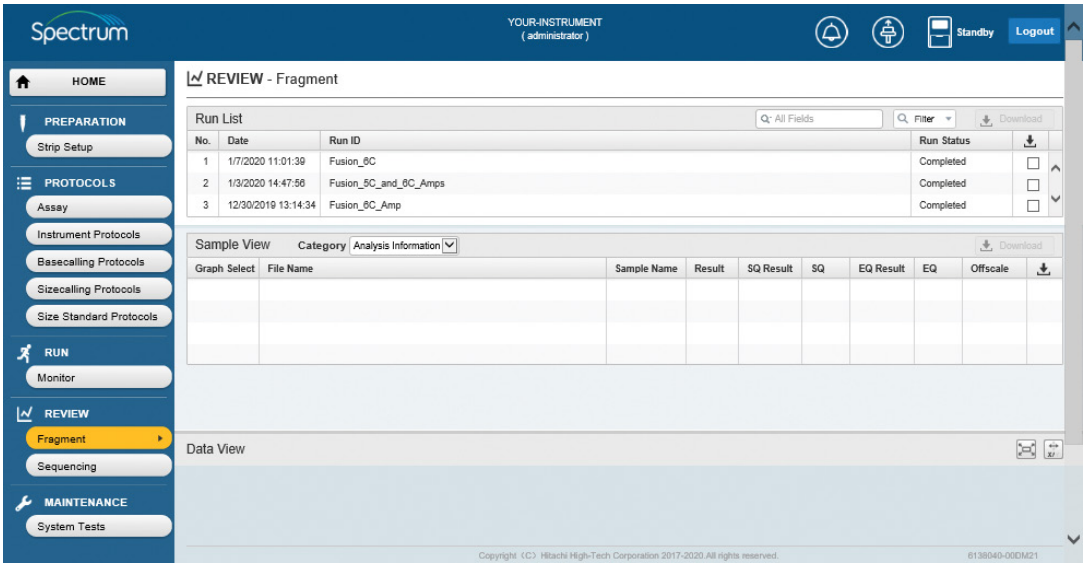

Figure 89. 'REVIEW-Fragment' screen.

2. The Run List contains all the completed runs on the Spectrum Compact CE System. The Run List is split into five columns as described in the following table.

Column Header	Description
No.	Run number in the order runs were performed with most recent being number 1.
Date	Time and date run was performed.
Run ID	Run ID of run.
Run Status	Indicates whether run was completed.
Download	Checking boxes in this column identifies which runs (includes all injections/samples) can be downloaded when selecting **Download**. **Note: Download** only becomes active after at least one run checkbox has been selected in the Download column.

3. Data in the Run List may be searched and filtered (i.e., searched for based on specific values and filtered such that only runs that meet those criteria are displayed in the Run List). Select the magnifying glass icon on the Select Search Field box to display a window with radio button selections that allows you to search by All Fields, Date, Run ID or Run Status (Figure 90).

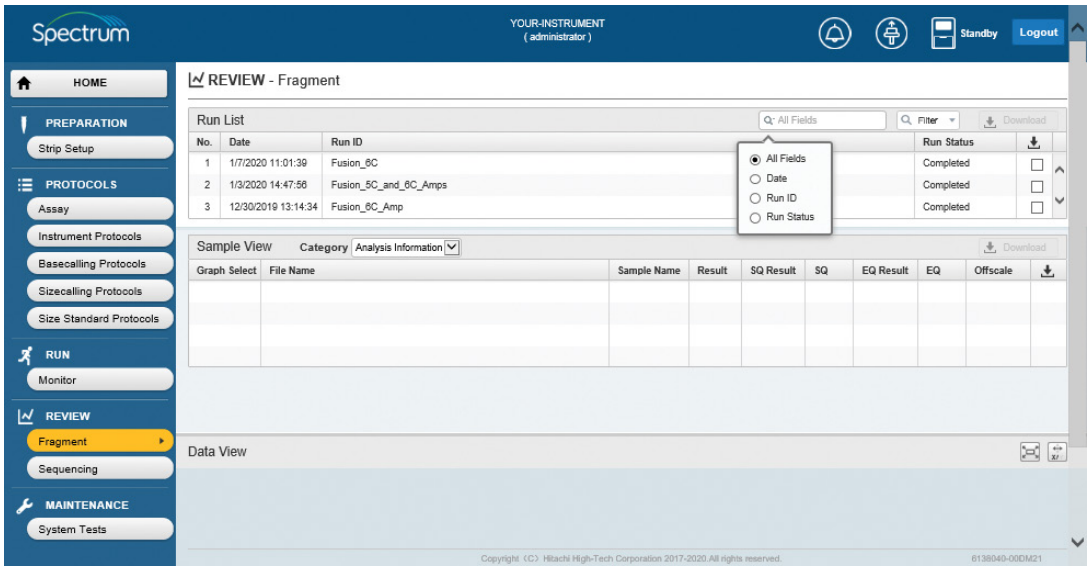

Figure 90. Run List select search field radio button window.

4. After selecting the appropriate search field, select the magnifying glass or down arrow icon in the **Filter** box to display filtering options by the different fields (Figure 91).

5. Search terms can be filtered by:

   - is
   - begins
   - contains
   - ends

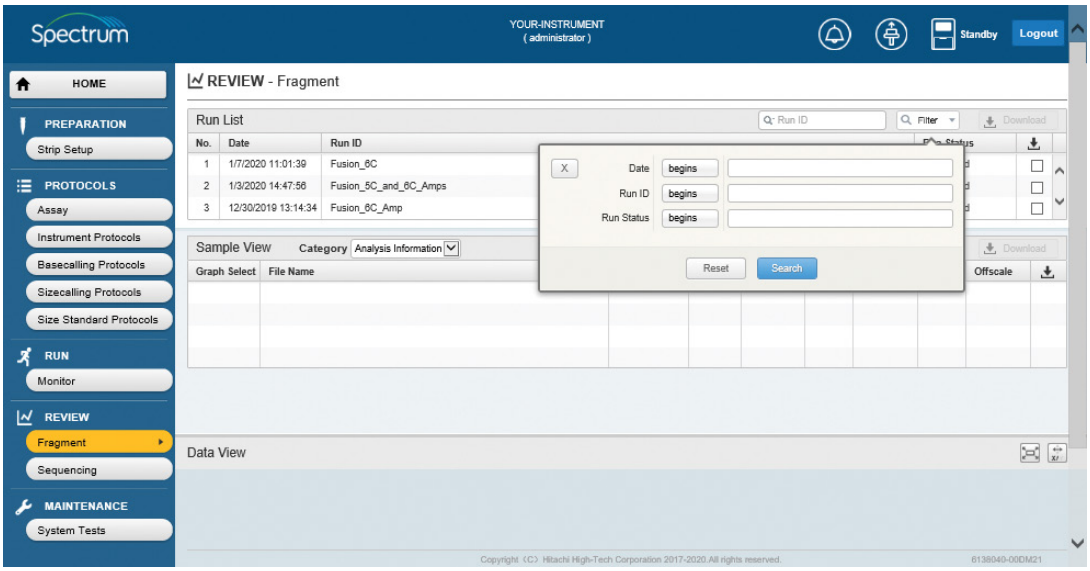

Figure 91. Run List search filter option selection.

6. After selecting the appropriate filter for search terms in the field being searched (i.e., Date, Run ID or Run Status), type the desired search term in the adjacent box and select **Search** (Figure 92). Alternatively, select **Reset** to exit.

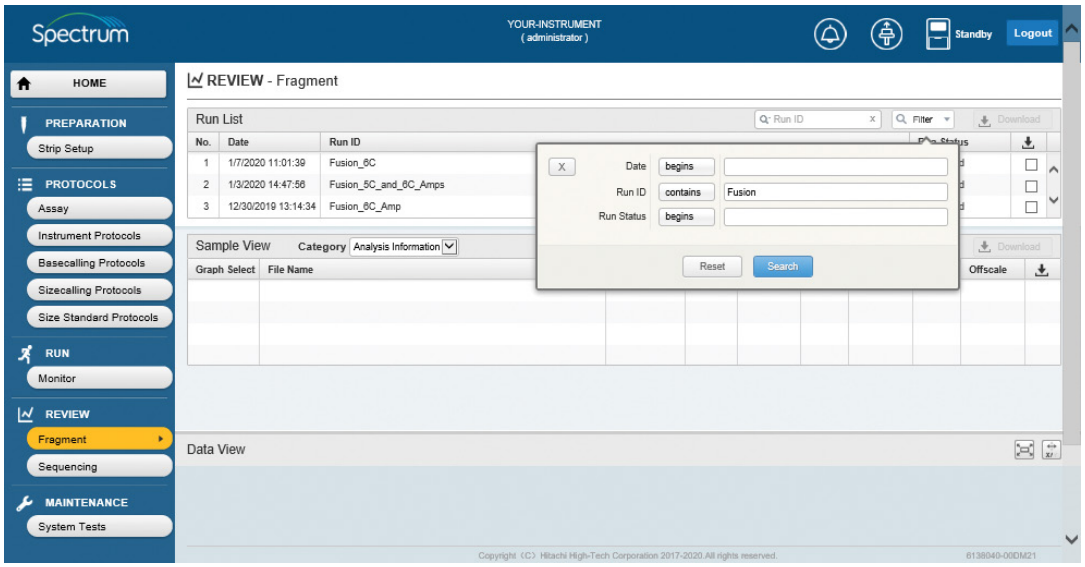

Figure 92. 'Run List' search filter option selection.

7. The runs that meet the desired search and filter parameters are displayed at the top of the Run List (Figure 93).

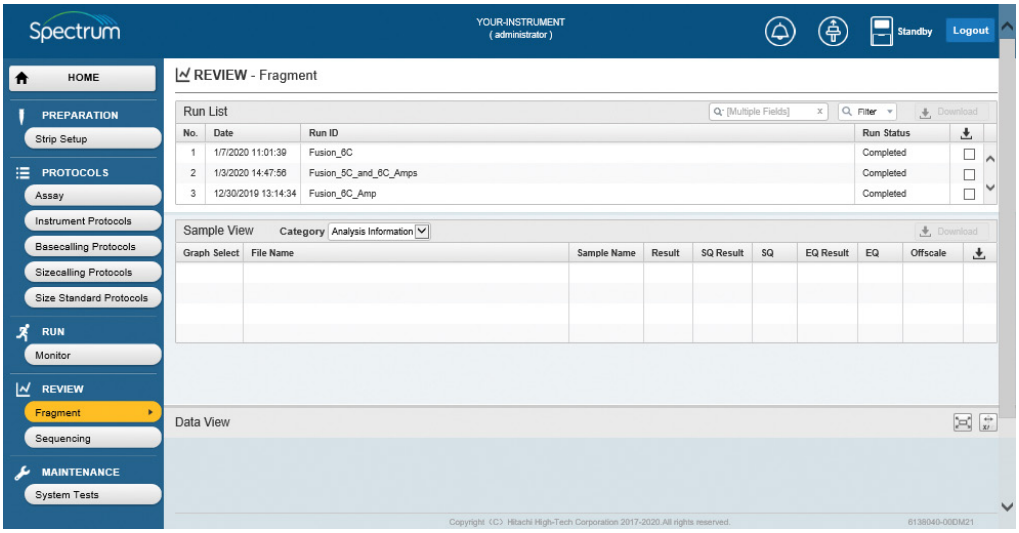

Figure 93. Searched and filtered runs.

8. Select a specific run in the Run List to display the list of samples in that injection in the Sample View section of the 'REVIEW-Fragment' screen (Figure 94). A scroll bar on the right side of the Sample View section of the 'REVIEW-Fragment' screen enables scrolling through the samples in the selected run.
9. The Sample View has a **Category** pull-down menu for choosing the following two options:
   - Analysis Information
   - Run Information
10. The Samples View section of the 'REVIEW-Fragment' screen will display the information for the selected category.

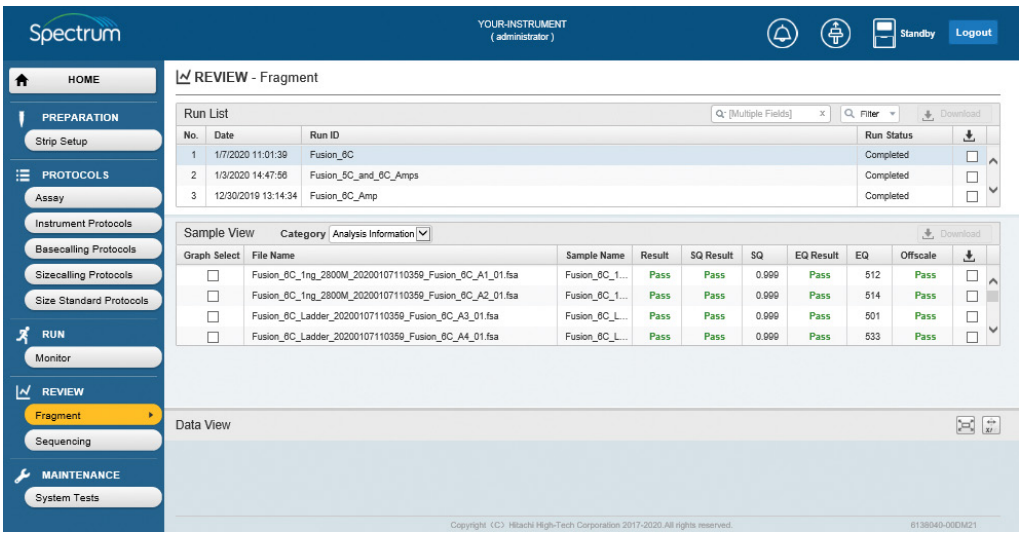

Figure 94. 'REVIEW-Fragment' screen with run selected.

11. When **Analysis Information** is selected, the Sample View is split into ten columns, as described in the following table.

Column Header	Description
Graph Select	Checking boxes in this column displays electropherogram images in Data View section of 'REVIEW-Fragment' screen. Multiple electropherogram images may be displayed in Data View. **Note:** Scroll to view the different electropherograms when multiple samples are selected for viewing in Data View section of 'REVIEW-Fragment' screen.
File Name	Name of the file for each sample and sample type (.fsa).
Sample Name	Name of sample as entered in Strip ID.
Result	Overall pass or fail based on SQ and EQ pass/fail values.
SQ Result	SQ pass, suspect, or fail result based on SQ settings in sizecalling protocol (see Section 5.3).
SQ	Calculated SQ value (upon which, the pass, suspect, or fail result is made based on SQ settings in sizecalling protocol).
EQ Result	EQ pass, suspect, or fail result based on EQ settings in sizecalling protocol (see Section 5.3).
EQ	Calculated EQ value (upon which, the pass, suspect, or fail result is made based on EQ settings in sizecalling protocol).
Offscale	Indicates whether any data in sample is offscale (fail) or below saturation (pass).
Download	Checking boxes in this column identifies which individual sample files in a run can be downloaded. **Note: Download** only becomes active after at least one sample check box has been selected.

12. When **Run Information** is selected, the Sample View is split into nine columns, as described in the following table.

Column Header	Description
Graph Select	Checking boxes in this column displays electropherogram images in Data View section of 'REVIEW-Fragment' screen. Multiple electropherogram images may be displayed in Data View. **Note:** Scrolling is required to view the different electropherograms when multiple samples are selected for viewing in Data View section of 'REVIEW-Fragment' screen.
File Name	Name of the file for each sample and sample type (.fsa).
Run ID	Run ID being injected.
Assay	Name of the Assay being used for each injection during the run.
Instrument Protocol	Name of the Instrument Protocol being used for each injection during the run.
Capillary	Capillary length being used.
Polymer	Polymer type used during run.
Capillary No.	Capillary number on which a particular sample was run.
Download	Checking boxes in this column identifies which individual sample files in a run can be downloaded. **Note: Download** only becomes active after at least one sample check box has been selected.

13. Check the box in the Graph Select column of the Sample View section of the 'REVIEW-Fragment' screen to display the electropherogram for that sample in the Data View section of the 'REVIEW-Fragment' screen (Figure 95).

    Note: Electropherogram images for up to four samples can be displayed at one time. Samples are displayed in the order they were selected. A scroll bar will appear to enable scrolling through the REVIEW window.

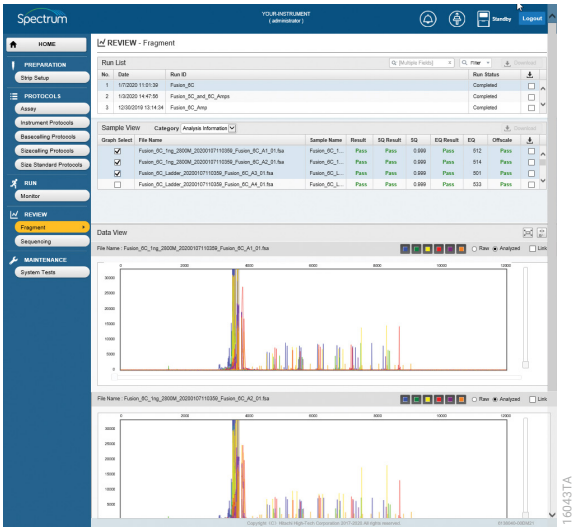

Figure 95. Electropherogram in the Data View section of the 'REVIEW-Fragment' screen.

14. The **Raw** and **Analyzed** radio buttons can be used to toggle between these two views of the data.

15. The **Link** check box allows for the same operations (shown below) to be applied across multiple electropherograms displayed in the Data View section of the 'REVIEW-Fragment' screen. Check the **Link** check box to link the desired electropherograms.

    - Data type shown (Raw or Analyzed).
    - X axis zoom in and out by mouse operation
    - Y axis zoom in and out using slider
    - X and Y axis dual zoom in and out by mouse operation

16. The Data View section of the 'REVIEW-Fragment' screen can be navigated using the icons on the screen.

Icon	Description
	Show/Hide Blue dye channel
	Show/Hide Green dye channel
	Show/Hide Yellow dye channel
	Show/Hide Red dye channel
	Show/Hide Purple dye channel
	Show/Hide Orange dye channel
	Show/Hide Aqua dye channel
	Show/Hide Brown dye channel
	Resets view after zooming (by mouse or using Y axis slider)
	Switch the zoom-in/zoom-out direction by mouse (X and Y axis together or X only)

17. Zoom in onto data by clicking on the mouse and drawing it across the region of the electropherogram of interest. Depending on the zoom selected (i.e., X and Y axis together or X axis alone) the image will be zoomed upon release of the mouse button.
18. Zoom in on the Y axis by moving the slider on the right hand side of the Data View section of the screen up (to increase peak heights) or down (to decrease peak heights).

7.2 Downloading Fragment Data

1. To download a completed run, check the box adjacent to that run in the Download column of the Run List section of the 'REVIEW-Fragment' screen, then select **Download** above this column (Figure 96).

   Notes:

   a. **Download** only becomes active after a check box has been selected in the Download column.

   b. Up to 10 runs can be downloaded at a time in one compressed .zip file.

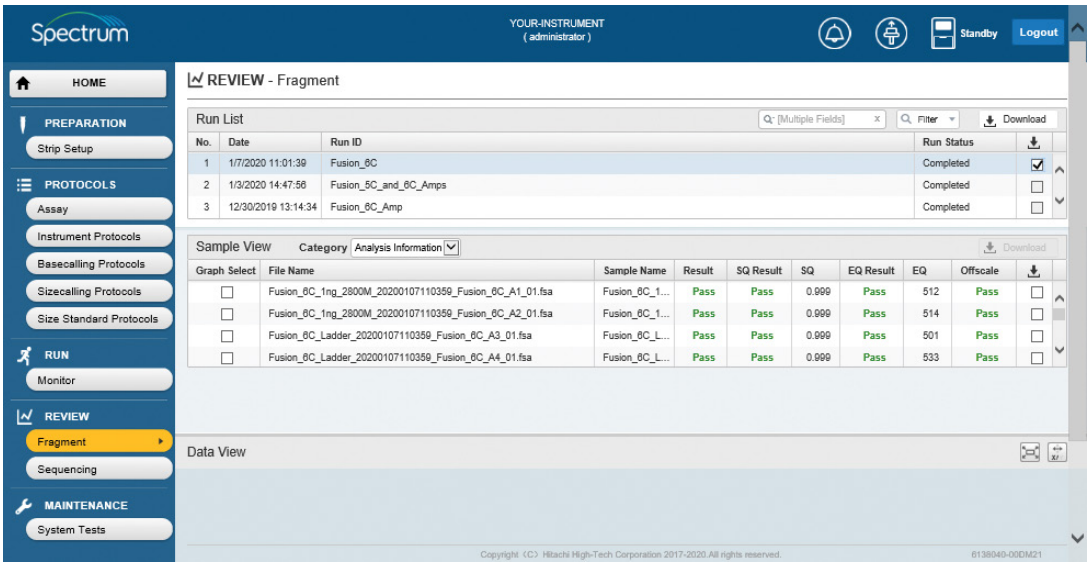

Figure 96. 'REVIEW-Fragment' screen with run selected for download.

2. To download an individual sample file or files from a completed run (i.e., a subset of files from a run), select the run containing those samples in the Run List section of the 'REVIEW-Fragment' screen. Check the appropriate box adjacent to the samples in the Download column of the Sample View section of the 'REVIEW-Fragment' screen, and select **Download** above this column (Figure 97).

   Notes:

   a. Individual samples can be downloaded from either the Run or Analysis Information category of the Sample View section.

   b. **Download** only becomes active after at least one sample check box has been selected.

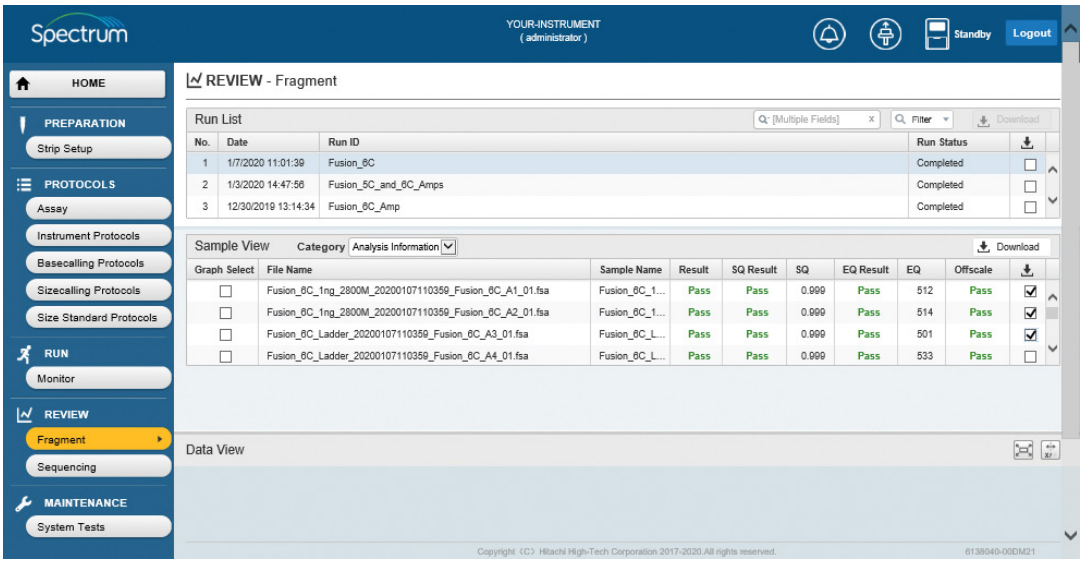

Figure 97. 'REVIEW-Fragment' screen with samples selected for download.

3. After selecting **Download**, a dialog box appears at the bottom of the 'REVIEW-Fragment' screen asking if you want to **Open, Save** or **Cancel** the .zip file containing the run information for the selected samples (Figure 98). When downloading individual samples, the .zip file is named with the date (Year/Month/Day) and time of export, followed by the RunID. The .zip file is named with the date and time of export followed by the word "RUN" when downloading a completed run.

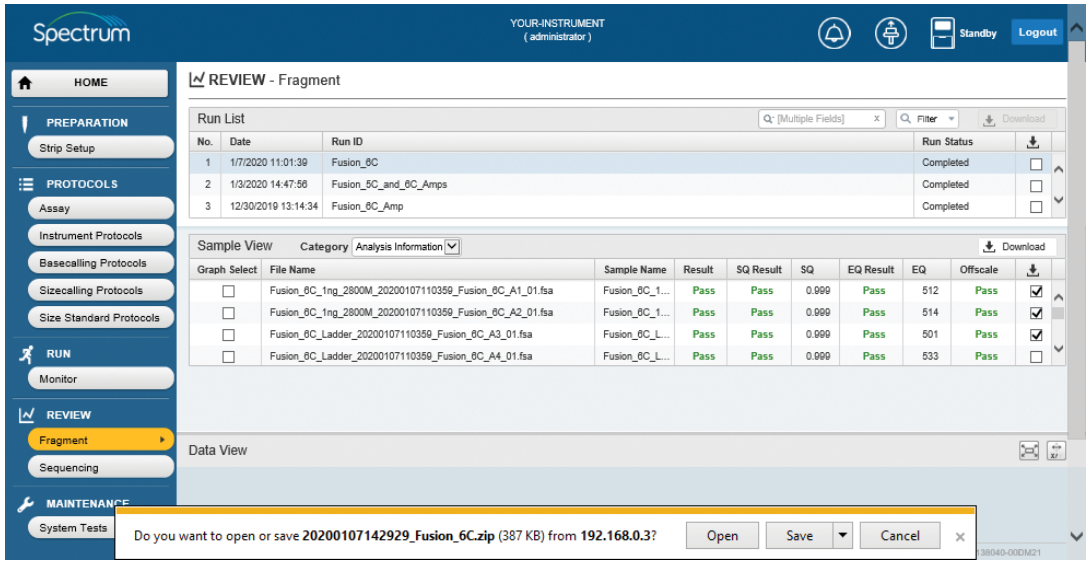

Figure 98. 'REVIEW-Fragment' screen with download window.

4. Selecting **Open** or **Save** opens a dialog box at the bottom of the 'REVIEW-Fragment' screen stating that the download is complete and asking if you want to **Open, Open Folder** or **View Downloads** (Figure 99). Selecting any one of these options allows you to access the downloaded run files. The files can be moved to another location on the PC or other network location. Selecting **Cancel** exits the download.

   Note: Data are downloaded as a compressed .zip file which may be unzipped after the download.

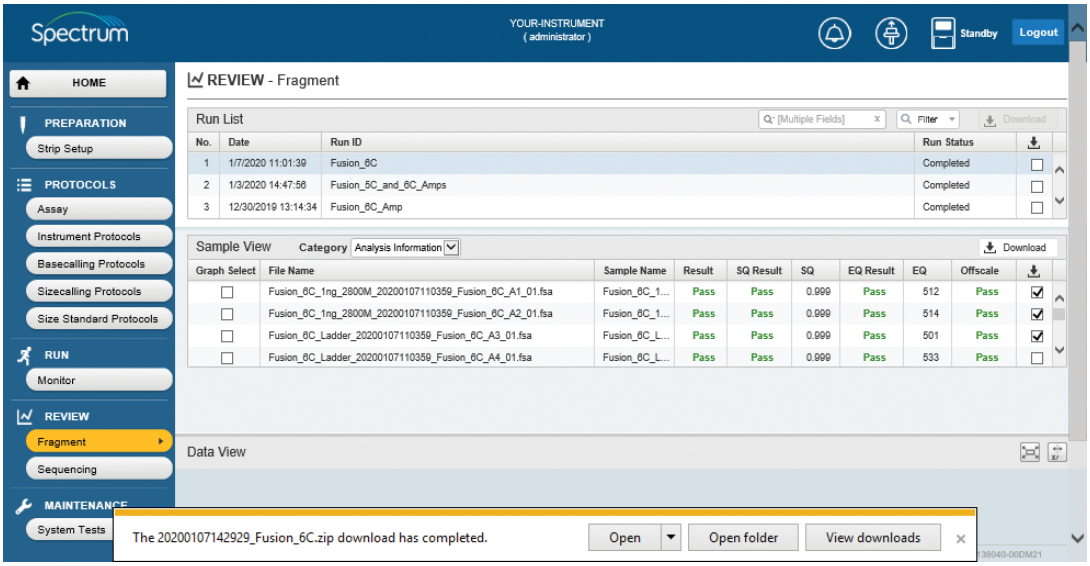

Figure 99. 'REVIEW-Fragment' screen with completed download window.

7.3 Reviewing Sequencing Data

1. Select **Sequencing** under REVIEW from the Main Menu of the 'HOME' screen (Figure 12) to reveal the 'REVIEW-Sequencing' screen (Figure 100). The 'REVIEW-Sequencing' screen is split into three sections from top to bottom:
   - Run List
   - Sample View
   - Data View

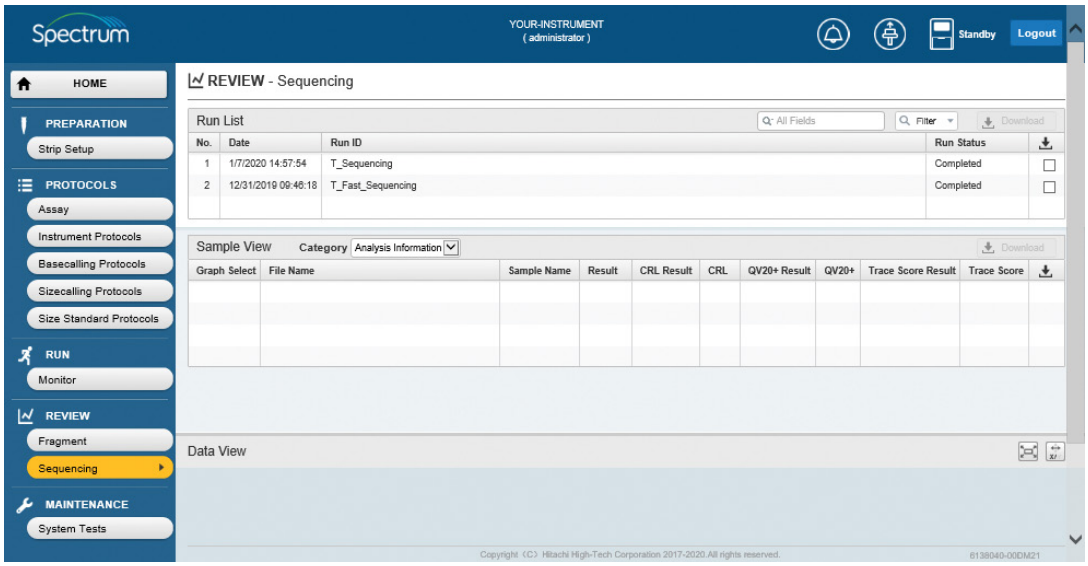

Figure 100. 'REVIEW-Sequencing' screen.

2. The Run List contains all the completed runs on the Spectrum Compact CE System. The Run List is split into five columns, described in the following table.

   Note: Data in the Run List may be searched and filtered in the same way as for fragment data, as described in Step 3–7 of Section 7.1.

Column Header	Description
No.	Run number in the order runs were performed, with the most recent being number 1.
Date	Time and date the run was performed.
Run ID	Run ID of the run.
Run Status	Indicates whether the run was completed.
Download	Checking boxes in this column identifies which runs can be downloaded when selecting **Download**. **Note: Download** only becomes active after at least one run check box has been selected in the Download column.

3. Select a specific run in the Run List to display the list of samples in that injection in the Sample View section of the 'REVIEW-Sequencing' screen (Figure 101). A scroll bar on the right side of the Sample View section of the 'REVIEW-Sequencing' screen enables scrolling through the samples in the selected run.
4. The Sample View has a **Category** pull-down menu that allows you to choose the following two options:
   - Analysis Information
   - Run Information
5. The Sample View section of the 'REVIEW-Sequencing' screen will display the information for the selected category.

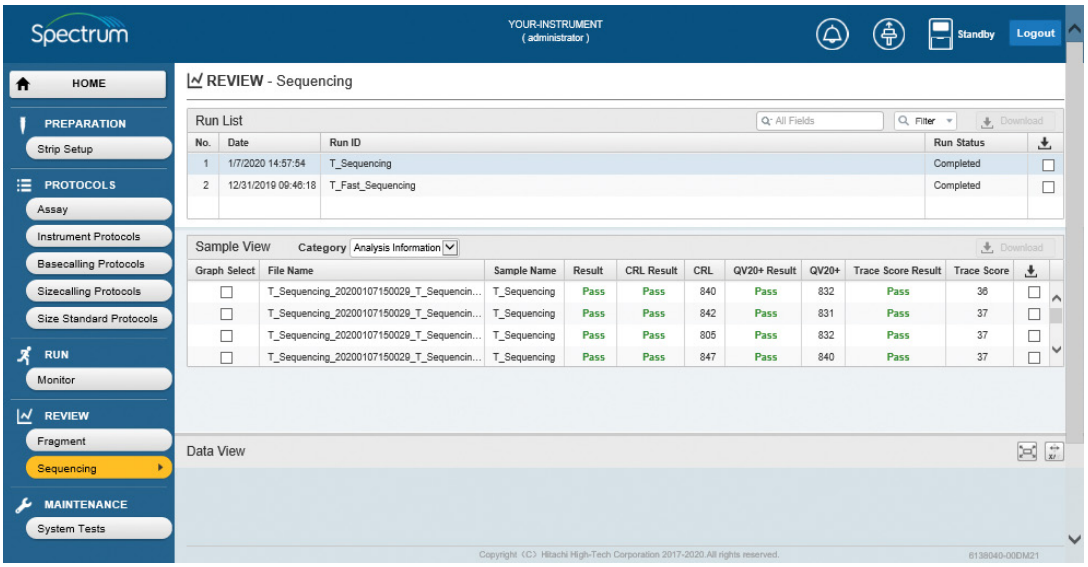

Figure 101. 'REVIEW-Sequencing' screen with run selected.

6. When **Analysis Information** is selected, the Sample View is split into eleven columns as described in the following table.

Column Header	Description
Graph Select	Checking boxes in this column displays electropherogram images in Data View section of 'REVIEW-Sequencing' screen. Multiple electropherogram images may be displayed in Data View. **Note:** Scrolling is required to view the different electropherograms when multiple samples are selected for viewing in Data View section of 'REVIEW-Sequencing' screen.
File Name	Name of the file for each sample and sample type (.ab1).
Sample Name	Name of sample as entered in Strip ID.
Result	Overall pass or fail based on CRL, QV20+, and Trace Score pass/fail values.
CRL Result	CRL pass, suspect, or fail result based on CRL settings in basecalling protocol (see Section 5.2).
CRL	Calculated CRL value (upon which, the pass, suspect or fail result is made based on CRL settings in basecalling protocol).
QV20+ Result	QV20+ pass, suspect, or fail result based on QV20+ settings in basecalling protocol (see Section 5.2).
QV20+	Calculated QV20+ value (upon which, the pass, suspect, or fail result is made based on QV20+ settings in basecalling protocol).
Trace Score Result	Trace Score pass, suspect, or fail result based on Trace Score settings in basecalling protocol (see Section 5.2).
Trace Score	Calculated Trace Score value (upon which, the pass, suspect or fail result is made based on Trace Score settings in basecalling protocol).
Download	Checking boxes in this column identifies which individual sample files in a run can be downloaded. **Note: Download** only becomes active after at least one sample check box has been selected in the Download column.

7. When **Run Information** is selected, the Sample View is split into nine columns, as described in the following table.

Column Header	Description
Graph Select	Checking boxes in this column displays electropherogram images in Data View section of 'REVIEW-Sequencing' screen. Multiple electropherogram images may be displayed in Data View. **Note:** Scrolling is required to view the different electropherograms when multiple samples are selected for viewing in Data View section of 'REVIEW-Sequencing' screen.
File Name	Name of the file for each sample and sample type (.ab1).
Run ID	Run ID being injected.
Assay	Name of the Assay being used for each injection during the run.
Instrument Protocol	Name of the Instrument Protocol being used for each injection during the run.
Capillary	Capillary length being used.
Polymer	Polymer type used during run.
Capillary No.	Capillary number on which a particular sample was run.
Download	Checking boxes in this column identifies which individual sample files in a run can be downloaded. **Note: Download** only becomes active after at least one sample check box has been selected in the Download column.

8. Check the box in the Graph Select column of the Sample View section of the 'REVIEW-Sequencing' screen to display the electropherogram for that sample in the Data View section of the 'REVIEW-Sequencing' screen (Figure 102).

   Note: Electropherogram images for up to four samples can be displayed at one time. As multiple samples are selected, a scroll bar will appear to enable scrolling through the 'REVIEW' window.

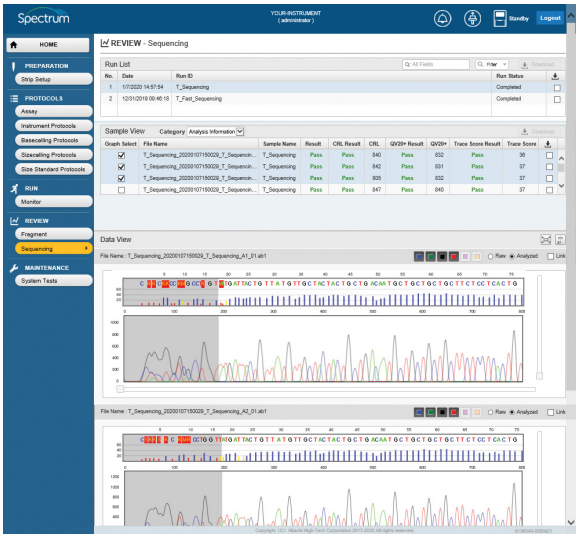

Figure 102. Electropherogram in Data View section of 'REVIEW-Sequencing' screen.

9. The **Raw** and **Analyzed** radio buttons can be used to toggle between these two views of the data.
10. The **Link** check box allows for the same operations (shown below) to be applied across multiple electropherograms displayed in the Data View section of the 'REVIEW-Fragment' screen. Check the **Link** check box for the desired electropherograms.
    - Data type shown (Raw or Analyzed).
    - X axis zoom in and out by mouse operation
    - Y axis zoom in and out using slider
    - X and Y axis dual zoom in and out by mouse operation

11. The Data View section of the 'REVIEW-Sequencing' screen can be navigated using the icons on the screen.

Icon	Description
	Show/Hide Blue dye channel
	Show/Hide Green dye channel
	Show/Hide Black dye channel
	Show/Hide Red dye channel
	Resets view after zooming (by mouse or using Y axis slider)
	Switch the zoom-in/zoom-out direction by mouse (X and Y axis together or X only)

12. Zoom in on data by clicking on the mouse and drawing it across the region of the electropherogram of interest. Depending on the zoom selected (i.e., X and Y axis together or X axis alone) the image will be zoomed upon release of the mouse button.
13. Zoom in on the Y axis by moving the slider on the right hand side of the 'Data View' section of the screen up (to increase peak heights) or down (to decrease peak heights).

7.4 Downloading Sequencing Data

1. To download a completed run, check the box adjacent to that run in the Download column of the Run List section of the 'REVIEW-Sequencing' screen, then select **Download** above this column (Figure 103).

   Notes:

   a. **Download** only becomes active after a run checkbox has been selected in the Download column.

   b. Up to 10 runs can be downloaded at a time in one compressed .zip file.

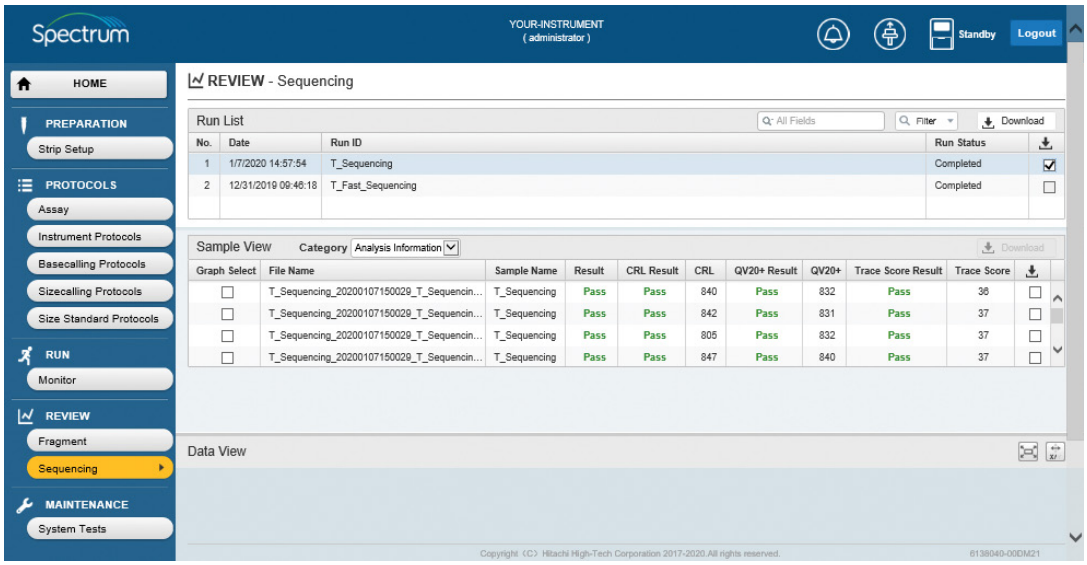

Figure 103. 'REVIEW-Sequencing' screen with run selected for download.

2. To download an individual sample file or files from a completed run (i.e., a subset of files from a run), select the run containing those samples in the Run List section of the 'REVIEW-Sequencing' screen. Check the box adjacent to that sample in the Download column of the Sample View section of the 'REVIEW-Sequencing' screen, and select **Download** above this column (Figure 104).

   Notes:

   a. Individual samples can be downloaded from either the Run or Analysis Information category of the Sample View section.

   b. **Download** only becomes active after at least one sample check box has been selected.

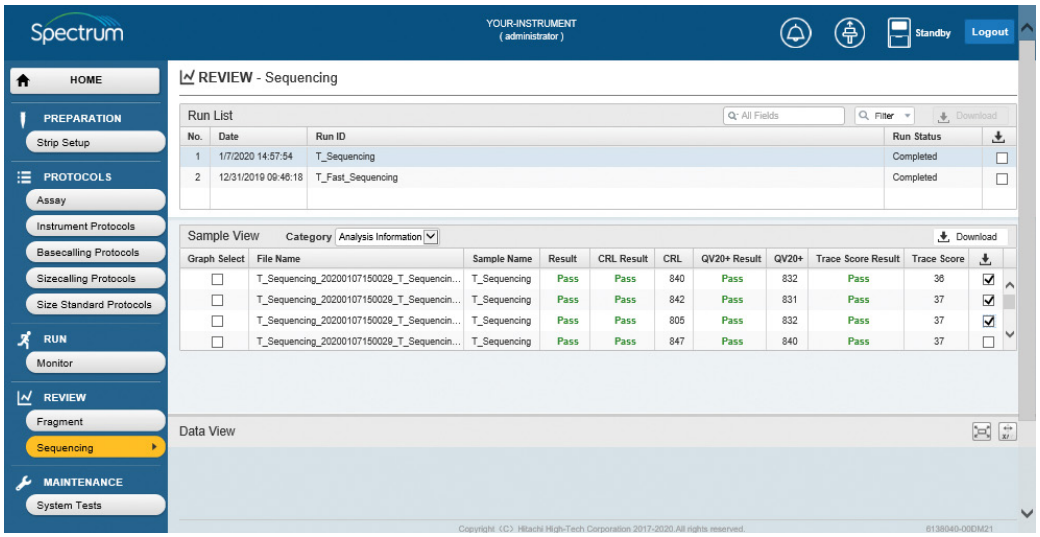

Figure 104. 'REVIEW-Sequencing' screen with run selected for download.

3. After selecting **Download**, a window appears at the bottom of the 'REVIEW-Sequencing' screen asking if you want to **Open, Save** or **Cancel** the .zip file (Figure 105). When downloading individual samples, the .zip file is name with the date (Year/Month/Day) and time of export, followed by the RunID. The .zip file is named with the date and time of export followed by the word "RUN" when downloading a completed run.

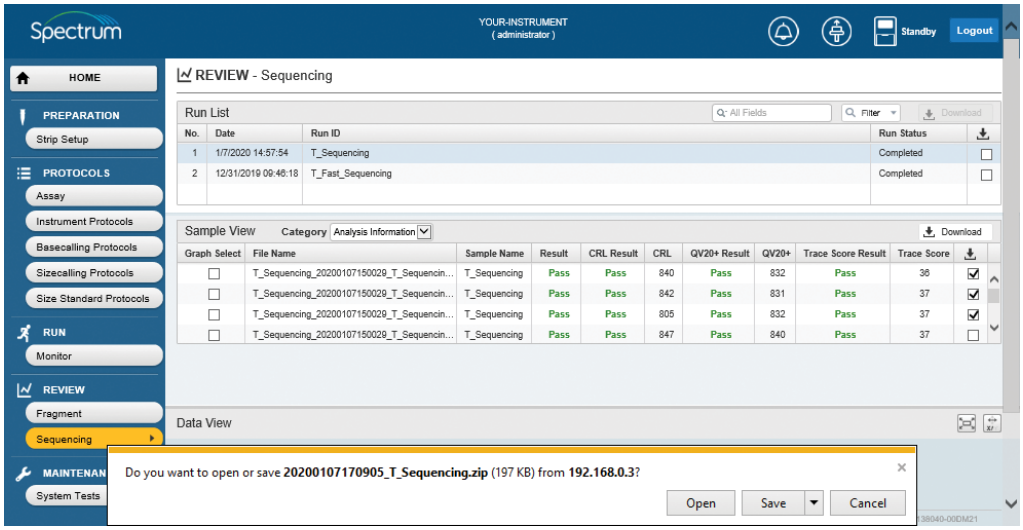

Figure 105. 'REVIEW-Sequencing' screen with download window.

4. Selecting **Open** or **Save** opens a dialog box at the bottom of the 'REVIEW-Sequencing' screen asking if you want to **Open**, **Open Folder** or **View Downloads** (Figure 106). Selecting any one of these options allows you to access the downloaded run files. The files can be moved to another location on the PC or other network location. Selecting **Cancel** exits the download.

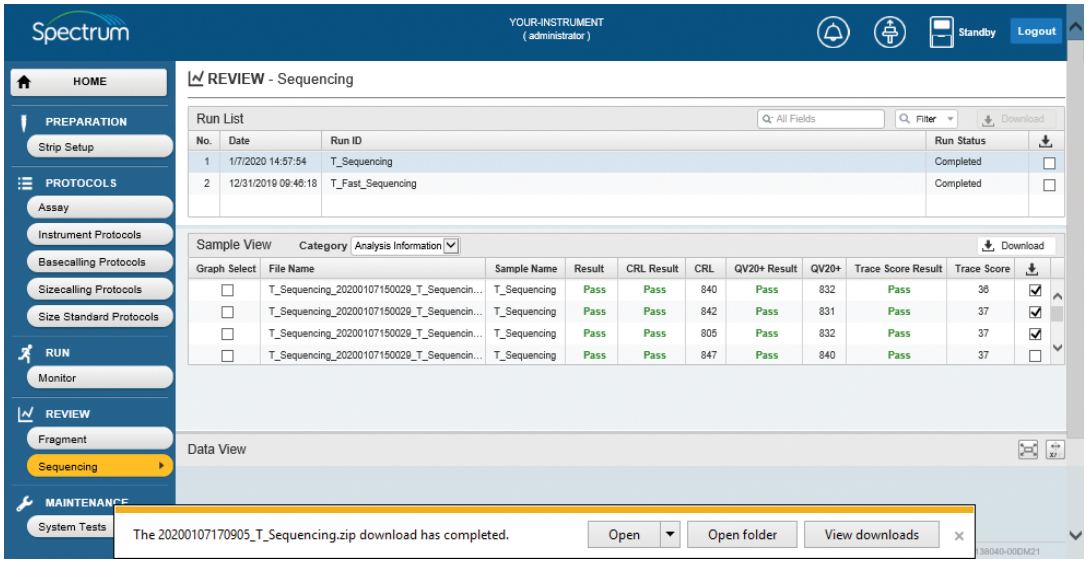

Figure 106. 'REVIEW-Sequencing' screen with completed download window.

Maintenance 8

8.1 System Tests

System Tests lets you review and download the information from System Tests performed on the instrument.

1. Select System Tests under MAINTENANCE from the Main Main of the 'HOME' screen (Figure 12) to reveal the 'MAINTENANCE-System Tests' screen (Figure 107).

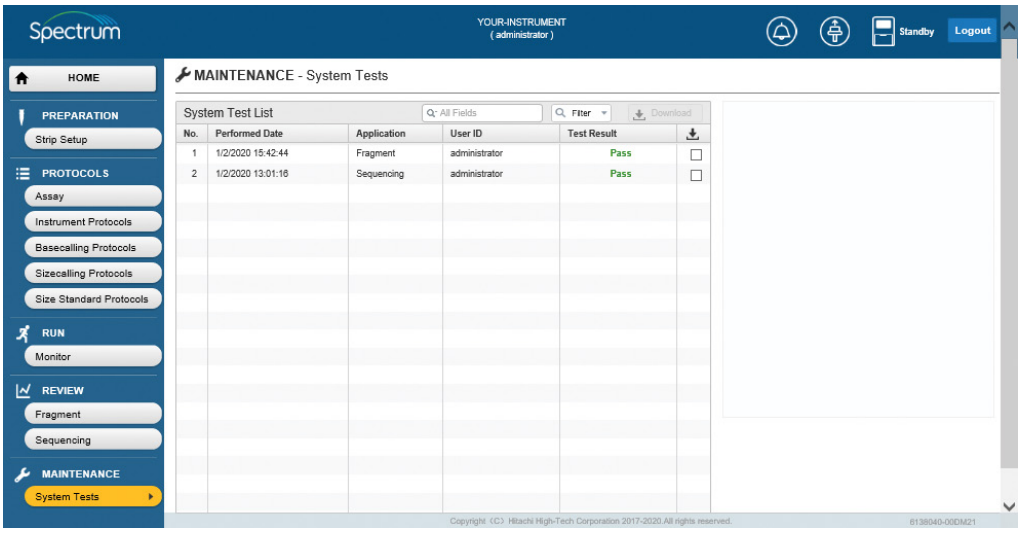

Figure 107. Maintenance System Test file download.

2. Data in the System Test List may be searched and filtered (i.e., searched for based on specific values and filtered such that ony runs that meet those criteria are displayed in the System Test List). Select the magnifying glass icon on the Select Search Field box to display a window with radio button selections that allows you to search by All Fields, Performed Date, Application, User ID or Test Result (Figure 108).

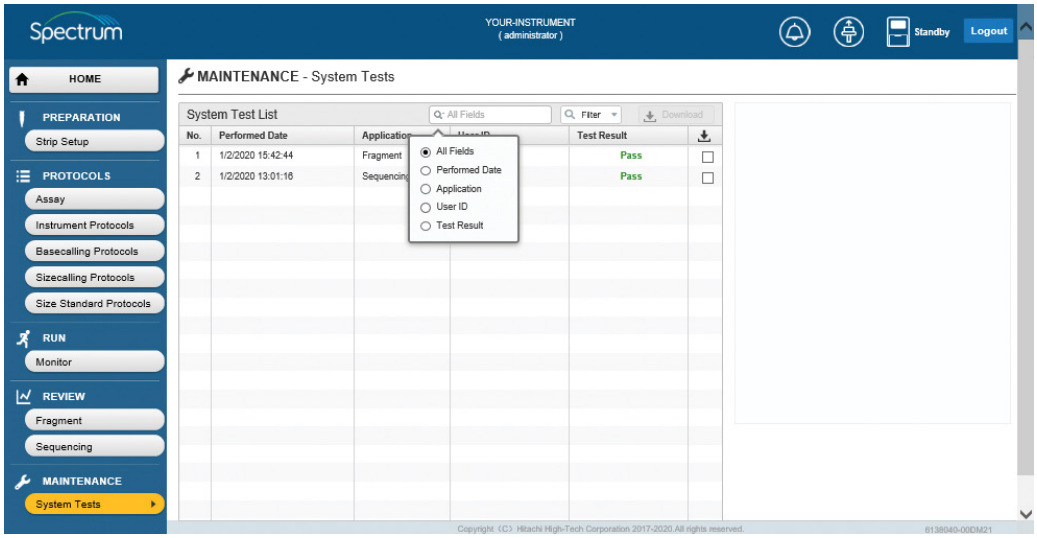

Figure 108. System Test List select search field radio button window.

3. After selecting the appropriate search field, select the magnifying glass or down arrow icon in the Filter box to display filtering options by the different fields (Figure 109).
4. Search terms can be filtered by:
   - is
   - begins
   - contains
   - ends

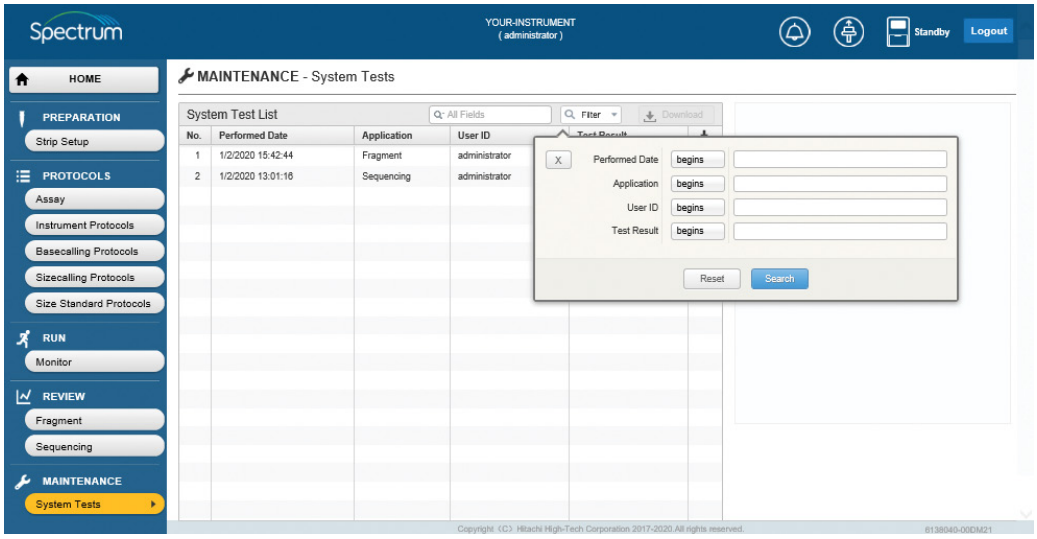

Figure 109. System Test List select search field radio button window.

5. After selecting the appropriate filter for search terms in the field being search (i.e., Performed Date, Application, User ID or Test Results), type the desired search term in the adjacent box and select **Search** (Figure 110). Alternatively, select **Reset** to exit.

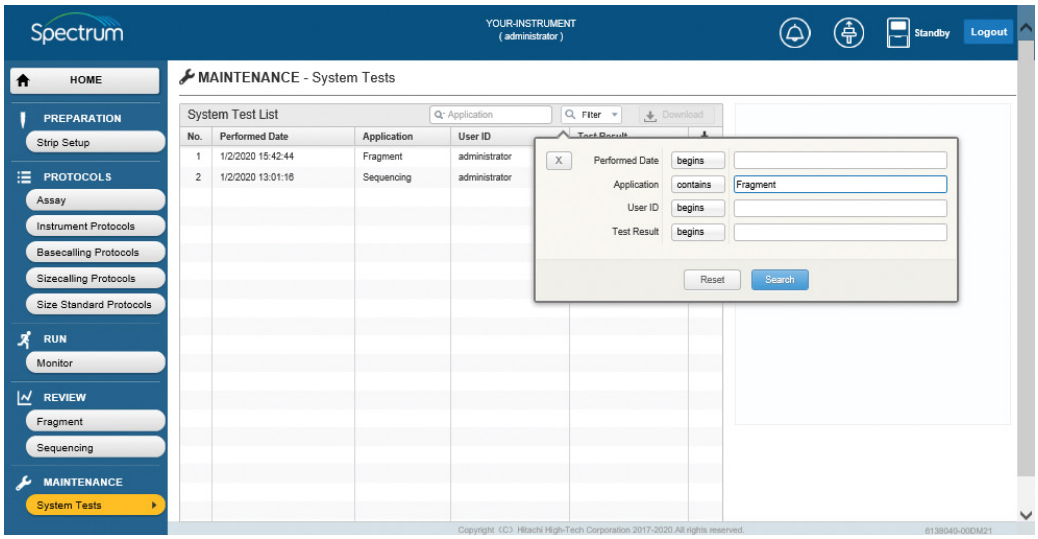

Figure 110. System Test List search filter option selection.

6. The System Tests that meet the desired search and filter parameters are displayed at the top of the System Test List (Figure 111).

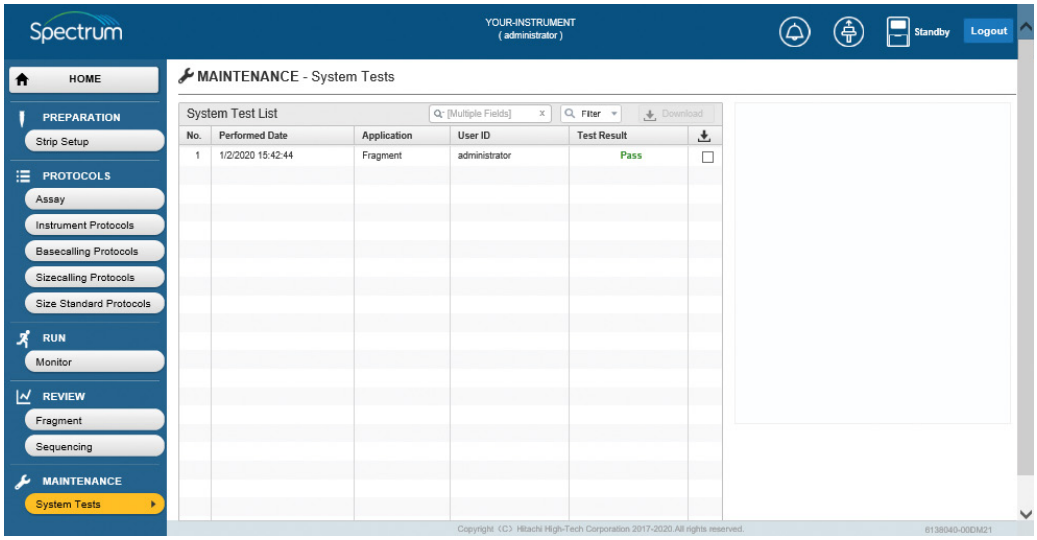

Figure 111. Searched and filtered System Tests.

7. Select a System Test file and check the **Download File** check box next to the selected file (Figure 112).

   Note: When a System Test file is selected, the system test details appear on the right side of the screen.

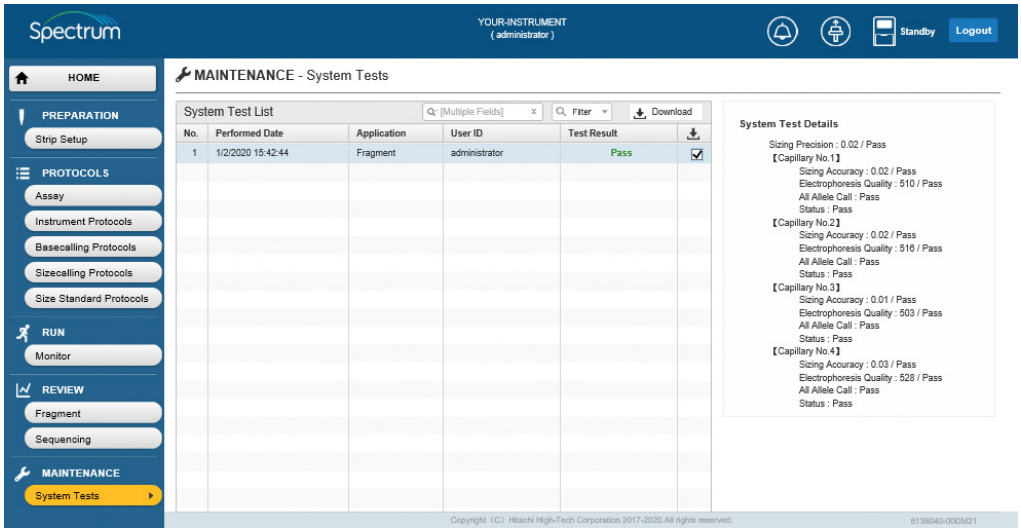

Figure 112. 'MAINTENANCE-System Tests' with System Test selected for download.

8. Select **Download** to download the system test report.
9. A window appears at the bottom of the screen asking if you want to **Open**, **Save** or **Cancel** (Figure 113).

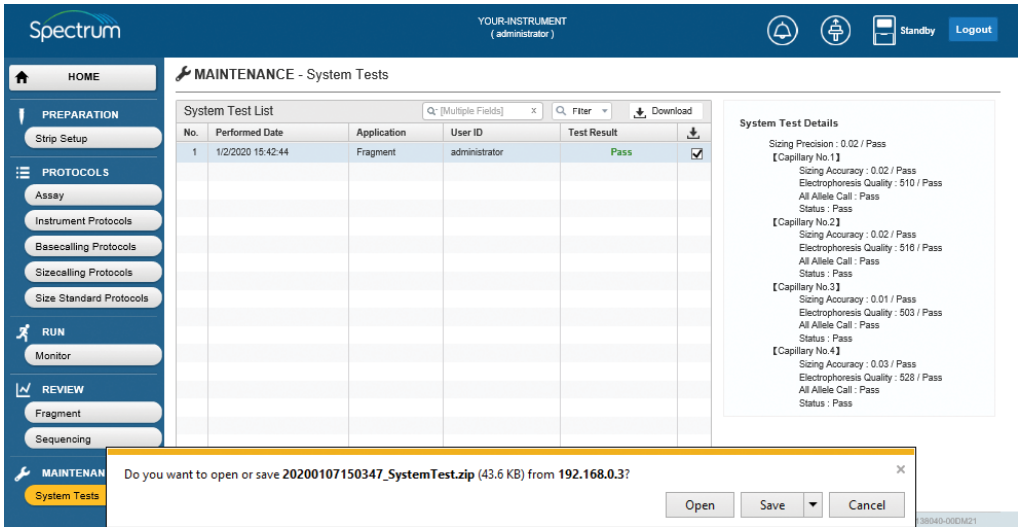

Figure 113. 'MAINTENANCE-System Tests' screen with download window.

10. Selecting **Open** or **Save** opens a dialog box at the bottom of the screen stating that the download is complete and asking if you want to **Open, Open Folder** or **View Downloads** (Figure 114). Selecting any one of these options allows you to access the downloaded system test files. The files may be moved to another location on the PC or other network location. Selecting **Cancel** exits the download.

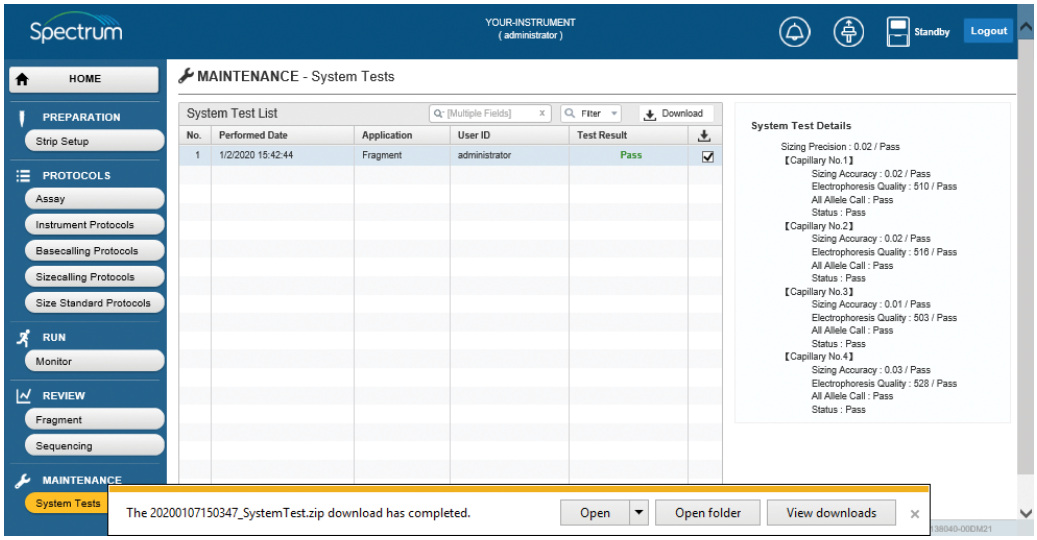

Figure 114. 'MAINTENANCE-System Tests' screen with completed download window.

Alarms and Consumables 9

The header on the 'HOME' screen of the Spectrum Compact CE System Remote Access Software (Figure 12) allows the user to access information about alarms that may have been triggered during a run, as well as the current status of consumables on the Spectrum Compact CE System.

9.1 Alarms

Alarms will provide information on any errors or actions on the Spectrum Compact CE System that require a user action (see Section 9.2 of the *Spectrum Compact CE System Operating Manual* #TMD058). Alarms can indicate when consumables need to be replaced, if there was an injection failure or if the system has encountered a critical error and requires Promega Technical Services to be contacted (see Section 11 of the *Spectrum Compact CE System Operating Manual* #TMD058).

1. Select the **Alarm** icon in the header of the 'HOME' screen to view the listing of current alarms (Figure 115).

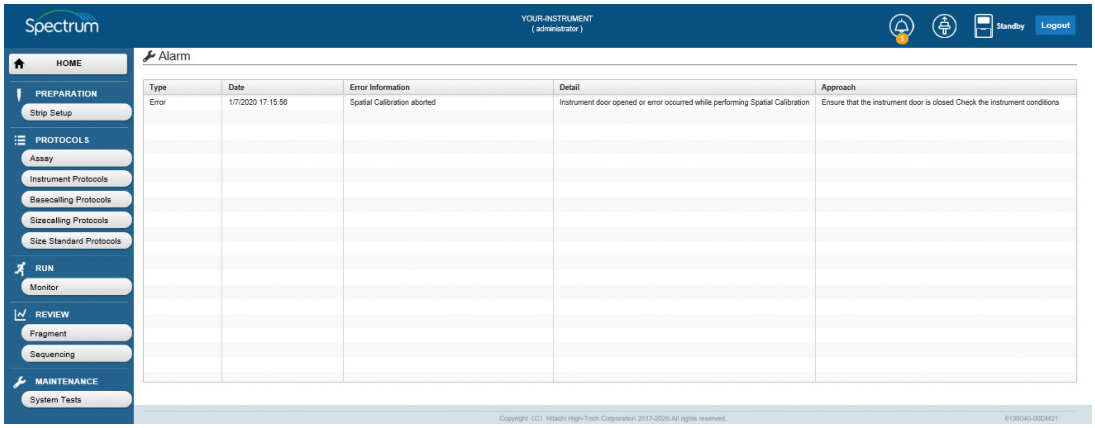

Figure 115. System Alarm list.

2. The ‘Alarm’ screen is split into five columns, as described in the following table.

Column Header	Description
Type	Type of alarm (Critical Alarm, Error Alarm or Warning).
Date	Time and date when alarm was generated.
Error Information	Summary of the alarm.
Detail	Detailed information on the alarm.
Approach	Recommended response to the alarm.

Note: Refer to Sections. 9.2 and 11 of the *Spectrum Compact CE System Operating Manual* #TMD058 for more information on alarms and error messages.

9.2 Consumables

Detailed information on each consumable installed on the Spectrum Compact CE System and which consumables may need to be replaced can be accessed using the Spectrum Compact CE System Remote Access Software.

Note: Replacement of consumables must be performed at the instrument using the integrated touch screen (see Section 3 of the *Spectrum Compact CE System Operating Manual* #TMD058).

1. Click the **Consumables** icon in the header of the ‘HOME’ screen to access a list of installed consumables (Figure 116).

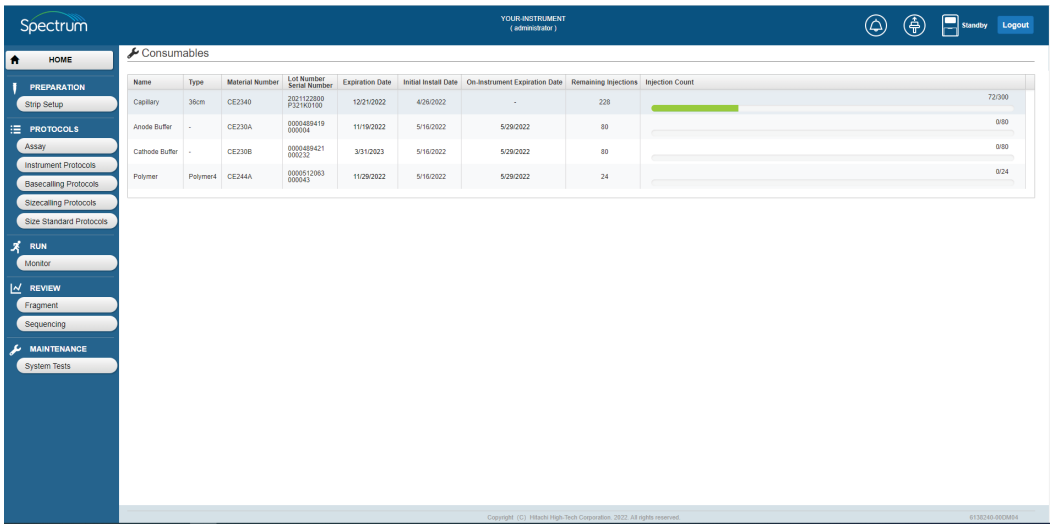

Figure 116. Consumables list.

2. The ‘Consumables’ screen is split into nine columns, as described in the following table.

Column Header	**Description**
Name	Consumable name (e.g., Capillary, Anode Buffer, Cathode Buffer, or Polymer).
Type	Length of capillary (e.g, 36cm), or type of polymer (e.g., Polymer4 or Polymer7).
Material Number	Part number for consumable.
Lot Number Serial Number	Lot number and serial number for installed consumable.
Expiration Date	Date when the consumable expires.
Initial Install Date	Date consumable was installed on Spectrum Compact CE System.
On-Instrument Expiration Date	Date on which the consumable expires after installation on Spectrum Compact CE System.
Remaining Injections	Number of injections left before installed consumable reaches its injection number limit.
Injection Count	Graphical representation of number of injections performed with each installed consumable.

Closing the Spectrum Compact CE System Remote Access Software 10

Users **must** logout of the Spectrum Compact Remote Access Software prior to closing the web browser.

1. Select **Logout** in the upper right corner of the header on the 'HOME' screen (Figure 117).

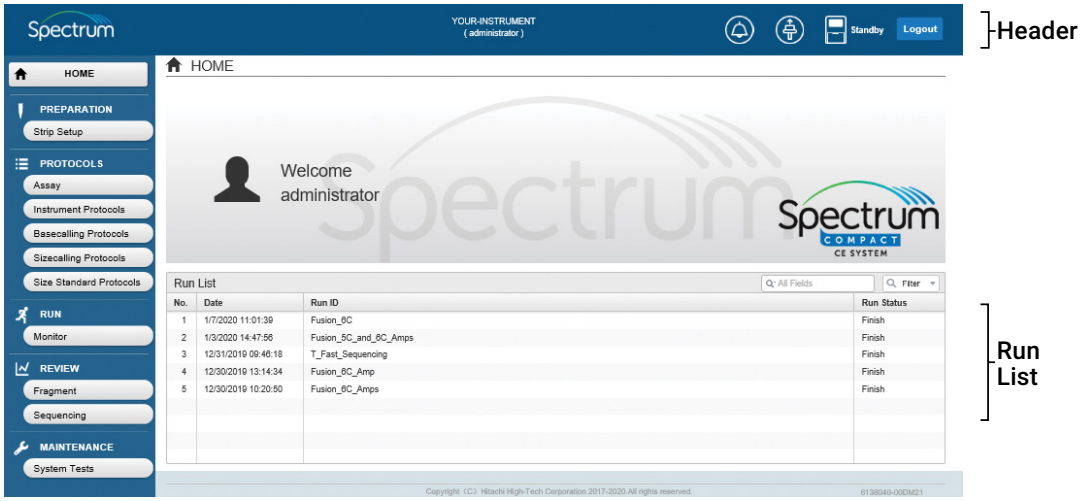

Figure 117. Spectrum Compact Remote Access Software 'Home' screen.

2. Once the user is logged out, the 'Login' screen appears (Figure 118).

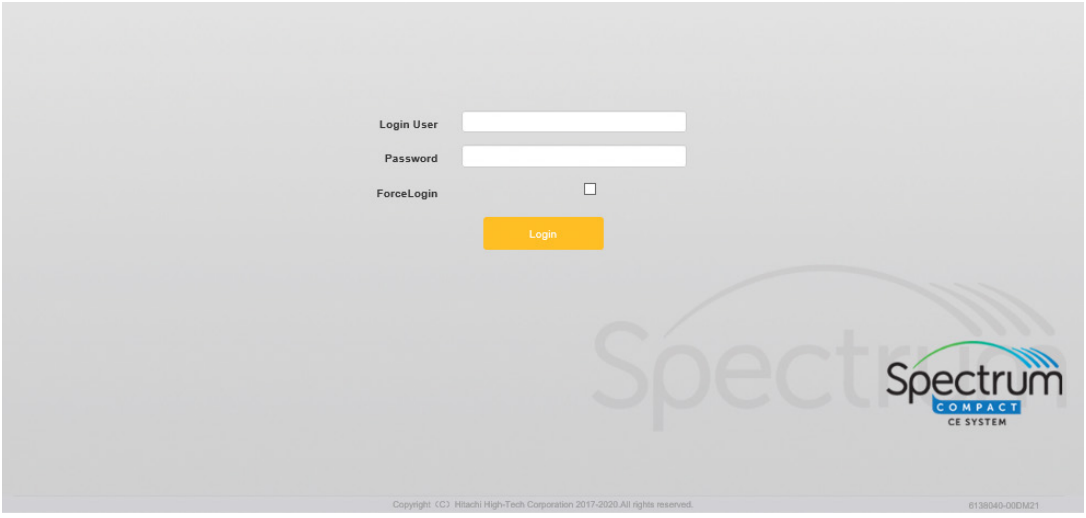

Figure 118. Spectrum Compact Remote Access Software 'Login' screen.

3. The web browser can now be closed.

   Note: If the Spectrum Compact CE System Remote Access Software was not properly closed, the following error will occur when attempting to login again: “Access is denied. This account already login.” (Figure 119). To correct the error, enter user name and password and check the “ForceLogin” box before selecting **Login**. The Spectrum Compact CE System Remote Access Software will start normally.

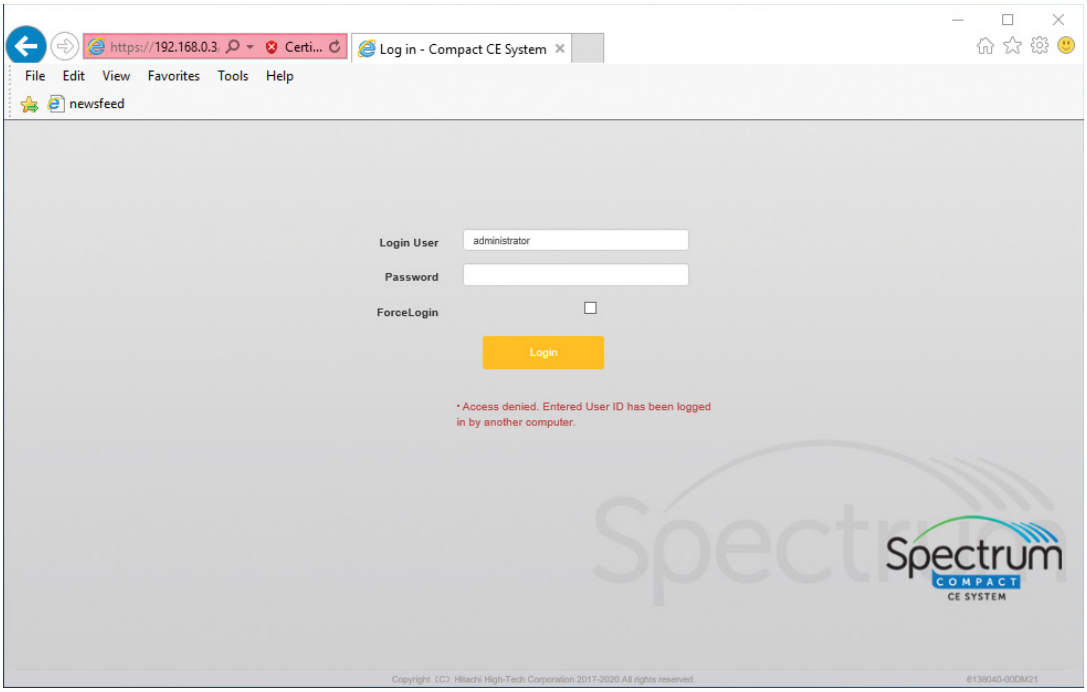

Figure 119. Improper shutdown error message.

Browser Settings 11

The Spectrum Compact CE System Remote Access Software version may be updated periodically as software for the Spectrum Compact CE System is updated. This is because the Spectrum Compact CE System Remote Access Software resides on the Spectrum Compact CE System and is accessed by the web browser via the network. After updating the Spectrum Compact CE System Remote Access Software, clear the web browser cache before logging into the updated version of the Spectrum Compact CE System Remote Access Software using the web browser.

Notes:

a. To determine version number of the Spectrum Compact CE System Remote Access Software, access the 'Instrument Information' screen through **About**, located in the footer on the 'Main Menu' screen of the Spectrum Compact CE System (see Section 9.1 of the *Spectrum Compact CE System Operating Manual* #TMD058). Check the version number of the Spectrum Compact CE System Remote Access Software. If version number has changed, follow the instructions below for clearing the browser cache.

b. The cache needs to be cleared on every PC that accesses the Spectrum Compact CE System following a software update.

11.1 Internet Explorer® Settings

1. Select **Internet Options** from the gear icon at the top right of the browser (Figure 120).

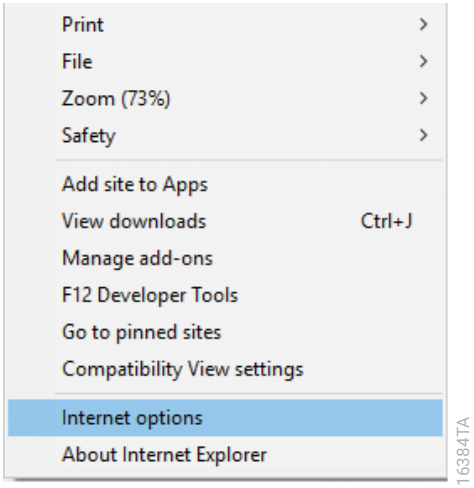

Figure 120. Selecting Internet options.

2. When the 'Internet Options' window is displayed, select **Delete** in Browsing History at the bottom of the 'General' tab (Figure 121). The 'Delete Browsing History' window pops up (Figure 122).

   Note: The cache has not been deleted yet.

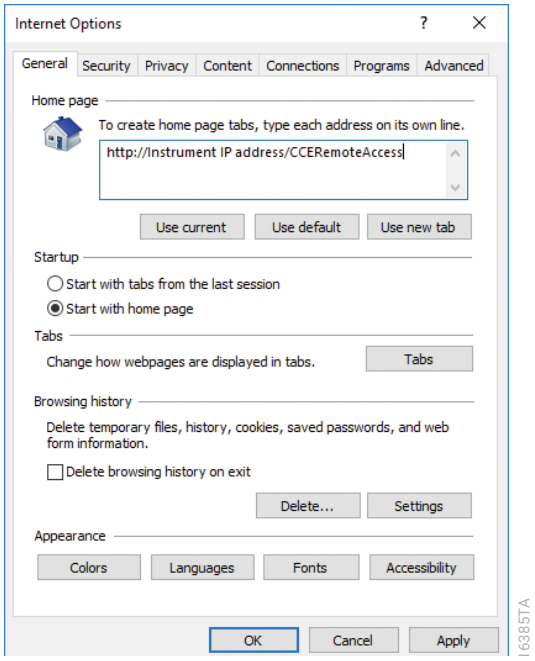

Figure 121. 'Internet Options' window.

3. Check **Temporary Internet files and Web site files**, and then select **Delete** at the bottom (Figure 122). The cache is now deleted.

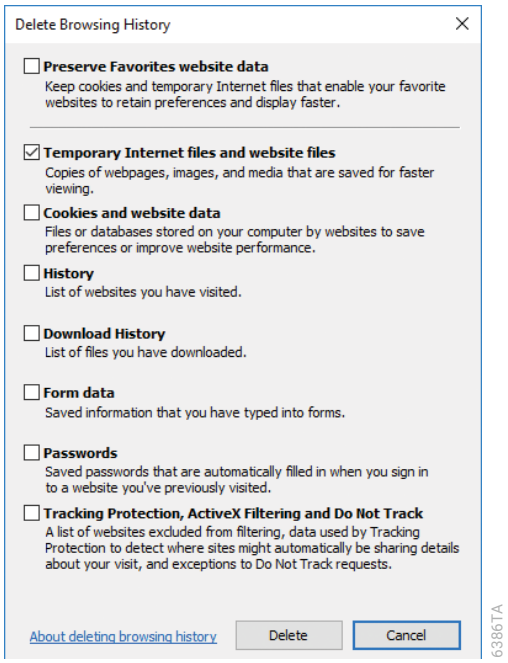

Figure 122. 'Delete Browsing History' window.

4. Select **OK** to close the 'Internet Options' window.

11.2 Google Chrome™ Settings

1. Select **Settings** from three dot leader icon at the top right of the browser (Figure 123).

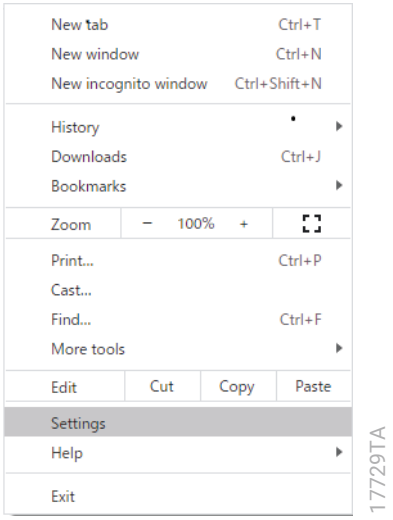

Figure 123. Google Chrome™ settings.

2. When the ‘Settings’ window is displayed, select **Clear browsing data** in Privacy and security (Figure 124). The ‘Clear browsing data’ window pops up (Figure 125).

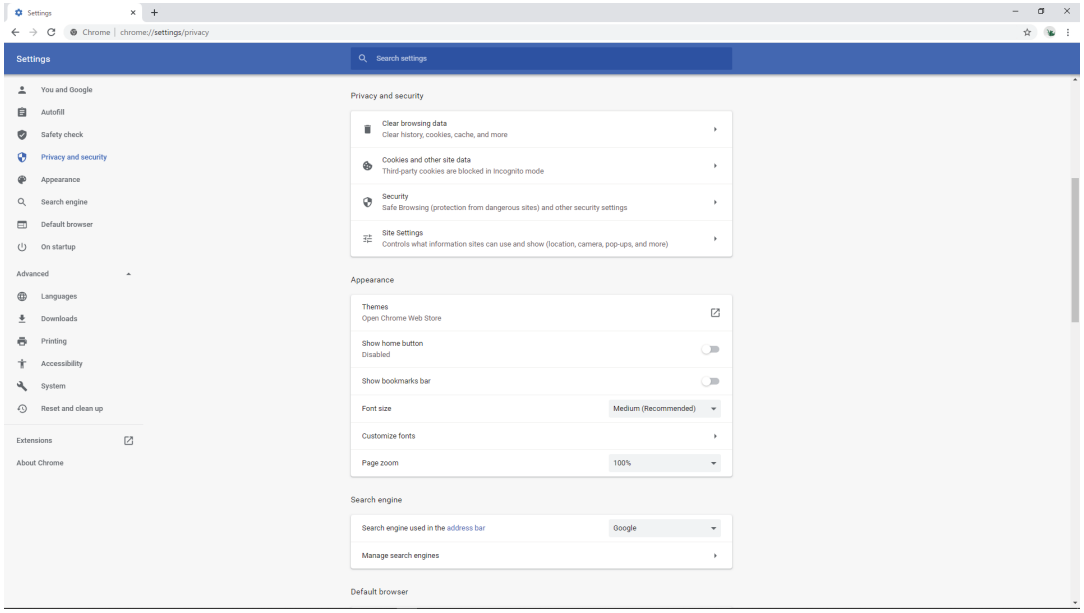

Figure 124. ‘Settings’ window.

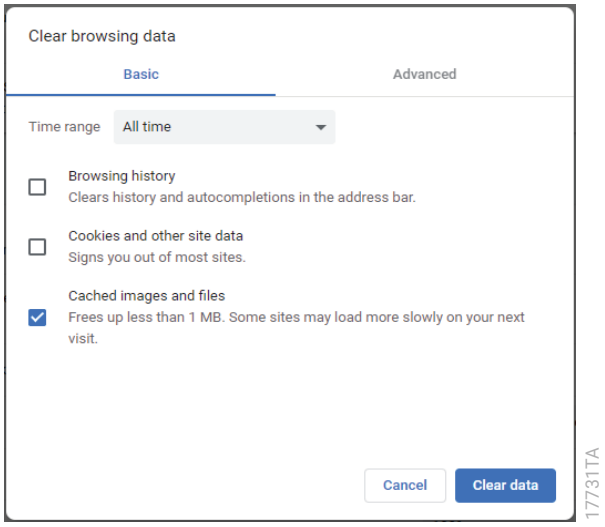

Figure 125. ‘Clear browsing data’ window.

3. Check “Cached images and files” at the bottom of the ‘Basic’ tab, and then select **Clear data** at the bottom (Figure 125). The cache is now deleted.

4. Select **X** to close the ‘Settings’ window.

11.3 Microsoft Edge® Settings

1. Select **Settings** from three dot leader icon at the top right of the browser (Figure 126).

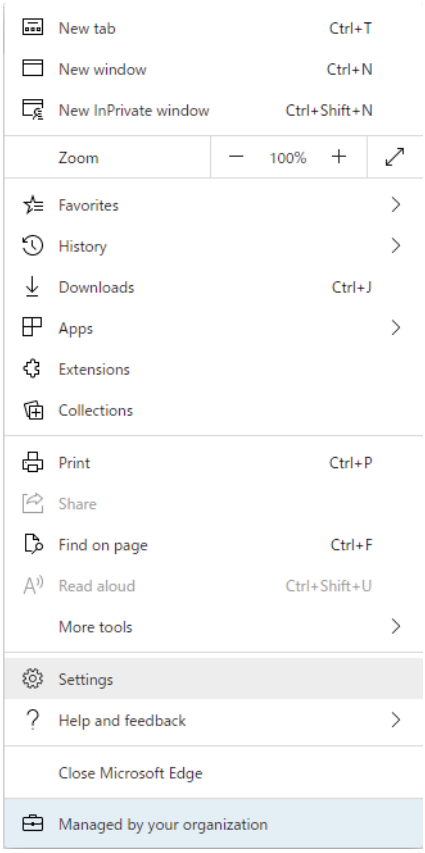

Figure 126. Microsoft Edge® settings.

2. When the ‘Settings’ tab is displayed, select **Privacy, search, and services** at the left of the ‘Settings’ window (Figure 127). The ‘Clear browsing data’ window pops up (Figure 128).

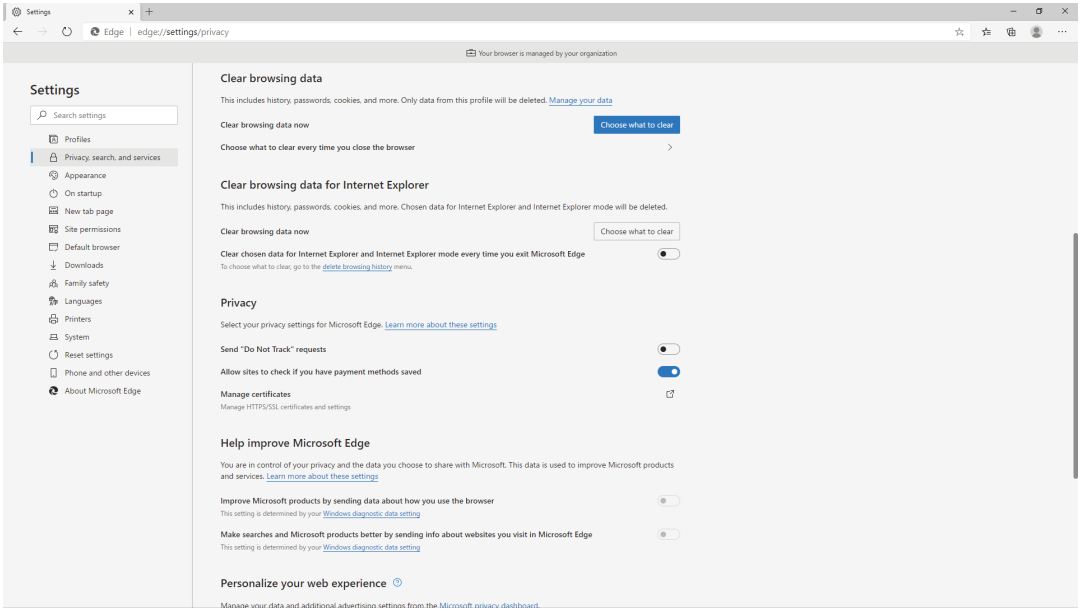

Figure 127. ‘Settings’ window.

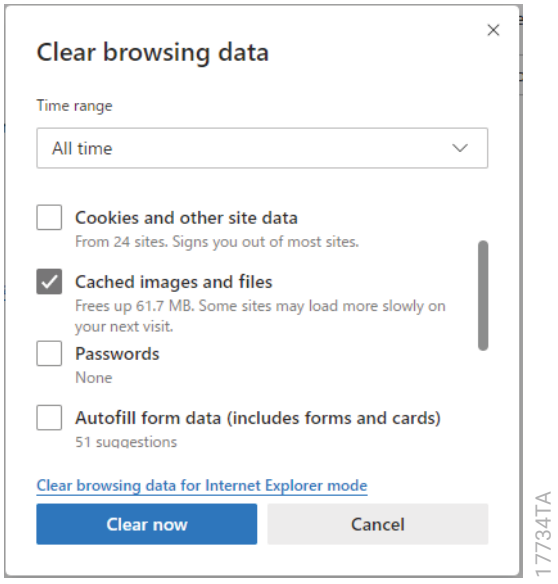

Figure 128. ‘Clear browsing data’ window.

3. Check “Cached images and files” at the second from the top, and then select **Clear now** at the bottom (Figure 128). The cache is now deleted.

4. Select **X** to close the ‘Settings’ window.

11.4 Mozilla Firefox® Settings

1. Select **Options** from hamburger icon at the top right of the browser (Figure 129).

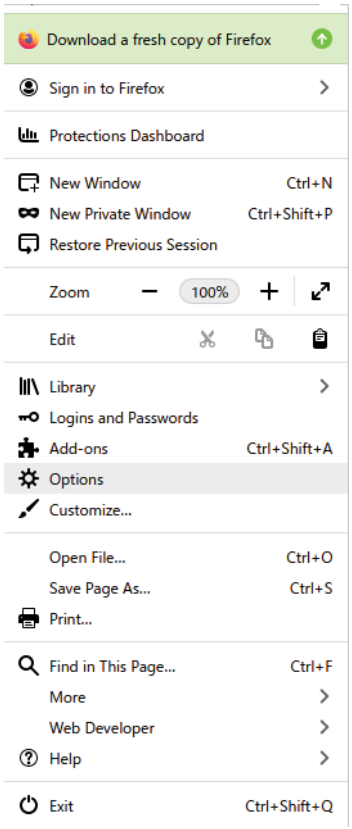

Figure 129. Mozilla Firefox® options.

2. When the ‘Options’ window is displayed, select **Privacy & Security** at the left of the ‘Options’ window (Figure 130). The ‘Clear data’ window pops up (Figure 131).

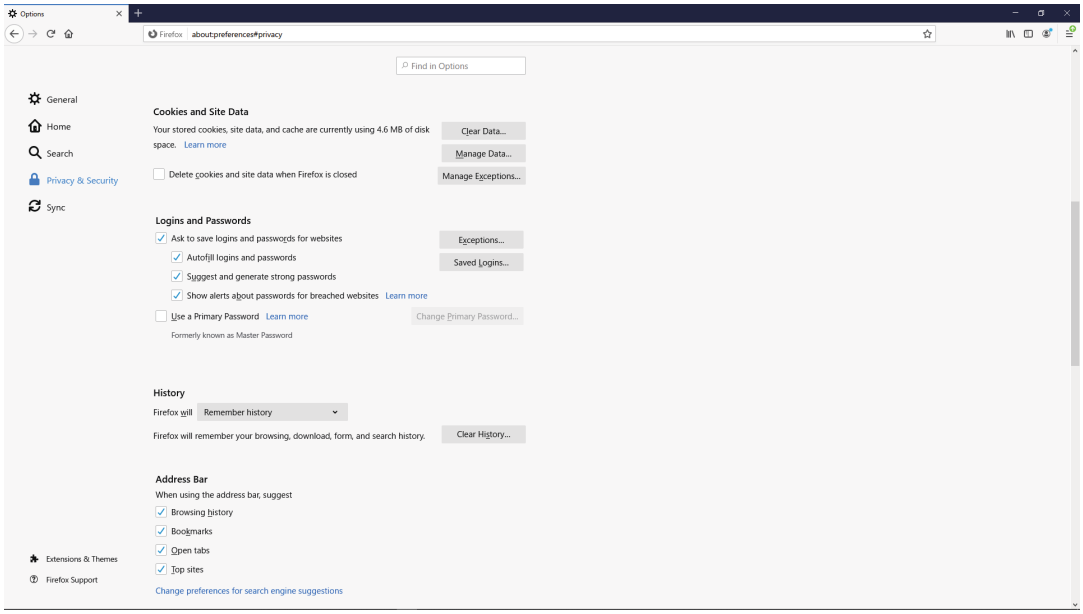

Figure 130. ‘Options’ window.

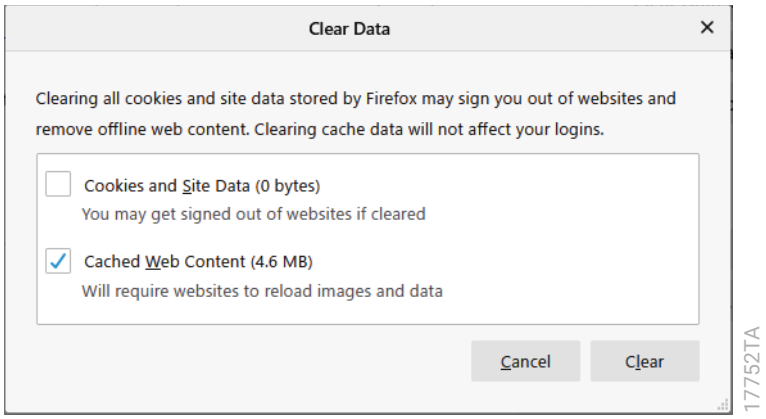

Figure 131. ‘Clear data’ window.

3. Check “Cached Web Content” at the window bottom, and then select **Clear** (Figure 131). The cache is now deleted.

4. Select **X** to close the ‘Options’ window.

Summary of Changes 12

The following changes were made to the 8/23 revision of this document:

Expanded the number of dye channels in Section 6.1, Step 7 and Section 7.1, Step 16.

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