SpectraMax® QuickDrop™

UV-Vis Spectrophotometer

User Guide

MOLECULAR DEVICES

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Chapter 1: Health and Safety

1

Safety Conformance

This equipment has been designed to conform to the following directives:

2014/35/EU Low voltage equipment safety directive

2014/30/EU EMC directive

2012/19/EU Directive on Waste Electrical and Electronic Equipment (WEEE)

2011/65/EU ROHS directive

2006/42/EC Machinery directive

Standards, to which conformity is declared include:

EN61010-1:2010 Safety requirements for electrical equipment for measurement, control, and laboratory use. General requirements

EN61010-2-101:2002 Safety requirements for electrical equipment for measurement, control, and laboratory use. Particular requirements for in vitro diagnostic (IVD) medical equipment

EN61326-1:2013 Electrical equipment for measurement, control, and laboratory use - EMC Requirements*

EN ISO 12100:2010 Safety of machinery: Basic concepts, general principles for design

* This equipment has been tested and found to comply with the limits for a CLASS A digital device, according to part 15 of the FCC Rules.

Hazards and Warnings

This section describes potential hazards which can exist in the operation of these units. Several warning labels and symbols are affixed to your instrument. These symbols are used to inform you of potential dangers which can exist or where caution is required. Before installing your new unit, take time to familiarize yourself with these warnings and symbols.

This instrument is subject to the following identified hazards:

This unit uses a Xenon lamp which is a high energy light source. DO NOT look closely at the cuvette holder or the micro-volume sample port when doing a measurement as prolonged exposure to the light source can result in permanent eye damage.

High voltages exist within the power supply unit and the Xenon lamp housing. Repair and maintenance must be done only by individuals trained to work on these instruments.

There are no bio-hazardous materials within the unit; however, this unit can be exposed to bio-hazardous samples during normal laboratory use. We recommend the following decontamination procedures of this instrument to protect users: remove cuvettes and cuvette holders and wash with appropriate disinfectant for the bio hazard in question, rinsed with distilled water and then allowed to dry. The exterior can be wiped with a suitable disinfectant cleaning wipe. In addition, we recommend the following:

- Include an appropriate decontamination certificate for equipment returned for repair.

- Ensure that the operator of the equipment is provided with a safe working environment.
- Use, store, and dispose of any chemicals in accordance with product guidelines and local safety regulations.
- Provide suitable ventilation when working with volatile solvents or toxic substances.
- Dispose of solvents and chemicals that can be classed as hazardous waste in accordance with local regulatory practice.
- Determine if personal protective equipment (PPE) is required for handling laboratory samples.

Emergency Procedure

In the event of contamination, malfunction or hazard occurring, disconnect the unit, by removing the power cord, and isolate for decontamination and/or repair.

Unpack and Install

- Units weigh less than 4 kg. No special handling is required.
- Please keep the original packaging for transport for service or repair as it has been specifically designed to protect the unit from damage during transit.
- Inspect the instrument and its power supply for any signs of damage caused during transit. If any damage is discovered, do not use the instrument and report the problem to your supplier.
- Ensure your proposed installation site conforms to the environmental conditions for safe operation.
  - Indoor use
  - 5 °C to 40 °C
  - Maximum relative humidity 90% up to 31 °C decreasing linearly to 50% at 40 °C
- Extremes of temperature may require recalibration of the unit for optimal performance.

- If the instrument has been stored in a cold environment then it should be allowed to come to room temperature before turning on the instrument to avoid compromising the internal calibration procedure.
- The instrument must be placed on a stable, level bench or table capable of taking its weight with sufficient space around the instrument for air to circulate freely.
- The equipment is operated using an 18 VDC power supply adapter unit. Always use the power supply adapter and mains cords supplied.
- Local mains power requirements are as follows:
- 100 to 240 VAC~
- 50 or 60 Hz
- The UK style mains cord plug has a user replaceable 3 A fuse. Replace only with the same rating and type 3 A BS1362.
- The unit maximum power rating is 50 VA.
- The instrument should be positioned so that the power supply cable may be readily removed in the event of a hazard or malfunction.
- Locate the instrument in an atmosphere free from dust and corrosive fumes. Use the dust cover to further protect the instrument when not in use or powered.

Back Connections

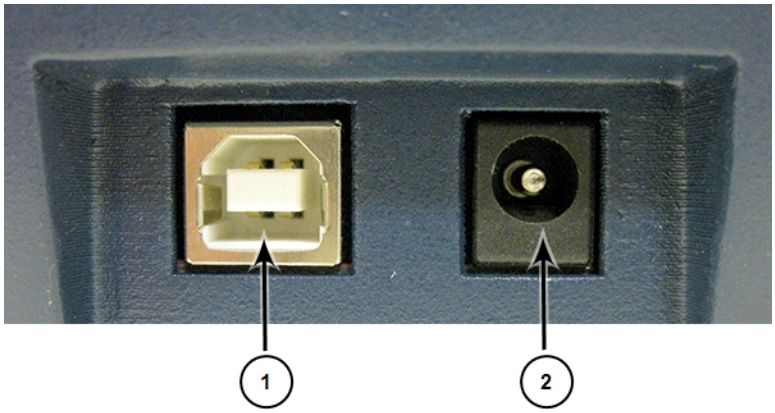


Table 1-1: Connection on the back of the instrument

Number	Description
1	USB connector for computer connection. See Print on page 99.
2	18 V power supply connector

Equipment Operation

The instrument has a sample port and a cuvette port for analysis.

Note: You cannot use both ports at the same time to do an analysis.

Table 1-2: Instrument Overview

Number	Description
1	Touchscreen display. Touch to power on the instrument.
2	LED indicator when USB is in use
3	Power button when on home screen, and return to home screen button when not on home screen
4	USB port for external data saving
5	Standard cuvette port
6	Micro-volume sample port

Intended Users

The instrument is intended to be used by scientists and technicians who possess basic laboratory and technical skills and have the knowledge and understanding of the hazards involved, with the unit and the samples used, to operate it in a safe manner.

Instrument Preparation

- Switch on the unit and allow it to finish the startup calibration.
- Select the appropriate application or method.
- Where relevant, set up the application parameters for the sample.
- Select the correct type. It is important to use cuvettes with the correct parameters. Most samples are measured using a standard 10 mm path length cuvette. It is important to use cuvettes of the correct type. Plastic used in many cuvettes absorb UV light and therefore are not suitable for UV sample measurement. Use dust-free, residue-free, and scratch-free cuvettes for measurement.
- Before preparing samples and sample reference blanks, familiarize yourself with hazards arising from handling the sample materials, and where required, observe local regulatory practice, personnel protection equipment and measures designed to ensure your safety.
- Prepare the sample blanks (reference) in the same solution used to dissolve the sample.
- Prepare the sample solutions.

When placing the cuvette in the equipment, ensure that the cuvette is orientated so that the light energy passes through the cuvette.

Post Operating Procedures

- Empty cuvette and rinse with deionized water.
- Clean cuvettes periodically with commercially available cleaning solution or dilute detergent solution followed by several thorough rinses in deionized water.
- Some samples and solvents might be classified as hazardous or bio hazardous waste. The disposal of such substances must be carried out in accordance with local regulatory practice.

Optical Validation

Good laboratory practice requires that the unit is periodically checked for optical operation.

- Switch on validation tests. When the unit is powered up, it does a wavelength accuracy and lamp energy test.
- Periodically test wavelength, stray light, and absorbance accuracy to ensure that the unit is operating to specification. Deterioration in operation might indicate that the instrument requires service. Optical validation can be done using reference materials.

User Maintenance

CAUTION! If the equipment is used in a way not specified, then the protection provided by the equipment can be impaired and the instrument warranty withdrawn.

- There are no user-serviceable parts in this instrument.
- To prevent cross-contamination and protect users from occupationally acquired infections, keep the unit clean and free from contaminates.
  - Remove and clean the cuvette holders with commercially available cleaning solution or dilute detergent followed by a thorough rinse in deionized water. Allow to dry thoroughly before use.
  - Casework and the sample compartment can be wiped down with commercially available disinfectant wipes.
  - Periodically validate the optical performance and refer the instrument for regular servicing and calibration.

Troubleshooting

CAUTION! Service or maintenance procedures other than those specified in this guide can be done only by Molecular Devices qualified personnel. When service is required, contact Molecular Devices technical support.

If the following problems happen, do the following troubleshooting corrections.

Negative Absorbance Readings

Sample measurements will read negative absorbance for the following reasons:

- The absorbance value of the reference is higher than the sample.
- The reference and the sample are interchanged.
- The sample is very dilute and close to the absorbance of the reference. The minimum concentration for the micro-volume sample port is 1 ng/µL (dsDNA) The minimum concentration for the 10 mm pathlength standard cuvette port is 0.5 ng/µL (dsDNA).

Unexpected Results

You will see unexpected results for the following reasons:

- There are bubbles or contamination in the sample or reference.
- The cuvette orientation is wrong.
- The cuvette material is not compatible with the experiment wavelength requirement.
- The pathlength selected in software is wrong.

- Both the cuvette and the micro-volume sample platform contain sample at the same time.

Absorbance Readings are Higher Than Expected

Absorbance readings will be higher than expected for the following reasons:

- The sample reference is wrong.
- The cuvette orientation is wrong.
- The cuvette material for the measurement wavelengths is wrong.
- The pathlength selected in software is wrong.
- Both the cuvette and the micro-volume sample platform contain sample at the same time.
- The sample or the cuvette is contaminated.
- In DNA applications, check 320 nm background, if the value is higher than 0, select a background correction in method set up.
- The optical alignment might be wrong. Contact technical support.

Absorbance Readings are Lower Than Expected

Absorbance readings will be lower than expected for the following reasons:

- The sample reference is wrong.
- The sample or the reference is contaminated.
- The sample and the reference samples are the same.
- The cuvette material is not compatible with the experiment wavelength requirement.
- The pathlength selected in software is wrong.
- The light beam might be missing the sample in the cuvette. Fill the cuvette with 20 mm of sample.
- On the micro-volume sample platform, the size or position of the droplet might be wrong.
- For DNA applications, check that the measurements at 230 nm and 320 nm are near 0.
- There might be a stray light issue. Contact technical support.

Poor Reproducibility

You will get poor reproducibility for the following reasons:

- More sample is needed in the cuvette or the micro-volume sample port.
- The cuvette orientation is wrong.
- The cuvette material for the measurement wavelengths is wrong.

- The concentration of the sample is either too low or too high. Using a 10 mm pathlength cuvette, the measured sample absorbance should be between 0.1 A and 2.0 A. If absorbance is > 2 A, the measurement is no longer in the linear range.
- There are particulates in the sample. Absorbance measurements will not be accurate in turbid samples.
- There might be noise or a measurement stability issue. Contact technical support.

Instrument Start Up Failure

The instrument should start up when you touch the power button or the touchscreen. The instrument might not start up for the following reasons:

- The sample paths are blocked or dirty. Dried DNA or Protein sample on the micro-volume head can cause start up calibration errors.
- The power supply is disconnected.

Report persistent failures to technical support.

Absorbance Readings are Stable but are Different Than Expected

Absorbance readings might be stable, but different than expected for the following reasons:

- Check that the Absorbance displayed is being normalized to a pathlength of 10 mm if a standard micro-volume cuvette is used.
- With a 0.5 mm pathlength, the ideal measurement range becomes equivalent when normalized to 2 A to 50 A and for a pathlength of 0.125 mm it becomes 8 A to 200 A.

For unresolved Absorbance issues, contact technical support. See Obtain Support on page 13.

Obtain Support

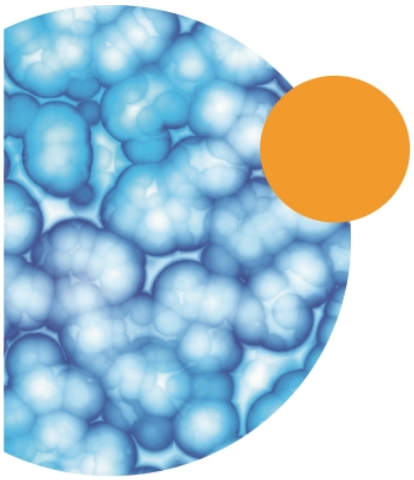
Molecular Devices is a leading worldwide manufacturer and distributor of analytical instrumentation, software, and reagents. We are committed to the quality of our products and to fully supporting our customers with the highest possible level of technical service.

Our support website, www.moleculardevices.com/support, has a link to the Knowledge Base with technical notes, software upgrades, safety data sheets, and other resources. If you still need assistance, click **Request Support** to submit a request to our technical support representatives.

To find regional support contact information, visit www.moleculardevices.com/contact.

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

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



Chapter 2: Introduction

2

The SpectraMax® QuickDrop™ UV-Vis Spectrophotometer is a standalone, split beam spectrophotometer with a high-resolution color touchscreen. The spectrophotometer offers a comprehensive range of spectrophotometric and life science applications. The instrument provides a sample port and standard cuvette port for rapid micro-volume analysis.

A spectrophotometer is an optical device that is designed to transmit a beam of light through a sample. Transparent solutions absorb specific wavelengths of light based on their unique molecular composition. Absorbance is proportional to concentration of a sample. Absorbance peaks of a sample can also be used to identify its molecular composition. In kinetic studies, the tracking of absorbance over time can be useful to study chemical reactions and biological processes.

The instrument emits light from the far ultraviolet (190 nm) to the visible light (1100 nm). Many materials, and in particular solutions of materials absorb light within this region. This makes the QuickDrop Spectrophotometer useful in a wide range of applications including life sciences, clinical, pharmaceutical, cosmetics, food and drink, agricultural, industrial, environmental, toxicology, water treatment, and teaching. There are numerous published methods and assays for these applications.

The icons described throughout this manual use the names listed in the Table of Icons on page 101. If you are unsure of any of their functions refer to the table.

For detailed descriptions of the functions of the parameter boxes, see Glossary of Boxes on page 105.

Frequently Used Icons

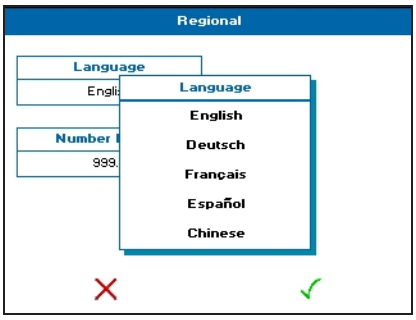
Icon	Name	Function
	Forward arrow	Navigates to the next screen in a sequence.
	Back arrow	Navigates back to the previous screen in a sequence.
	OK / Accept	Use to confirm or accept any changes. Saves and exits.
	Exit	Exits from a read type or other dialog. If exit is selected without saving, any changes are lost.
Icons on the Sample Measurement Screen		
	Take reference measurement	Starts a reference measurement.
	Take sample measurement	Starts a sample measurement. A reference measurement must be taken prior to a sample measurement
	Open Options menu	Opens the Options menu on the Sample Measurement screen.
Icons on the Options Menu		
	View Method parameters	Takes you from the Sample Measurement screen to the first Method parameter screen.
	Save sample data	Use to manually specify a save location for the sample data.
	Save method parameters	Use to manually specify a save location for a method.
	Sample Manager	Opens the Sample Manager. Displays the sample data held in the either the internal memory or on a USB flash drive.
	Trace Manager	Available in the Wavescan and Kinetics read types only. Use to overlay up to 8 samples data files and use to chooses what type of data is displayed, such as, raw data, smoothed data, or 1st derivative.

First Time Powered on

When you push the power button or touch the touchscreen to start the instrument for the first time, you are prompted to set your regional setting preferences for language and local date and time.

Regional

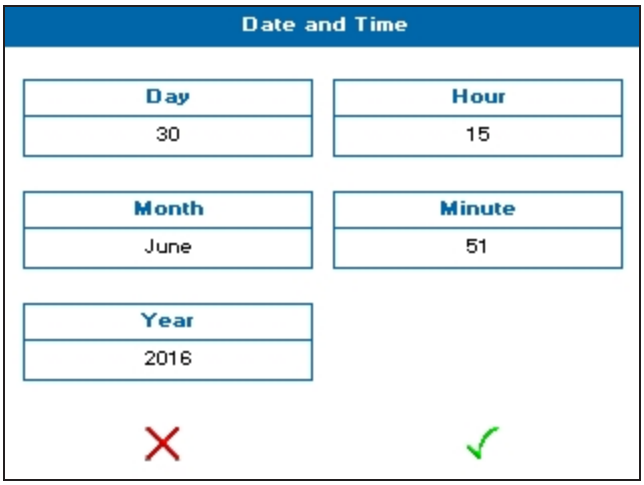
The language preference is set to English by default. This can be changed by touching **Settings**, then touching **Regional**, then touching the **Language** box, then touching a different language option from the list. The options include: English, German, French, Spanish, and simplified Chinese.



To save your change, touch the ✓. To exit without saving, touch the ✗.

Date and Time

The date and time preference is set to Pacific Time (PT) by default. This can be changed by touching **Settings**, then touching **Date and Time**. You can change the following settings: **Day**, **Month**, **Year**, **Hour**, and **Minute**. Touch the setting box you want to change. If it is a number, enter the new value using the numeric keypad that is displayed, otherwise, touch a new setting from the options list that is displayed.



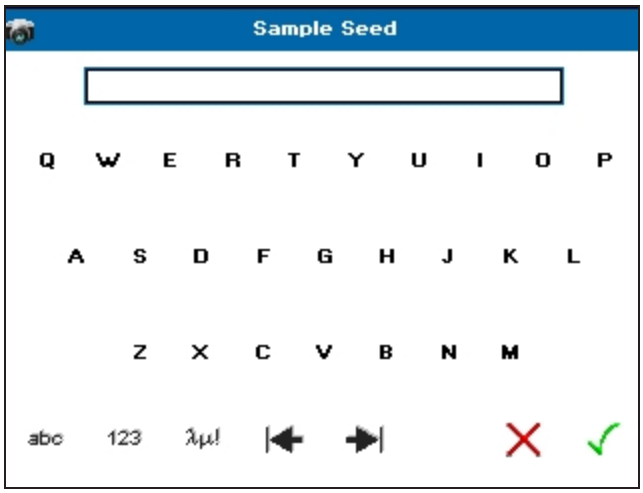
To save your change, touch the ✓. To exit without saving, touch the ✗.

Types of Boxes

The QuickDrop Spectrophotometer software uses different kinds of boxes for parameter selection and data entry depending on what you are doing.

Alphanumeric Text Entry

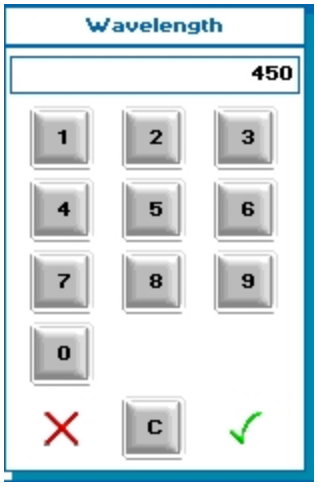
The alphanumeric text entry box lets you enter letters, numbers and symbols by touching **abc**, **123** and **λμ!**, respectively. You can toggle between upper and lower case letters and through a list of symbols by touching **abc** and **λμ!** twice.



Note: The layout of the screen depends on the text entry mode set in **Settings** in **User Interface** .

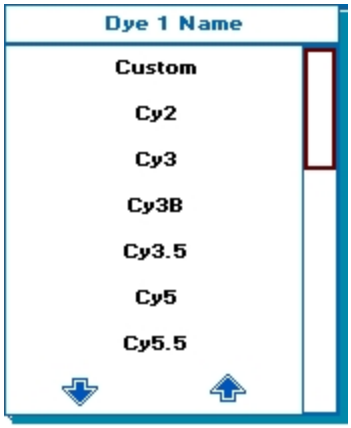
Numeric Entry

The numeric entry box lets you enter numbers in the Method parameters. Depending on the numeric box selected, you can add both positive and negative numbers.



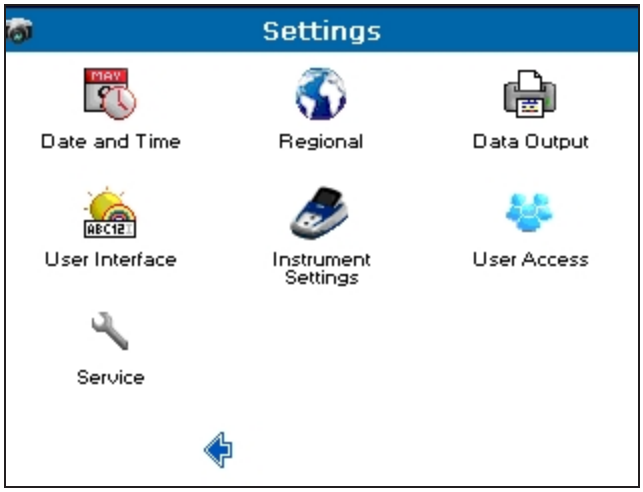
Selection List and Combination Box

When there are more than two options, you get a list. If there are more than 8 options, you can scroll through the options by touching either the page up and page down arrows. When there are only two options, touching the box toggles between the two options, such as On or Off.



Settings

From the main screen, touch **Settings** to view or change the instrument operational preferences.



The choices include:

- **Date and Time**—Use to specify the **Day**, **Month**, **Year**, **Hour**, and **Minute**.
- **Regional**—Use to specify the **Language** and **Number Format**.
- **Data Output**—Use to specify if **Auto-Print** is **On** or **Off** for all read types. Use to also specify where data **Print to**, either **PC Via USB** or **USB Mass Storage**, for all read types. See Print on page 99. Use to also specify if **Auto Save** is on or off for all read types. Use to also specify where data and methods **Save to**, either **USB CVS**, **USB**, or **Internal**, for all read types.

- **User Interface**—Use to specify screen **Brightness**, **Text Entry Mode** touch-keypad style, and **Screensaver** activation time.
- **Instrument Settings**—Use to view **Instrument Information** and **Lamp Settings**. Use to also manage the **Temporary Baseline**, **Permanent Baseline**, and **Restore** the original baseline. You can also view the **Service Date** set by the last service engineer.
- **User Access**—Use to add users and set limitations on software functionality according to user group, such as **Administrator**, **Supervisor**, or **Limited**. Only the Administrator users have access to all the software functionality. When User Access is in use, the User Access icon appears only if your login name has the Administrator setting assignment.
- **Service**—For use only by a trained service engineer or upon recommendation of technical support.

To change settings:

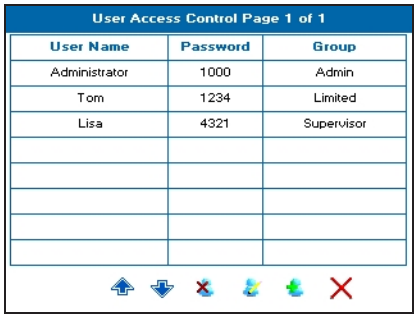
1. From the **Settings** screen, touch one of the available choices.
2. From the setting choice screen, touch the available setting parameter you want to change. Generally a list of options is displayed for you to select by touching. Some settings only toggle between on or off. Some settings require that you enter your change on the keypad that displays.
3. Make your change by touching, toggling or typing, as appropriate.
4. To save your changes and return to the **Settings** screen, touch ✓. To cancel your setting changes and return to the **Settings** screen, touch ✗.

To exit the **Settings** screen and return to the main screen, touch .

User Access Control Settings

By default the QuickDrop Spectrophotometer is set to work as an unrestricted Administrator user. You can set up user login requirements and assign access rights for up to 16 users, if you need to protect saved sample data, saved methods, instrument settings, and user access settings.

Note: After you set up user access controls, the **User Access** icon is only visible to the Administrator login user in **Settings**. Also everyone is prompted to log on or switch user, until the requirement is disabled. See Edit User Access on page 24.



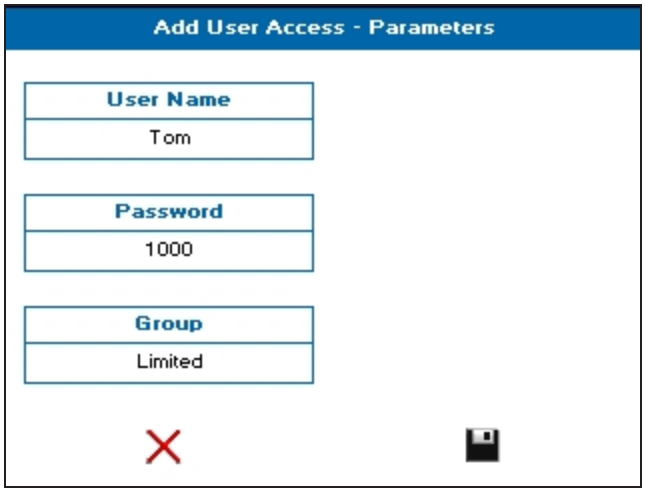
There are three levels of user access:

- **Administrator**—Unrestricted access
- **Supervisor**—Can run read types and saved methods. Can save sample data. Can save methods. Can delete sample data from the internal memory.
- **Limited**—Can run read types and can run saved methods, and can save sample data.

Add Users

The instrument can store up to 16 individual users. Give each user a **User Name** (using alphanumeric entry), a 4-digit **Password** and assign a **Group**, one of three user groups depending on the access level they need.

Note: Only the **Administrator** login user can add users.



User Group	Run Read Types and Saved Methods	Save Sample Data	Delete Sample Data From Instrument Memory	Save Methods	Access Settings Menu	Access User Settings
Limited	Yes	Yes	No	No	No	No
Supervisor	Yes	Yes	Yes	Yes	No	No
Administrator	Yes	Yes	Yes	Yes	Yes	Yes

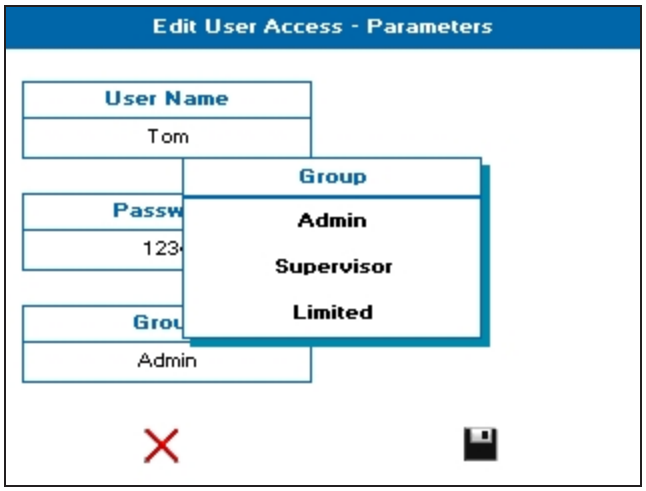
To add a user:

1. From the main screen, touch **Settings**.
2. From the **Settings** screen, touch **User Access**.
3. From the **User Access Control** screen, touch to add user.
4. From the **Add User Access** screen, touch **User Name**, then enter an alphanumeric user name.

5. Touch **Password**, then enter a 4-digit number.
6. Touch **Group**, then touch one of the three user group options: **Limited**, **Supervisor**, or **Administrator**.
7. Touch to save the user addition settings. Touch to exit the screen without saving.
8. When you are finished adding users, to exit the **User Access Control** screen, touch .

Edit Users

Note: Only the **Administrator** login user can edit users.



To edit a user:

1. From the main screen, touch **Settings**.
2. From the **Settings** screen, touch **User Access**.
3. From the **User Access Control** screen, touch the name needing the edit to highlight the line selection.
4. Touch to edit the user settings.
5. From the **Edit User Access** screen, touch the box needing the edit, **User Name**, **Password**, or **Group**, then enter or select as needed.
6. Touch to save the edits. Touch to exit the screen without saving.
7. When you are finished editing users, to exit the **User Access Control** screen, touch .

Delete Users

Note: Only the **Administrator** login user can delete users.

Deleting a user only removes the login name, password and group assignment. Any methods or sample data saved on the instrument by this user is still saved on the instrument.

Note: The default Administrator user cannot be deleted.

To delete a user:

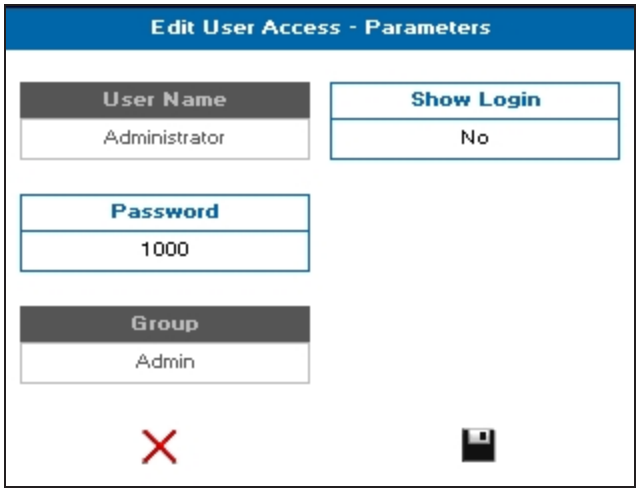
1. From the main screen, touch **Settings**.
2. From the **Settings** screen, touch **User Access**.
3. From the **User Access Control** screen, touch the name needing the delete to highlight the line selection.
4. Touch to delete the user login name and settings.
5. When prompted to delete the selected user, touch to confirm. If you want to cancel the user delete, touch .

6. When you are finished deleting users, to exit the **User Access Control** screen, touch .

Edit User Access

If you have set up **User Log On** as a requirement on your instrument, you can disable the login requirement and return the instrument to continually operate in Administrator mode.

Note: Only the **Administrator** login user can disable user login requirements.



To disable the user login requirement:

1. From the main screen, touch **Settings**.
2. From the **Settings** screen, touch **User Access**.
3. From the **User Access Control** screen, touch the default **Administrator** to highlight the line selection.
4. Touch to edit the user settings.
5. From the **Edit User Access** screen, touch **Show Login**, when **No** is displayed, the requirement is disabled.

   Note: Any time you add a user, **Show Login** automatically changes to **Yes**. Deleting the last user does not automatically change **Show Login** to **No**. It must be manually changed.

6. Touch to save the edits. Touch to exit the screen without saving.
7. When you are finished disabling the user login requirement, to exit the **User Access Control** screen, touch .

Chapter 3: Take Sample Measurements

3

The QuickDrop Spectrophotometer is a split-beam UV-visible spectrophotometer that uses a single cuvette holder for both reference and sample measurements. You can take a measurement from either a cuvette or from the micro-volume sample port. Before taking sample measurements, you must take a reference measurement to correct for solvent and cuvette effects. As long as you continue to use the same solvent or buffer, you only need to take one reference measurement.

Cuvette Sample Measurement

To take a cuvette sample measurement:

1. Insert a cuvette containing solvent or buffer in to the cuvette holder. Use the directional arrows next to the holder as your cuvette orientation guide for proper cuvette insertion.

2. Touch to take the reference measurement.
3. When the reference measurement is finished, remove the cuvette containing solvent or buffer from the cuvette holder, then insert a cuvette containing your sample solution.
4. Touch to take the sample measurement.
5. You can continue with replacing the sample cuvette with other sample cuvettes and taking sample measurements until all your data is collected.
6. For saving cuvette measurement sample data, see Save Sample Data on page 77.

Micro-Volume Sample Measurement

To take a micro-volume sample measurement:

1. Load 2 µl (0.5 µl minimum) of reference in the sample port.

2. Touch to take the reference measurement.
3. When the reference measurement is finished, remove the reference by wiping the sample port clean with a lint-free cloth, then using the same volume as the reference, load the sample of interest.

4. Touch to take the sample measurement.
5. You can continue taking measurements by wiping the sample port clean with a lint-free cloth, then load another sample onto the sample port until all your data is collected.
6. For saving micro-volume sample measurement sample data, see Save Sample Data on page 77.

Chapter 4: Read Types

4

The QuickDrop Spectrophotometer includes the following read types:

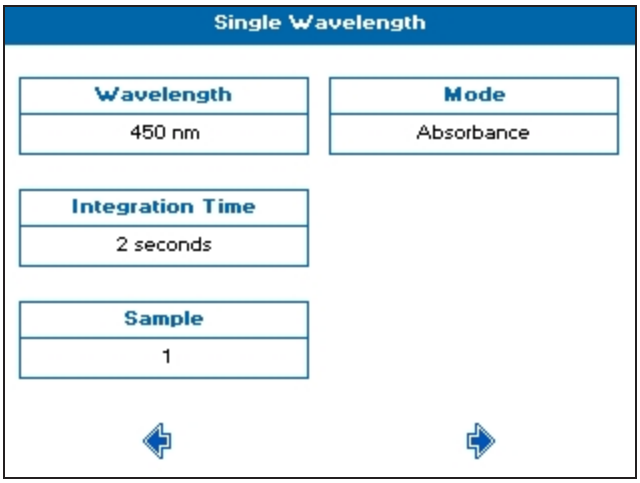
- **Single Wavelength**—Absorbance, % transmission or concentration measurements at a single, specified wavelength.
- **Wavescan**—Wavelength scan between two, user-defined wavelengths in the range 190 nm to 1100 nm. Can also do data overlay, post-scan data manipulation and user-configurable peak and valley functions.
- **Kinetics**—Measurements of Absorbance over time to determine rate or end points. Can also do data overlay, post-scan data manipulation and user-defined sectors.
- **Standard Curve**—Concentration measurement at a single wavelength determined by the generation of a calibration curve of known standards.
- **Equation Editor**—Create your own unique methods including calculations and thresholds.

Single Wavelength

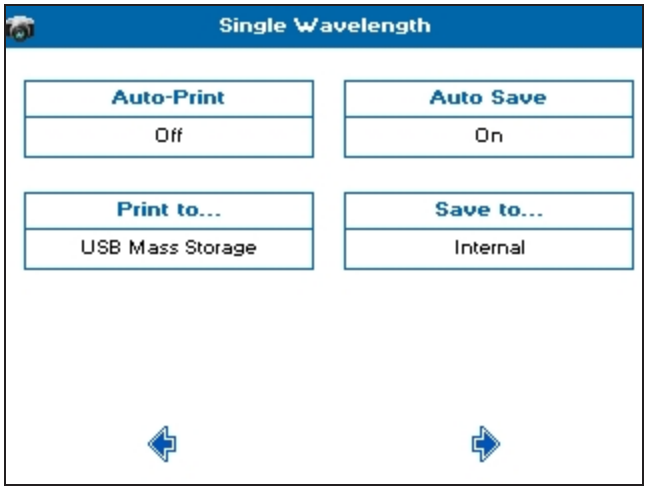
The Single Wavelength read type performs simple absorbance (A) and % transmission (%T) measurements on samples, measuring the amount of light that has passed through a sample relative to a reference, which can be air.

To use single wavelength:

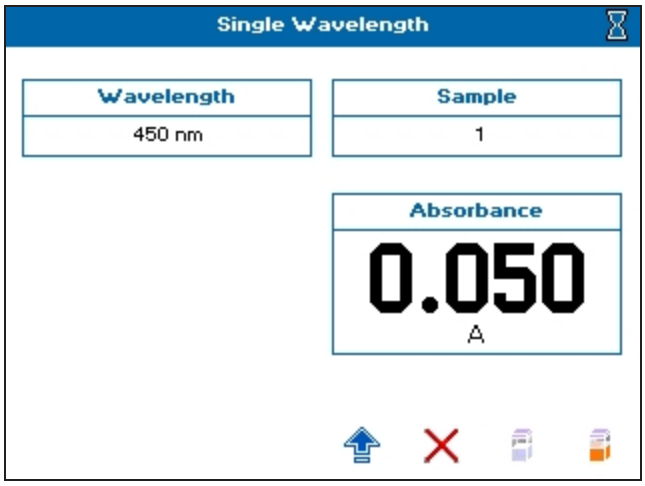
1. From the main screen , touch **Read Type**, then touch **Single Wavelength**.
2. Set **Mode** to either **Absorbance**, **%Transmission**, or **Concentration**.
3. Set **Wavelength**, and **Integration Time** as needed.
4. The **Sample Seed** entered under **Sample** becomes the file name used for any data file saved automatically.



5. When finished setting method parameters, touch to go to the next screen.
6. Set how you want the sample data to be saved. See Save Sample Data on page 77.



7. Touch to go to the next screen, and take a measurement.



8. See Take Sample Measurements on page 25.

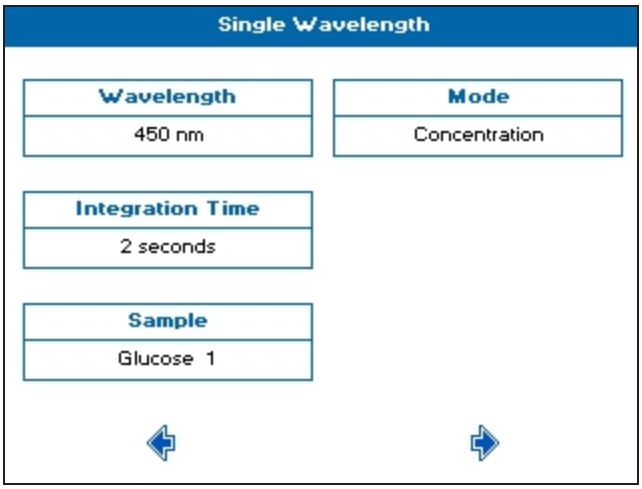
Concentration via Factor

Concentration mode within the Single Wavelength read type makes simple concentration measurements on samples. The measurement is done by multiplying the measured absorbance at a specific wavelength by a factor. The factor can be known in advance or can be calculated by the instrument by measuring a standard of known concentration. Examples of concentration measurements include DNA or protein.

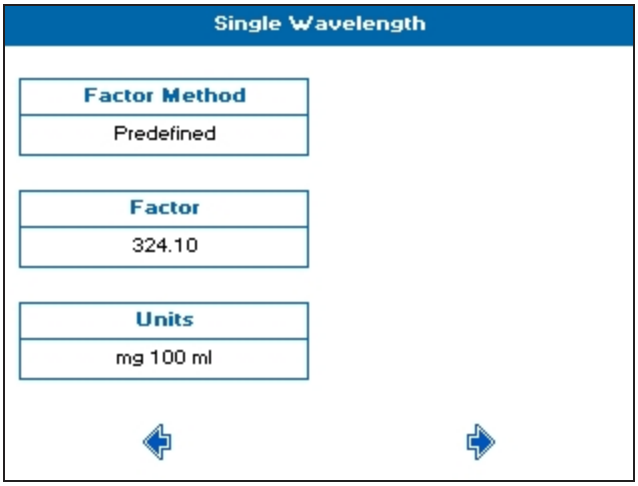
To use Single Wavelength in Concentration mode:

1. From the main screen , touch **Read Type**, then touch **Single Wavelength**.
2. Set **Mode** to **Concentration**.

3. Set **Wavelength**, and **Integration Time** as needed.
4. The **Sample Seed** entered under **Sample** becomes the file name used for any data file saved automatically.

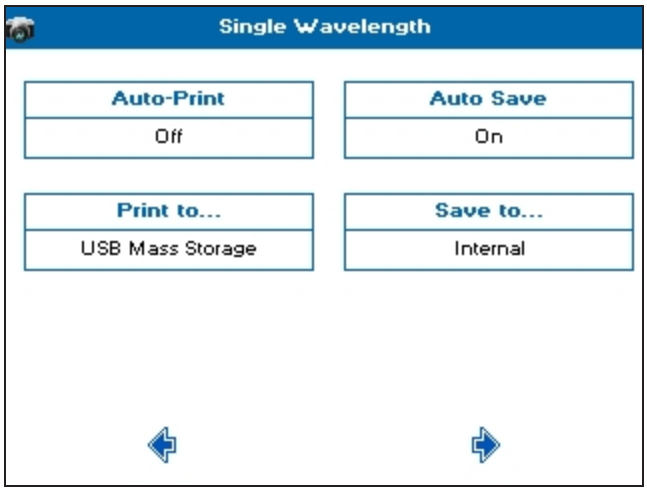


5. When finished setting method parameters, touch to go to the next screen.
6. Set **Factor Method**, **Factor**, and **Units** as needed.

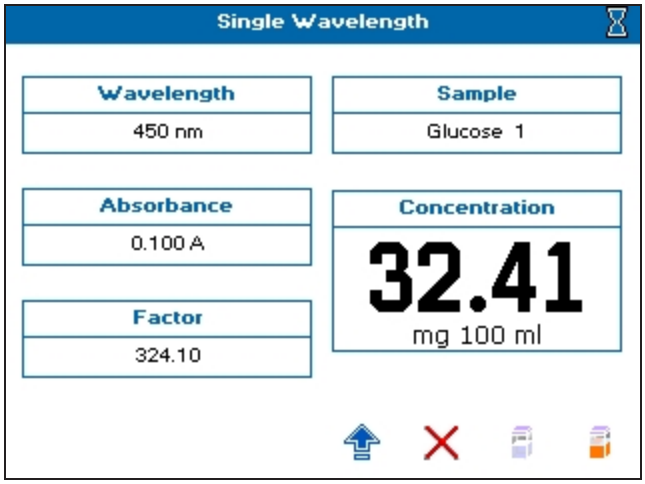


7. When finished setting method parameters, touch to go to the next screen.

8. Set how you want the sample data to be saved. See Save Sample Data on page 77.



9. Touch to go to the next screen, and take a measurement.



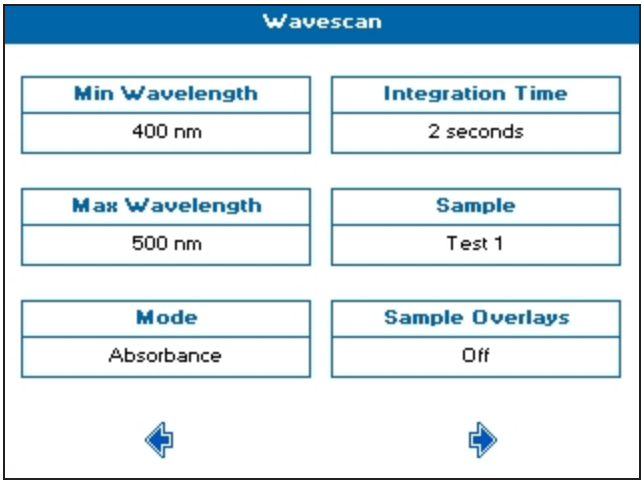
10. See Take Sample Measurements on page 25.

Wavescan

A measurement of absorbance or % transmission of a sample over a specified wavelength range is one of the most useful physical characteristics of a compound, both as means of identification (qualitative analysis) and of estimation (quantitative analysis). The observed features arise due to the various electronic transitions that are possible within a molecule. You can also do a range of post-scan data manipulation options including: 1st order derivative, enabling identification of multiple, unresolved peaks; 2nd order derivative, enabling identification of peak shoulders (inflections); 4th order derivative, which identifies both multiple peaks and inflections at the same time; Smoothing, utilises the Savitzky-Golay algorithm to smooth data and increase the signal to noise ratio; Enhanced, which enhances features, sharpening peaks and valleys.

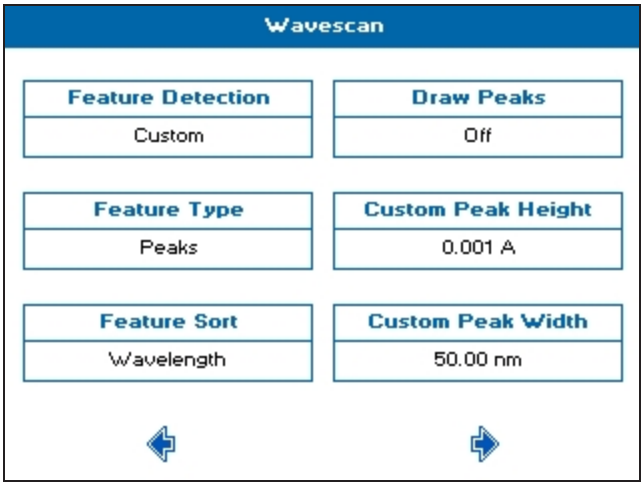
To use Wavescan:

1. From the main screen , touch **Read Type**, then touch **Wavescan**.
2. Set **Max Wavelength** and **Min Wavelength** to the needed wavelength range.
3. Set **Wavelength**, and **Integration Time** as needed.
4. The **Sample Seed** entered under **Sample** becomes the file name used for any data file saved automatically.
5. If needed, set **Sample Overlays**. When you set Sample Overlays to 2 or more, all of the wavelength scans automatically save to the internal instrument memory, and are displayed in Trace Manager. See Trace Manager - Overlay and Manipulate Wavescan and Kinetic Files on page 81 for more details.

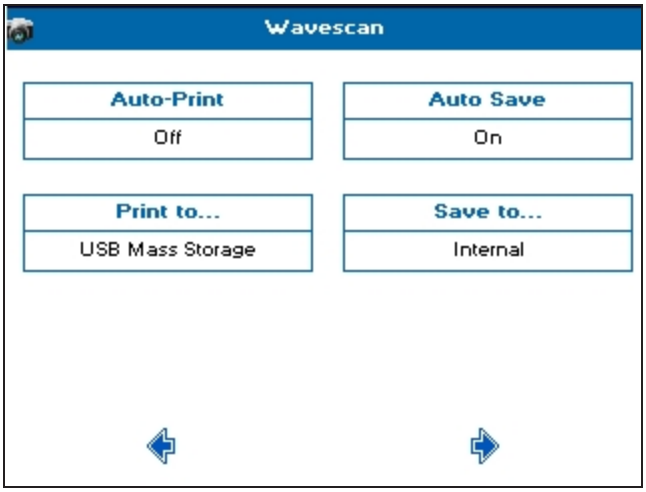


6. When finished setting method parameters, touch to go to the next screen.
7. Set **Feature Detection** as needed to determine the number of peaks or valleys that are automatically detected. Choices include: **Coarse**, **Sensitive**, or **Custom**.
8. Set **Feature Type** as needed to specify the feature needing detection. Choices include: **Peaks**, or **Valleys**.
9. Set **Feature Sort** as needed to determine how the features are displayed in the data table. **Wavelength** shows the peaks in ascending wavelength, and **Magnitude** shows them in descending size.
10. Set **Draw Peaks** as needed. **On** shows the width of the peak and the height of the detected peaks using dashed lines.
11. Set **Custom Peak Height** as needed Only available when **Feature Detection** is set to **Custom**. Specifies the minimum height the peak has to be above the higher of the two adjacent minima for the peak to be detected.

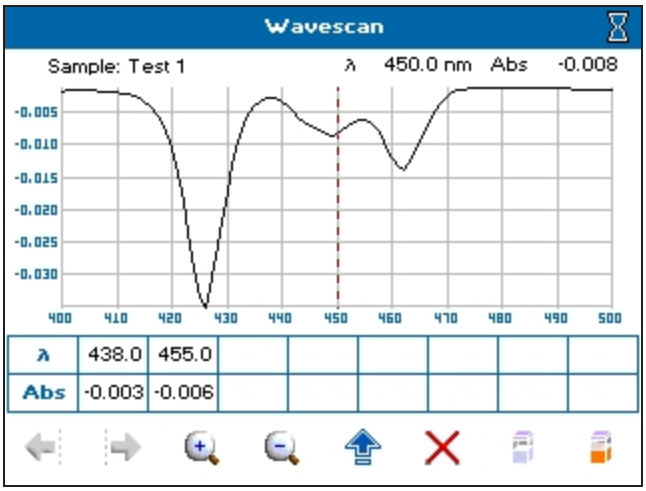
12. Set **Custom Peak Width** as needed. Only available when **Feature Detection** is set to **Custom**. Specifies the minimum width of the peak as determined by the difference in wavelength between the higher of the two adjacent minima and the opposing intersection of that higher minimum level and the peak profile.



13. When finished setting method parameters, touch to go to the next screen.
14. Set how you want the sample data to be saved. See Save Sample Data on page 77.



15. Touch to go to the next screen, and take a measurement.



16. See Take Sample Measurements on page 25.
17. With **Feature Detection** set to **Coarse**, **Sensitive** or **Custom**, the sample measurement screen shows a table below the scan. This table shows the **Feature Type** selected in the method parameters. To manually add a peak or valley to the table, position the cursor over the desired feature by either touching the feature, or touching or to move the cursor, then touch an empty cell in the table.
18. To add overlays, do data manipulation, or select saved files, see Trace Manager - Overlay and Manipulate Wavescan and Kinetic Files on page 81.

Kinetics

Kinetics measurements made using a UV-visible spectrophotometer measure the change in absorbance at a single, fixed wavelength over a specified period. This can be used to provide useful information when an appropriate factor, defined in a reagent kit protocol, is applied. Reagent test kits are routinely used for the enzymatic determination of compounds in food, beverage and clinical laboratories.

UV-visible spectrophotometric kinetic assays are considered one of the most convenient measurements for enzymatic assays since they allow the rate of the reaction to be measured continuously.

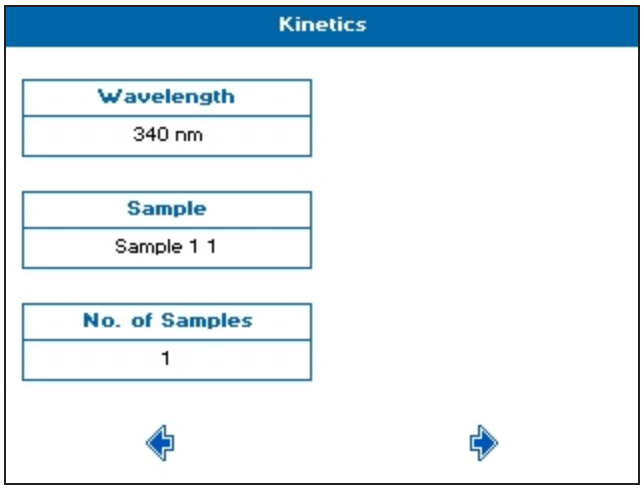
Serial Kinetics Measurments

Serial kinetics is the measurement of the absorbance of a single sample over a specified duration at a specified interval. Since the instrument can take up to 1 reading per second, serial kinetics measurements can be used for rapid rate reactions.

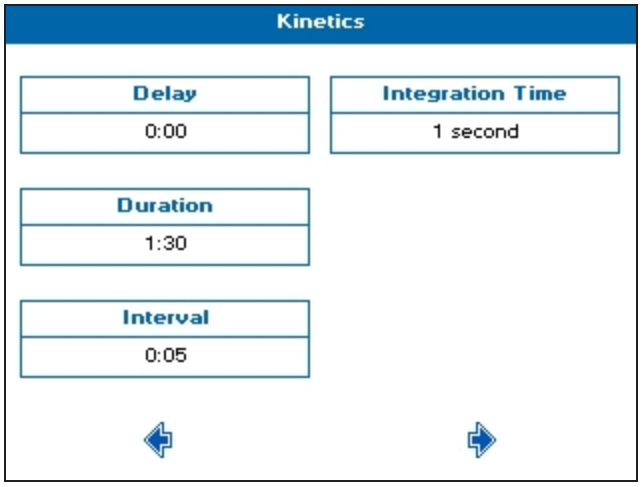
To use Kinetics:

1. From the main screen , touch **Read Type**, then touch **Standard Curve**.
2. Set **Wavelength** as needed.

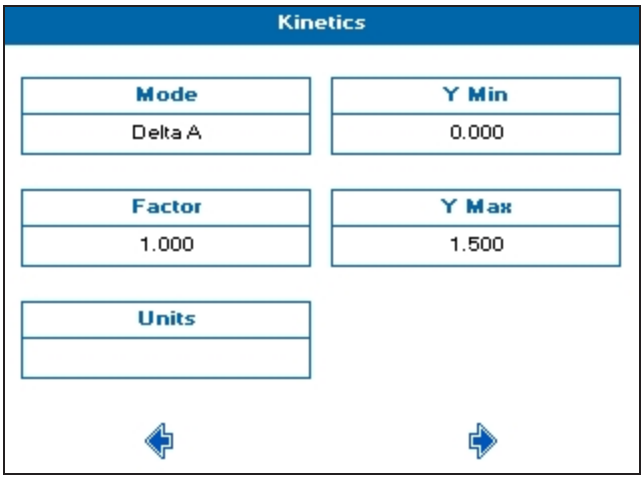
3. The **Sample Seed** entered under **Sample** becomes the file name used for any data file saved automatically.
4. For **No. of Samples**, when measuring more than 1 sample, all data is overlaid at the end of the measurement and automatically saved to the internal instrument memory. Sample 1 is measured for the full duration at the specified interval, and when finished, sample 2 is measured for the full duration at the specified interval. The measurement continues in this way until all samples have been recorded. You can choose up to 7 samples for consecutive measurement.



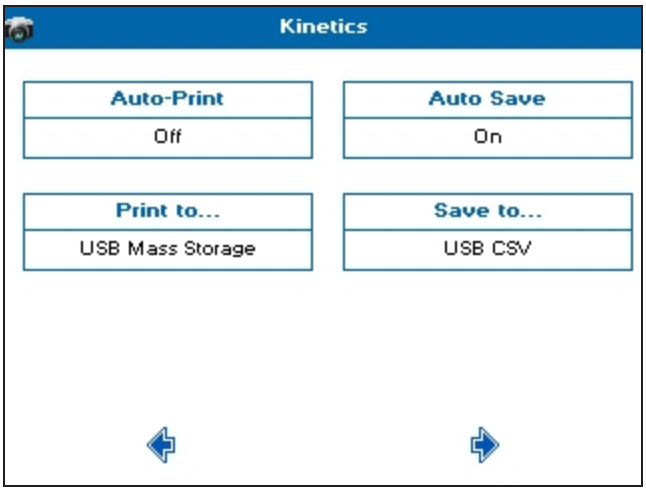
5. When finished setting method parameters, touch to go to the next screen.
6. Set **Delay** as needed to specify the time before the first measurement starts.
7. Set **Duration** as needed to specify the total measurement time, up to 180 minutes.
8. Set **Interval** as needed to specify the time between readings, from 1 second to the total duration.
9. Set **Integration Time** as needed. Time choices are determined by the interval. The maximum integration time is half of the interval time.



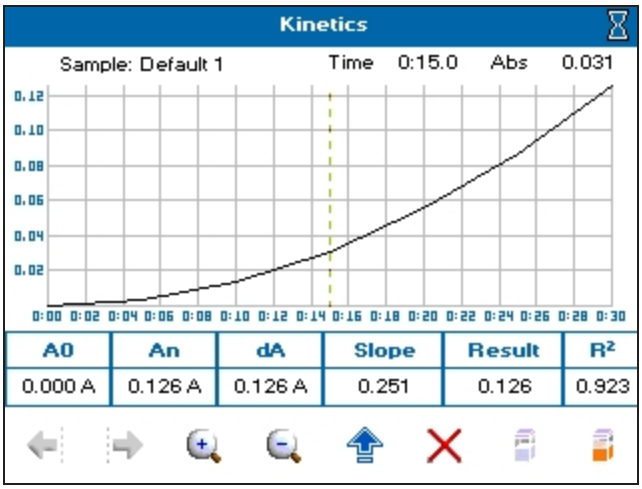
10. When finished setting method parameters, touch to go to the next screen.
11. Set **Mode** as needed. Choices include: **Delta A**, **Final A**, or **Slope**.
12. Set **Factor** as needed as the multiplier for **Mode** to calculate the **Result** value on the sample measurement screen.
13. Set **Units** as needed to label any exported data.
14. Set **Y Min** and **Y Max** as needed. These values are shown during the measurement. The y axis auto-scales upon completion.



15. When finished setting method parameters, touch to go to the next screen.
16. Set how you want the sample data to be saved. See Save Sample Data on page 77.



17. Touch to go to the next screen, and take a measurement.



18. See Take Sample Measurements on page 25. If you set a **Delay**, the measurements start after your specified time.

19. To stop the measurement at any time , touch . All the data collected up to the stop point is displayed on screen and can be saved.

20. The data displayed in the table below the scan refers to the full measurement range. To get data for a specific section, you have to add sections. Do the following:

    a. Set the cursor to the needed start position by either touching the scan or using the cursors.

    b. Touch to open the Options menu, then touch .

    c. Use the cursor to set the needed end position.

    d. Touch to open the Options menu, then touch .

    e. If needed, repeat to add up to 4 discrete sections. Sections must be added in numerical order.

    f. With sections defined, the data shown in the table below the scan is determined by the position of the cursor. Position the cursor in the section of interest to see the data.

21. To add a line of best fit to any section, position the cursor in the section of interest, touch to open the Options menu, then touch .

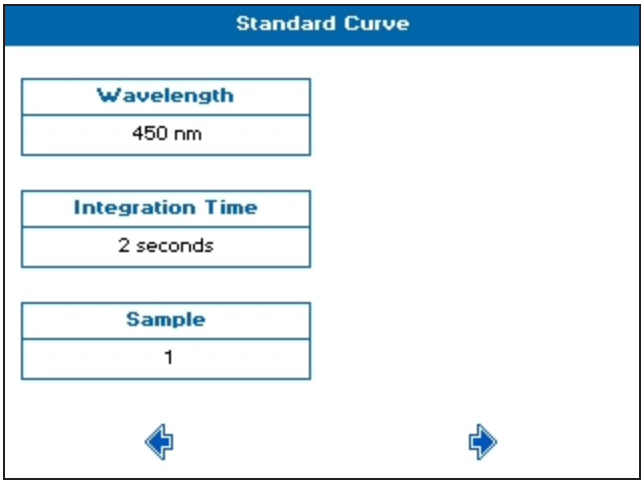
22. To add overlays, do data manipulation, or select saved files, see Trace Manager - Overlay and Manipulate Wavescan and Kinetic Files on page 81.

Standard Curve

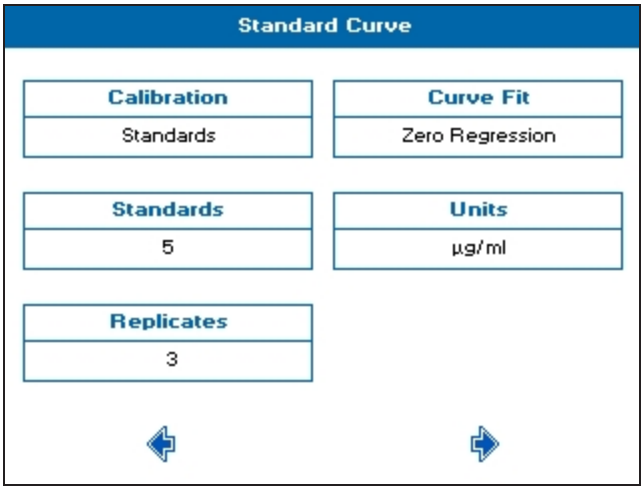
The construction of a multi-point calibration curve from standards of known concentration to quantify unknown samples is a fundamental use of a spectrophotometer. The instrument can store calibration curves with a method. Each calibration curve can be created using up to 9 standards with each standard measurement being made of up to 3 replicates.

To use Standard Curve:

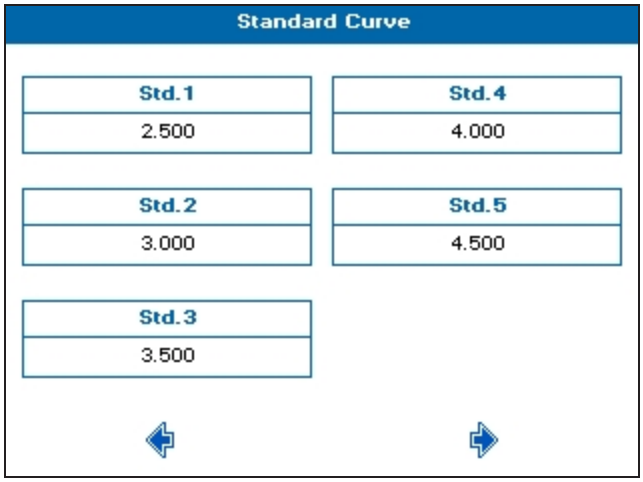
1. From the main screen, touch **Read Type**, then touch **Standard Curve**.
2. Set **Wavelength**, and **Integration Time** as needed.
3. The **Sample Seed** entered under **Sample** becomes the file name used for any data file saved automatically.



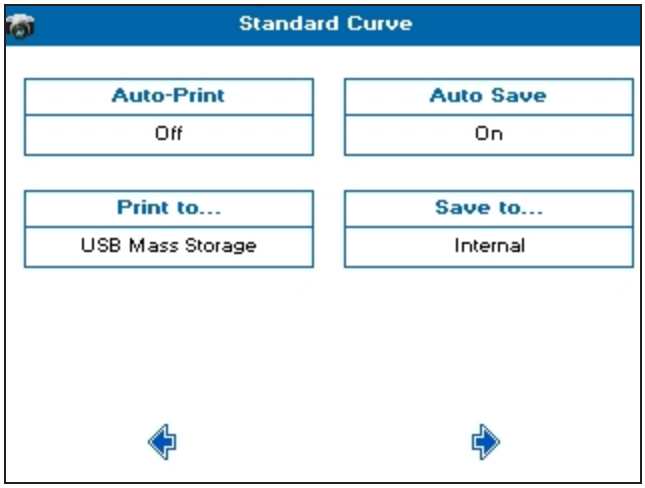
4. When finished setting method parameters, touch to go to the next screen.
5. Set **Calibration** as needed. Choose either **Standards** to prepare and measure standards, or **Manual** to enter both standard concentrations and standard absorbances.
6. Set **Standards**, **Replicates**, **Curve Fit**, and **Units** as needed.



7. When finished setting method parameters, touch to go to the next screen.
8. Set the concentration values for each of the standards.

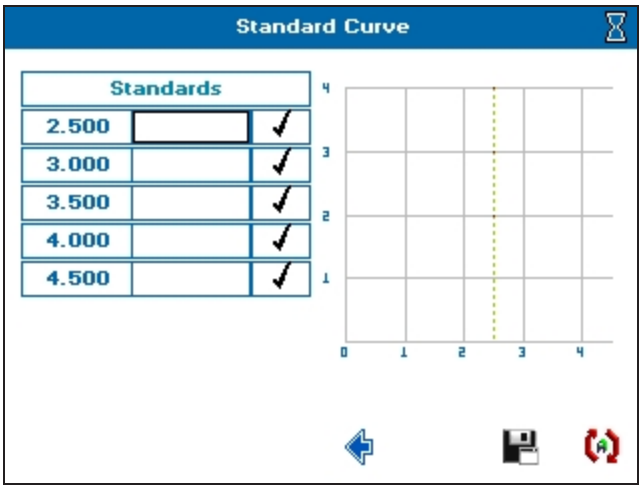


9. When finished setting method parameters, touch to go to the next screen.
10. Set how you want the sample data to be saved. See Save Sample Data on page 77.

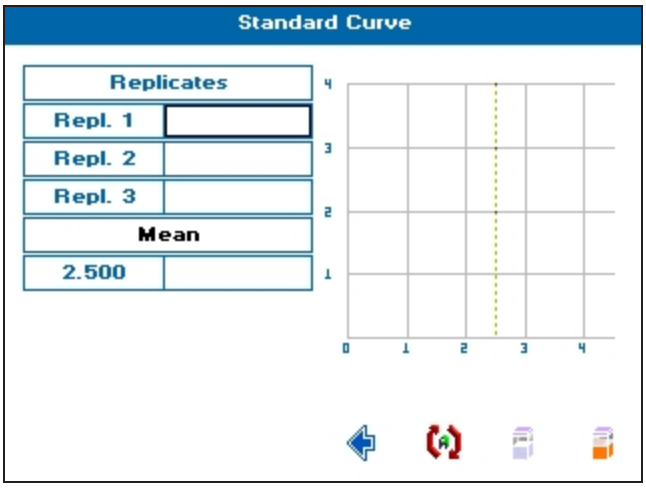


11. When finished setting method parameters, touch to go to the next screen.

12. To save the method before any standards are measured, touch . Recalling the method parameters only requires you to make a standard curve before measuring samples.

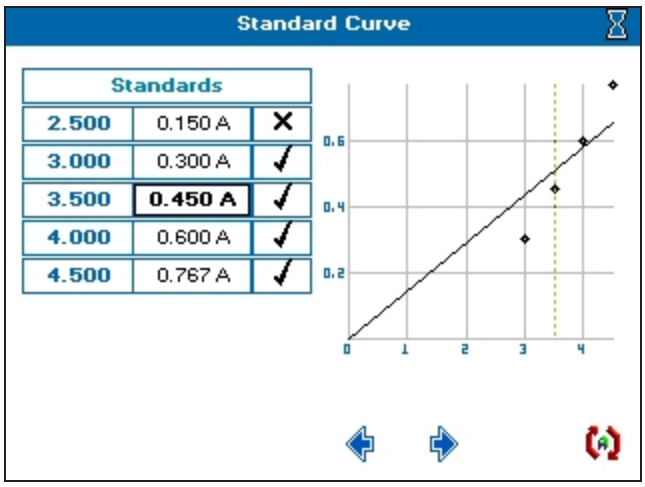


13. To create the standard curve using replicates, touch .

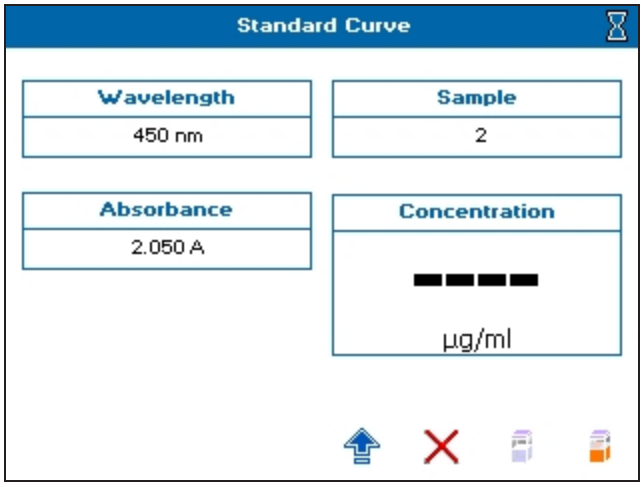


14. To create a standard curve, insert a cuvette containing the reference solution in the cuvette holder, then touch , and wait for the reference measurement to finish.
15. Remove the reference cuvette, replace with a cuvette containing the first standard in the replicate series, then touch to take the measurement.
16. Repeat step 15 until the all of the standards in the replicate series are measured.
17. If needed, to repeat any standard measurement, touch the result box ,insert the cuvette, then touch to take the measurement again.
18. When all replicates have been taken for a particular standard, touch to go to the next standard specified in the method.

19. To ignore any outlying standard measurements, touch the check mark in the needed row to toggle it to an **X**. Any ignored measurement is automatically removed from the standard curve. Ignored measurements can be reinstated by touching the **X** to toggle it back to a check mark.

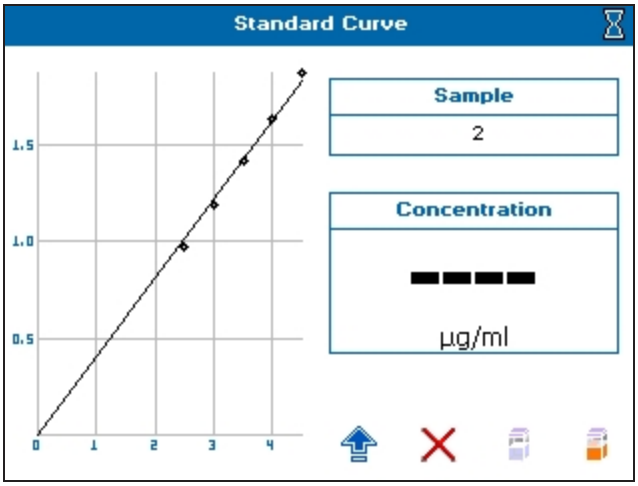


20. Touch to go to the next screen, and take a measurement.



21. See Take Sample Measurements on page 25.

22. To see the Standard Curve on the sample measurement screen, touch to open the Options menu, then touch .



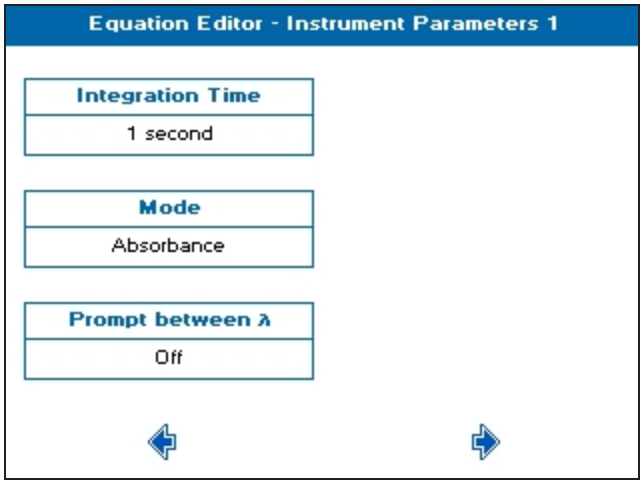
23. To save the method and the standard curve, from the sample measurement screen , touch to open the Options menu, then touch . Recalling a method with method parameters and standard curve lets you measure samples directly.

Equation Editor

The Equation Editor read type lets you create their own unique methods that include calculations and thresholds. Examples of methods that can be created using Equation Editor include percentage strength calculations and calculations for chlorophyll analyses.

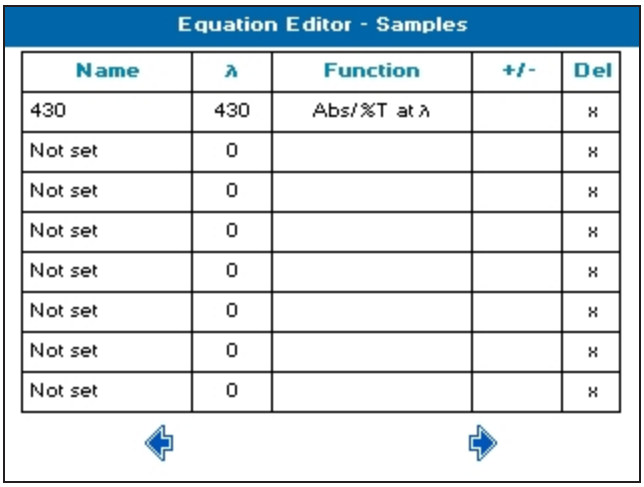
To use Equation Editor:

1. From the main screen, touch **Read Type**, then touch **Equation Editor**.
2. Set **Integration Time** and **Mode** as needed.
3. Set **Prompt between λ** either **On** or **Off**. Use **On** for equations that require wavelength measurements of different samples, like chlorophyll analysis.



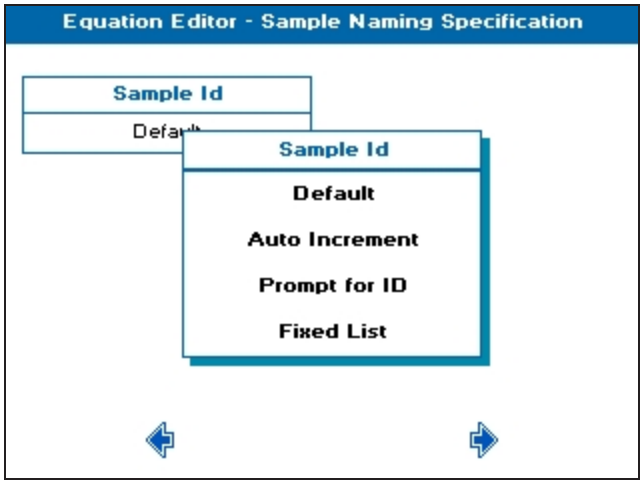
4. When finished setting method parameters, touch to go to the next screen.

5. Enter all the measurements that are required in the method on the **Samples** table screen. Before any data is entered, **Name** shows *Not set* and will not show in the Sample Data list in the Equation Builder. The following explains the data to enter:
   - **Name**—Touch one of the boxes that shows *Not set* and touch-enter a name you need for the measurement. The name entered here is used as the Sample Data in the Equation Builder.
   - **λ**—Touch the box and enter the wavelength value for the measurement named.
   - **Function**—Touch the box, then touch a choice to set. Choices include:
     - **Abs / %T at λ**—The measurement at the wavelength entered by you.
     - **Peak closest to λ**—The instrument automatically finds the peak closest to the entered wavelength.
     - **Valley closest to λ**—the instrument automatically finds the valley closest to the entered wavelength.
   - **+/-**—Only use with the functions **Peak closest to λ** and **Valley closest to λ** to specify the range over which the instrument scans for a peak or valley for the specified wavelength.
   - **Del**—Touch the **X** to delete the row. If the data is used in an equation, it is also be deleted.

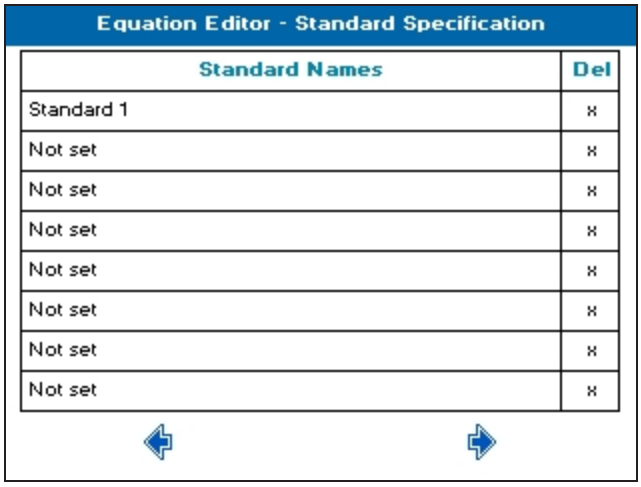


6. When finished setting method parameters, touch to go to the next screen.

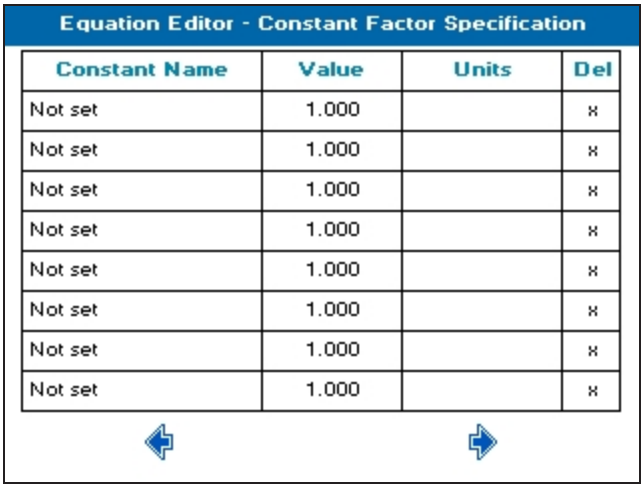
7. From the **Sample Naming Specification** screen, touch **Sample ID**, then touch a choice. Choices include:
   - **Default**—The sample name consists of Sample and an incrementing number.
   - **Auto Increment**—The sample name is a combination of sample seed and an incrementing sample number. You are prompted to enter the sample seed for each new batch of samples.
   - **Prompt for ID**—You are prompted to enter the sample name before running each sample.
   - **Fixed List**—You are prompted to enter the number of samples required. Sample names for each sample are then entered on the subsequent screens. The entered sample names save for each method.



8. When finished setting, touch to go to the next screen.
9. From the **Standard Specification** screen, declare a list of all of the standard solutions that will be referenced when creating an equation. Touch a **Standard Names** row and touch-enter the name. Standard measurements can be made for any measurements specified in the Samples table.

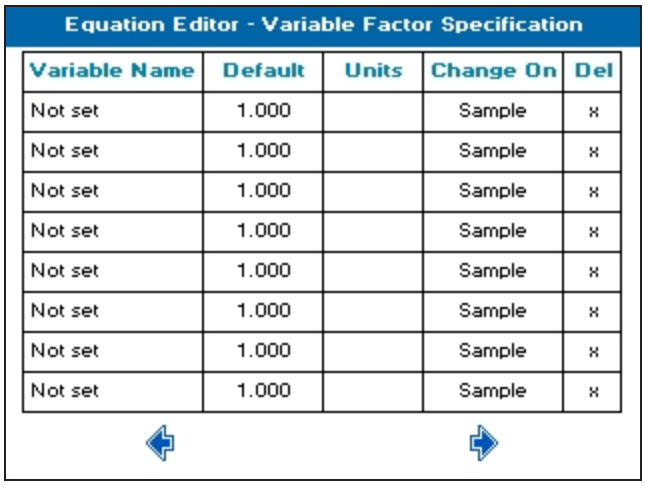


10. When finished setting, touch to go to the next screen.
11. From the **Constant Factor Specification** screen, declare any constants used in the equation. Before any data is entered, **Constant Name** shows *Not set* and will not show in the Constants list in the Equation Builder. The following explains the data to enter:
    - **Constant Name**—Touch one of the boxes that shows *Not set* and touch-enter a name you need for the constant. The name entered here is used as the Constant in the Equation Builder.
    - **Value**—Touch to enter the value of the constant.
    - **Units**—Touch to touch-enter the units for the constant. If this column is left blank, no units show on exported data.
    - **Del**—Touch the **X** to delete the row. If the constant is used in an equation, it is also be deleted.



12. When finished setting, touch to go to the next screen.

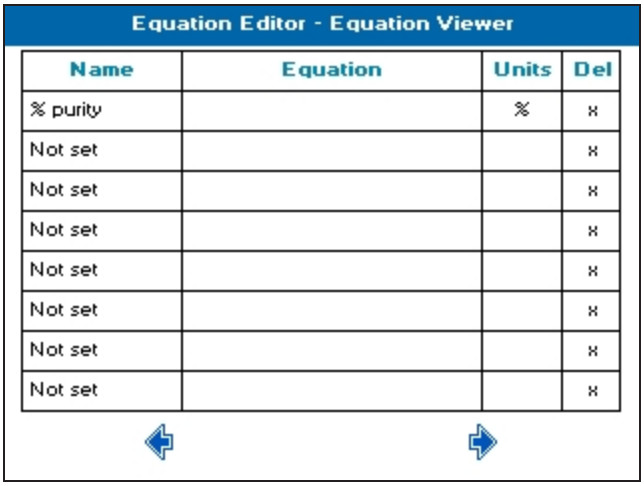
13. From the **Variable Factor Specification** screen, declare any variables used in the equation. Before any data is entered, **Variable Name** shows *Not set* and will not show in the Variables list in the Equation Builder. The following explains the data to enter:
    - **Variable Name**—Touch one of the boxes that shows *Not set* and touch-enter a name you need for the variable factor. The name entered here is used as the Variable in the Equation Builder.
    - **Default**—Touch to enter the default variable factor. Default values can be edited during the measurement.
    - **Units**—Touch to touch-enter the units for the variable factor. If this column is left blank, no units show on exported data.
    - **Change On**—Touch to set either **Sample** or **Batch**.
    - **Del**—Touch the **X** to delete the row. If the variable is used in an equation, it is also be deleted.



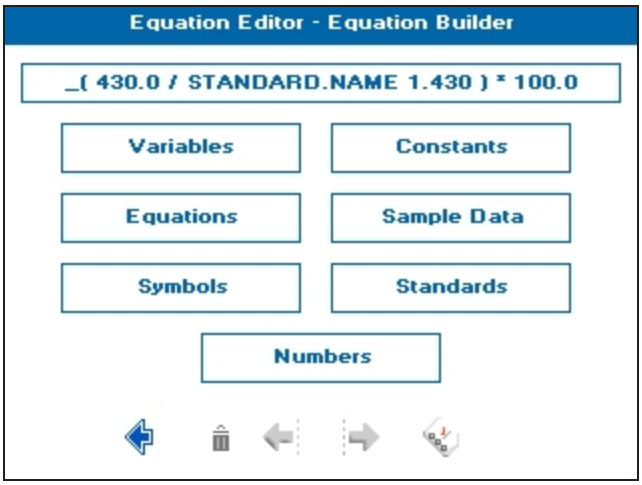
14. When finished setting, touch to go to the next screen.

15. The **Equation Viewer** screen, shows an overview of any equations created, and lets you create new or edit existing equations. Before any data is entered **Name** shows *Not set* and will not show on the results screen. The following explains the data to enter:

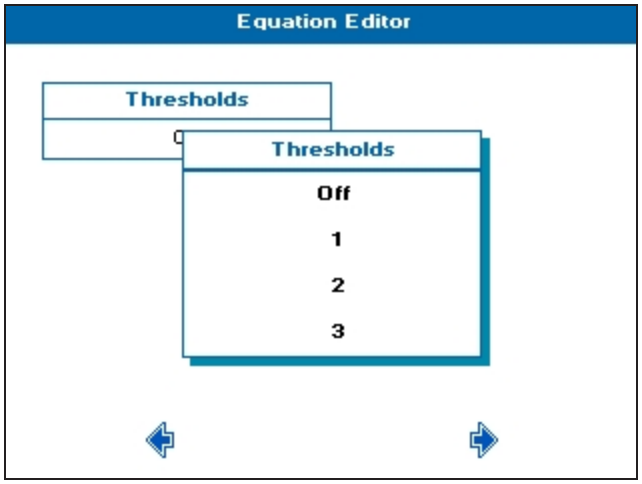
    - **Name**—Touch one of the boxes that shows *Not set* and touch-enter a unique name for the equation so that any equation can be easily identified when using it in other equations. The names entered here show in the equations field on the Equation Builder screen and the results screens.
    - **Equation**—Touch the box in the row you named to open the **Equation Builder** screen. Any equation constructed in the Equation Builder is displayed in this box.
    - **Units**—Touch to touch-enter the units for the result of the equation. If this column is left blank, no units show next to the result.
    - **Del**—Touch the **X** to delete the row and remove the equation.



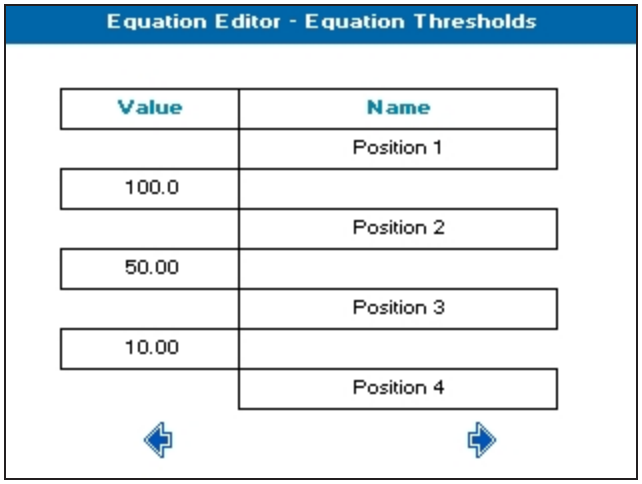
16. Use the **Equation Builder** to create any equations required in the method. Touch the cursor or to specify where the data is to be inserted in the equation field, as needed. If needed, to delete data in the equation field, move the cursors and touch . The following explains the data choices to enter:
    - **Variables**—If needed, to add a variable to the equation field, touch this box, then touch the required variable name choice.
    - **Constants**—If needed, to add a constant to the equation field, touch this box, then touch the required constant name choice.
    - **Equations**—If needed, to add an equation to the equation field, touch this box, then touch the required equation name choice.
    - **Sample Data**—If needed, touch this to show a list that contains all of the readings specified by you in the Sample Measurement table, then touch one of the reading choices to add it to the equation field.
    - **Symbols**—Touch this box to enter logic gates, AND, OR, and mathematical symbols into the equation field.
    - **Numbers**—Touch this box to enter a number into the equation field.



17. If the result needs to be viewed with a specified pass/fail limit, touch to set appropriate thresholds for the measurement. Do the following to set thresholds:
    a. On the first Thresholds screen, touch **Thresholds**, then touch the number of thresholds required for your result, up to 3.



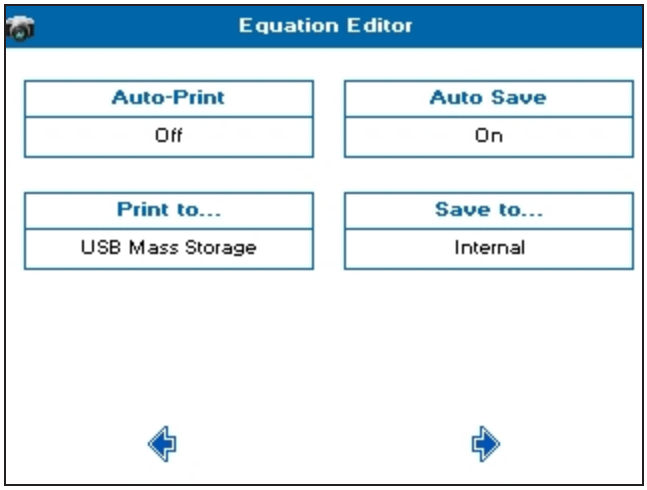
    b. When finished setting, touch to go to the next screen.
    c. On the **Equation Thresholds** screen, a table shows that requires your input. Enter the required **Value** for the threshold, and **Name** for the result.



    d. When finished setting, touch to return to the **Equation Builder** screen.

18. When you finish building the equation, touch to return to the **Equation Viewer** screen, and view the equation you just built in the table row you specified.
19. Repeat steps 5 through 18 as needed until all needed equations are created. Otherwise , when finished setting equations, touch to go to the next screen.

20. Set how you want the sample data to be saved. When the **Sample Naming Specification** is set to **Prompt for ID**, or **Fixed List**, the sample name entered first saves as the file name. See Save Sample Data on page 77.



21. Touch to go to the next screen, and take a measurement.
22. See Take Sample Measurements on page 25.
23. From the measurement results screen, to save the method, touch , then touch .
24. When taking a measurement using a method that includes standards, the first touch of prompts you to insert a specific standard. After all standards have been measured, subsequent touches of takes sample measurements.

Chapter 5: Life Science Read Types

5

Life Science Read Types contain two sub-folders, Nucleic Acids and Protein. The following is an outline of the sub-folders and the contents.

Nucleic Acids

DNA—Uses the absorbance measurements at 230, 260 & 280 nm with optional background correction to perform a concentration and purity check for DNA samples.

RNA—Uses the absorbance measurements at 230, 260 & 280 nm with optional background correction to perform a concentration and purity check for RNA samples.

Oligo—Uses the absorbance measurements at 230, 260 & 280 nm with optional background correction to perform a concentration and purity check for oligo samples.

Cydye DNA—Measures the labeling efficiency of fluorescently labeled DNA probes to ensure that there is sufficient amount of each probe to give satisfactory signals. The DNA yield is measured at 260 nm whilst the incorporation of the dyes is measured at the absorption maxima. This method is also useful for measuring the yields and brightness of fluorescently labeled in-situ hybridization probes.

TM Calc—The Tm Calculation read type calculates the theoretical melting point from the base sequence of a primer. It is done using nearest neighbor thermodynamic data for each base in the nucleotide chain in relation to its neighbor.

Protein

BCA—Quantitative determination of protein concentration using the absorbance measurement at 562 nm

Bradford—Quantitative determination of protein concentration using the absorbance measurement at 595 nm

Lowry—Quantitative determination of protein concentration using the absorbance measurement at 750 nm

Biuret—Quantitative determination of protein concentration using the absorbance measurement at 546 nm

Protein UV— Direct UV determination of protein concentration at 280 nm using the Christian Warburg calculation

Protein A280—Direct UV determination of protein concentration using BSA, IgG, Lysozyme, Molar Extinction. Mass Extinction or E1% calculations

Nucleic Acid Read Types

DNA, RNA and Oligo

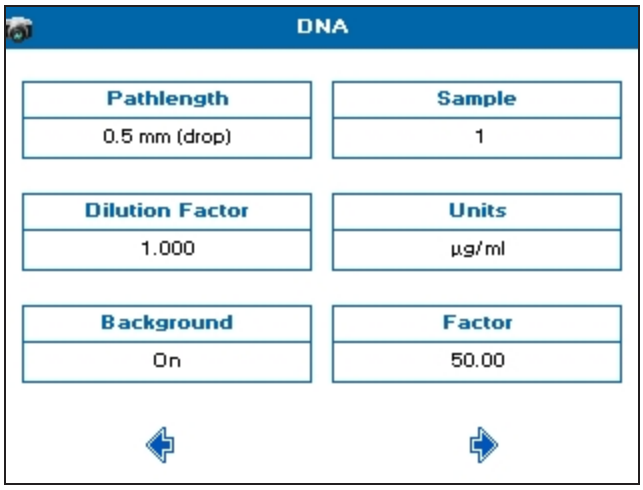
Nucleic acids can be quantified at 260 nm because it is well established that solutions of DNA and RNA in 10 mm pathlength cuvettes with an optical density (absorbance) of 1.0 have concentrations of 50 µg/ml and 40 µg/ml, respectively. Oligonucleotides typically have a factor of 33 µg/ml, although this does vary with base composition and can be calculated if the base sequence is known.

Concentration = A260 × Factor

The instrument uses the default factors 50, 40 and 33 for DNA, RNA and oligonucleotides, respectively. Compensation for dilution and pathlength can also be entered.

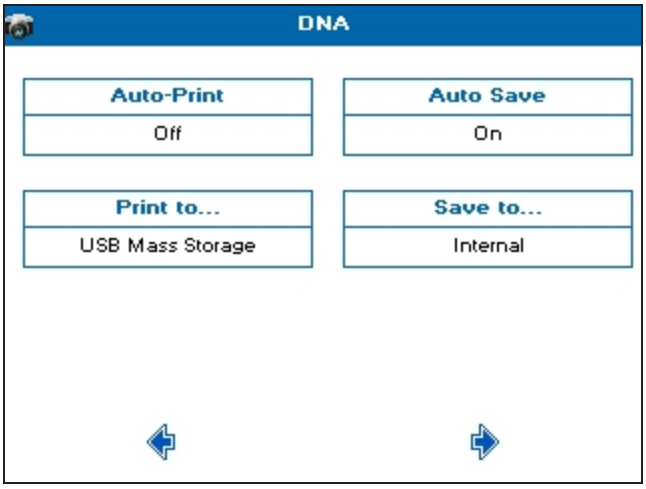
To use DNA, RNA, and Oligo:

1. From the main screen, touch **Life Science**, then touch **Nucleic Acids**, then touch either **DNA**, **RNA**, or **Oligo**.
2. Set **Pathlength** to match the cuvette in use and **Dilution Factor** as needed.
3. If using low-volume cuvettes, set **Background** correction to **On**.
4. Set **Units** to the expected concentration of your samples.
5. The default **Factor** updates automatically depending on the units selected, for example, for units of µg/ml the default factor is 50.00. If the required **Factor** differs from the default value, edit using numeric entry.
6. The **Sample Seed** entered under **Sample** becomes the file name of any saved file.



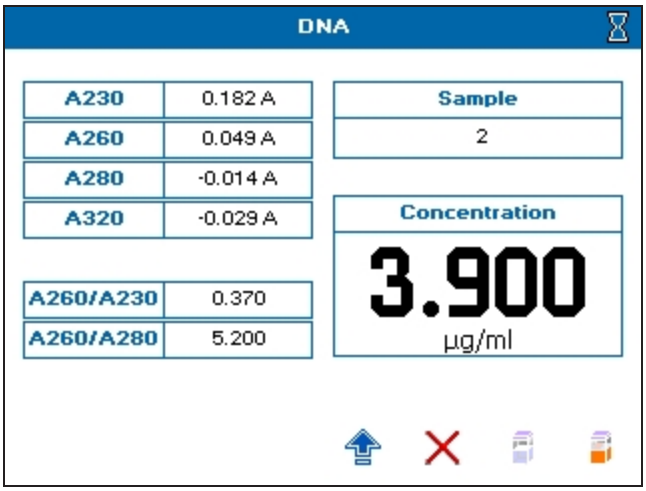
7. When finished setting, touch to go to the next screen.

8. Set the outputs required in your method. For saving methods, see Save and Delete Methods on page 87.



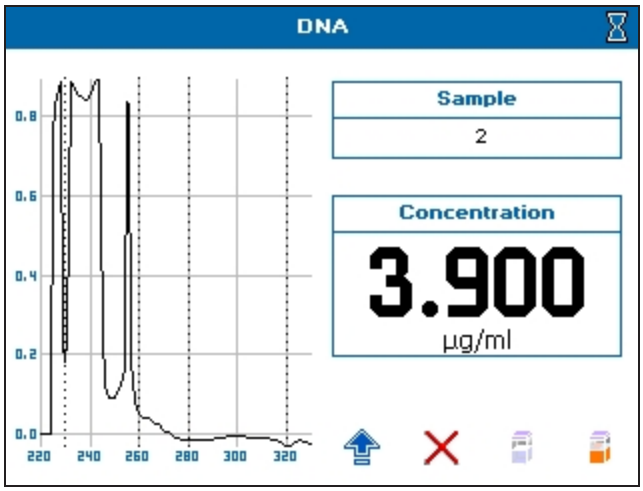
9. Touch to go to the next screen, and take a measurement.

10. See Take Sample Measurements on page 25.



If the **Background** parameter is set to **On**, the A320 result is included in the left results column, and automatically subtracted from the displayed A230, A260, A280, A260/A230, A260/A280 results.

11. To view a scan of the most recently run sample, touch to open the Option menu, then touch to view scan.



Note: When saving sample data, scan files are not saved. The Wavescan read type should be used to save scans of nucleic acid samples.

Nucleic Acid Purity Checks

- Nucleic acids extracted from cells are accompanied by proteins and extensive purification is required to separate these protein impurities. The ratio of A260/A280 gives an indication of a sample's purity, with pure DNA and RNA preparations typically having ratios of ≥ 1.8 and ≥ 2.0, respectively. Deviations from these values indicate the presence of impurities, but care must be taken when interpreting results.
- Concentration also affects both the A260 and A280 readings. If a solution is too dilute, the readings may be at the instrument's detection limit and results may vary as there is less distinction of the A260 peak and A280 slope from the background absorbance. For accurate measurements A260 should always be greater than 0.1.
- Elevated A230 values can also indicate the presence of impurities (230 nm is near the absorbance maximum of peptide bonds and also indicates buffer contamination since EDTA and other buffer salts absorb at this wavelength). When measuring RNA samples, the A260/A230 ratio should be > 2.0. Ratios lower than 2.0 generally indicate contamination with guanidinium thiocyanate, a reagent commonly used in RNA purification and which absorbs over the 230 nm to 260 nm range. A wavelength scan of the nucleic acid is particularly useful for RNA samples.

Background Correction

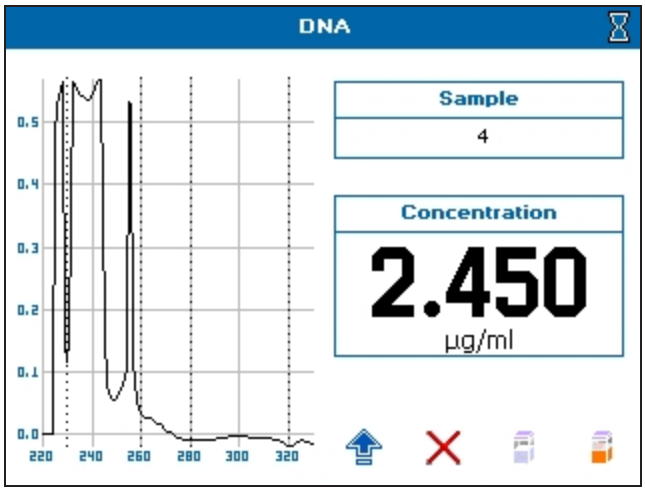
- Compensate for the effects of background absorbance caused by turbibity by using high absorbance buffer solutions, reduced aperture cuvettes, or background correction at 320 nm.
- When used, A320 is subtracted from A260 and A280 prior to use so that:
  Concentration = (A260 - A320) × Factor

  Abs ratio = (A260 - A320) / (A280 - A320)

  Abs ratio = (A260 - A320) / (A230 - A320)
- The use of background correction can remove variability due to handling effects of low-volume disposable cuvettes.

Spectral Scan of Nucleic Acid

An absorbance maximum near 260 nm and absorbance minimum near 230 nm, a flat peak near 260 nm and steep slope at 280 nm and very little absorbance at 320 nm.



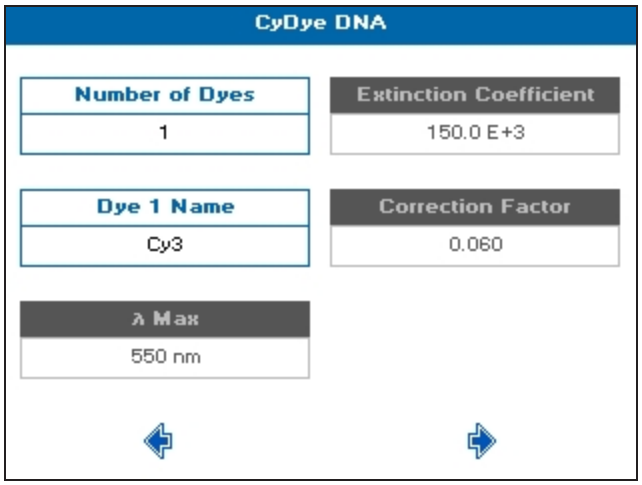
CyDye DNA

The measurement of the labeling efficiency of fluorescently labeled DNA probes before 2-color micro-array hybridization ensures that there is sufficient amount of each probe to give satisfactory signals. The data also provides an opportunity to balance the relative intensities of each fluorescent dye by adjusting the concentration of each probe before hybridization. The DNA yield is measured at 260 nm whilst the incorporation of the dyes is measured at the absorption maxima. This method is also useful for measuring the yields and brightness of fluorescently labeled in-situ hybridization probes.

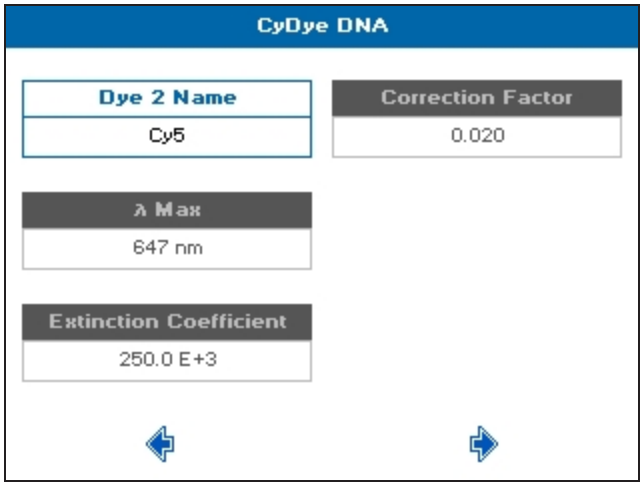
To use CyDye DNA:

1. From the main screen, touch **Life Science**, then touch **Nucleic Acids**, then touch **CyDye DNA**.
2. Set **Number of Dyes** as needed, **1** or **2**.

3. Set **Dye 1 Name** as needed. There are 19 pre-programmed dyes to choose from and a **Custom** option to enter your own.
4. You can only set **λ Max**, **Extinction Coefficient**, and **Correction Factor** if you selected **Custom** as your dye.

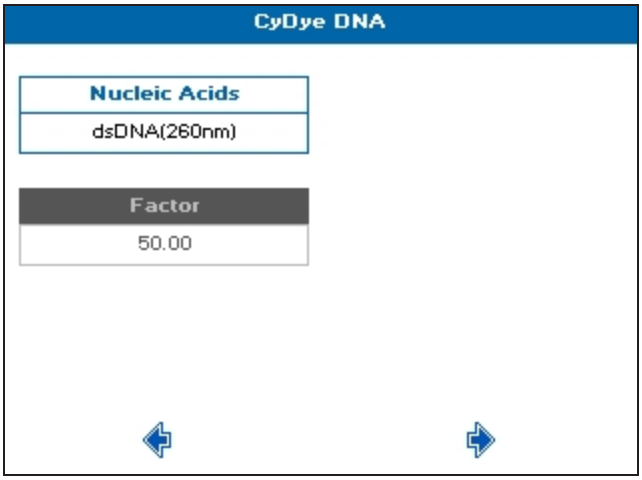


5. When finished setting, touch to go to the next screen.
6. If you set **Number of Dyes** to **2**, the next method parameter screen is for setting **Dye 2 Name**. Set as needed, like **Dye 1 Name**.

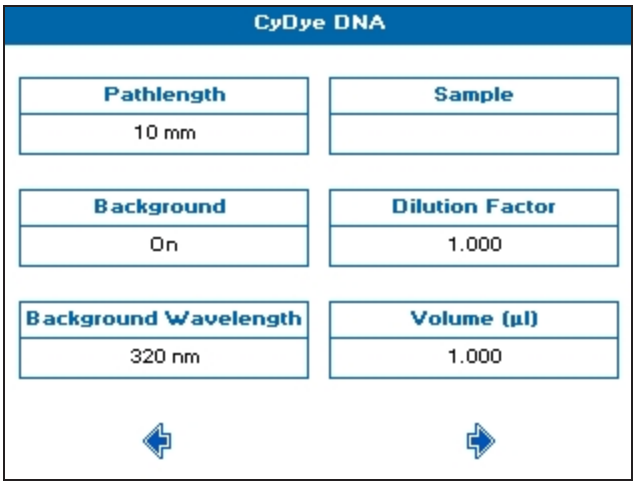


7. When finished setting, touch to go to the next screen.

8. If your measurement requires the calculation of DNA Concentration or DNA Quantity, you can choose the relevant nucleic acid by touching the **Nucleic Acids** box, then choosing from the list. Choose **Custom** if you need to enter a custom factor.

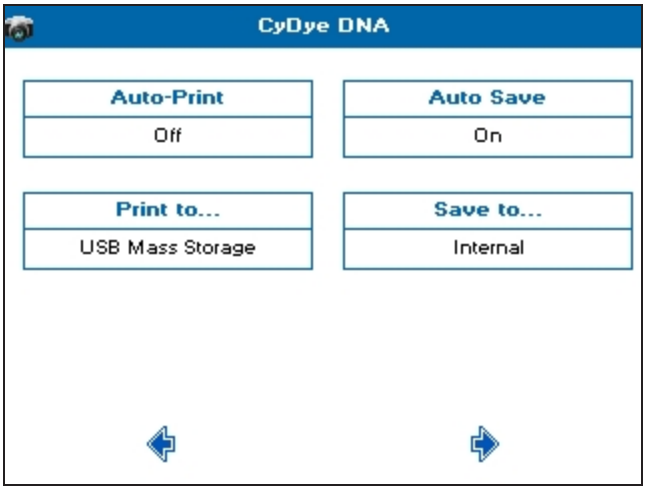


9. When finished setting, touch to go to the next screen.
10. Set **Pathlength** for the cuvette being used. This parameter is used in the calculations.
11. If needed, set **Background Correction** to **On**, then set the **Background Wavelength**. These parameters are used in the calculations.
12. The **Sample Seed** entered under **Sample** becomes the file name of any saved file.
13. Set **Dilution Factor** and **Volume** of the sample as needed in µl. These parameters are used in the calculations.



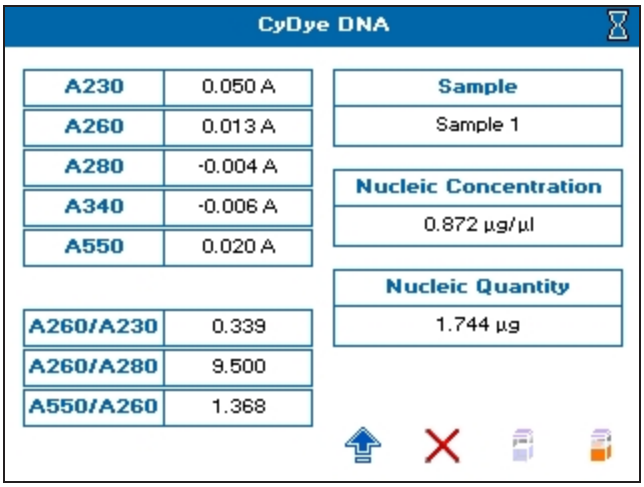
14. When finished setting, touch to go to the next screen.

15. Set the outputs required in your method. For saving methods, see Save and Delete Methods on page 87.



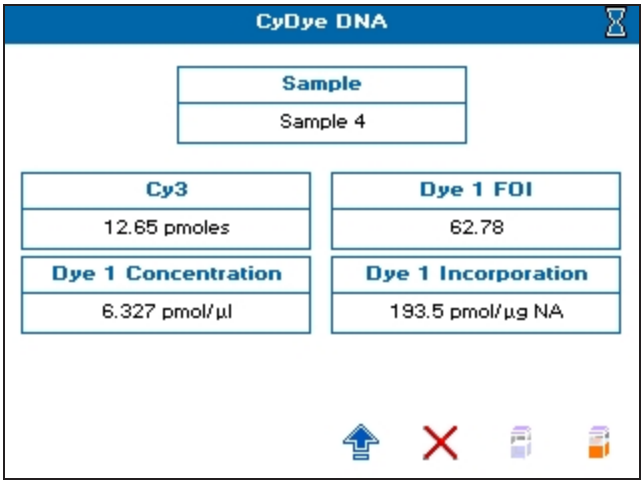
16. Touch to go to the next screen, and take a measurement.

17. See Take Sample Measurements on page 25.

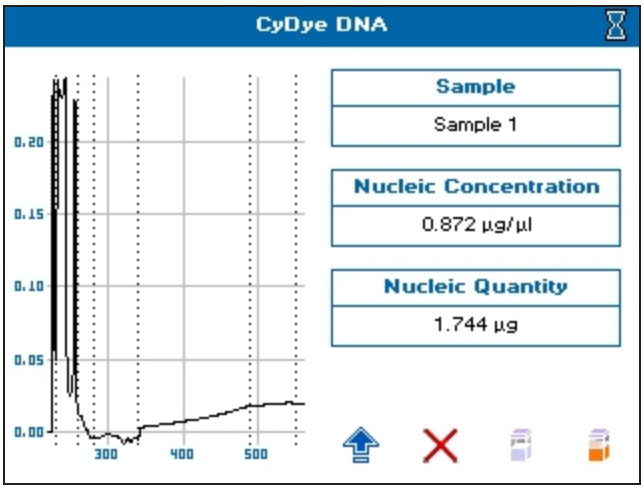


If **Background Correction** is set to **On**, the **Background Wavelength** set in the method is included in the left column in the results and automatically subtracted from all results.

18. To toggle between DNA and dye parameters, touch to open the Option menu, then touch .



19. To view a scan of the most recently run sample, touch to open the Option menu, then touch to view scan.



Tm Calculation

The Tm Calculation read type calculates the theoretical melting point from the base sequence of a primer. It is done using nearest neighbour thermodynamic data for each base in the nucleotide chain in relation to its neighbour (Breslauer et al, *Proc.Natl. Acad. Sci. USA*, 1986, 83, 3746). The data obtained are useful in both the characterisation of oligonucleotides and in calculating Tm for primers used in PCR experiments.

The ACGT/U sequence entered in the method parameters is used to calculate the theoretical Tm, the theoretical absorbance (Absorbance units/mmol) and the conversion factor (mg/ml). This is possible as the stability of a bent and twisted sequence of bases such as an oligonucleotide is dependent on the actual base sequence. These calculated thermodynamic interactions between adjacent base pairs have been shown to correlate well with experimental observations.

The Tm Calculation read type uses matrices of known, published thermodynamic values and extinction coefficients to calculate Tm and the theoretical absorbance/factor of an entered base sequence.

Tm is calculated using the equation:

$$Tm = \frac{\Delta H \times 100}{\Delta S + (1.987 \times \log_e(\mathbf{c}/4 + 53.0822)} - 273.15 + \log \mathbf{[salt]}$$

where ΔH and ΔS are the enthalpy and entropy values, respectively summed from respective 2 × 4 × 4 nearest neighbour matrices

c is the Primer concentration of oligonucleotide (pmoles/ml) in the calculated Tm or the measured concentration in measured Tm. In the latter case, concentration is obtained from the equation:

$$c = \frac{\text{Abs(260 nm)} \times \text{Calculated factor} \times \text{pathlength multiplier} \times 10\,000}{\mathbf{MW}}$$

Calculated factor and MW are defined as:

[salt] is the buffer molarity plus total molarity of salts in the hybridization solution (moles/l).

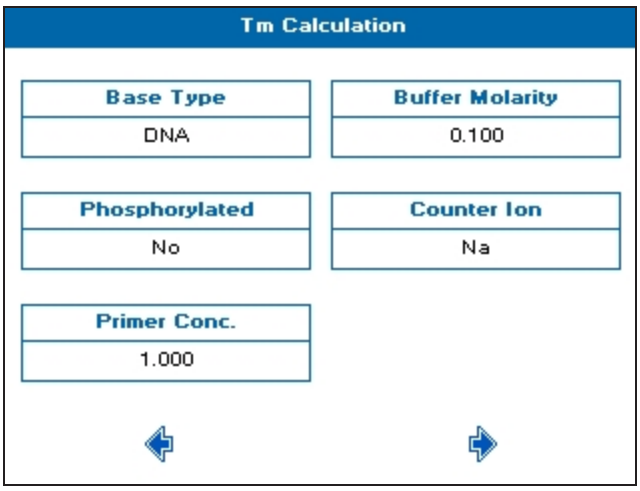
Weights for ΔS are indexed by adjacent paired bases. A similar equation applies to weights for ΔH, again indexed by adjacent bases.

Note: Bivalent salts might need normalizing using a multiplying factor of 100 because of their greater binding power.

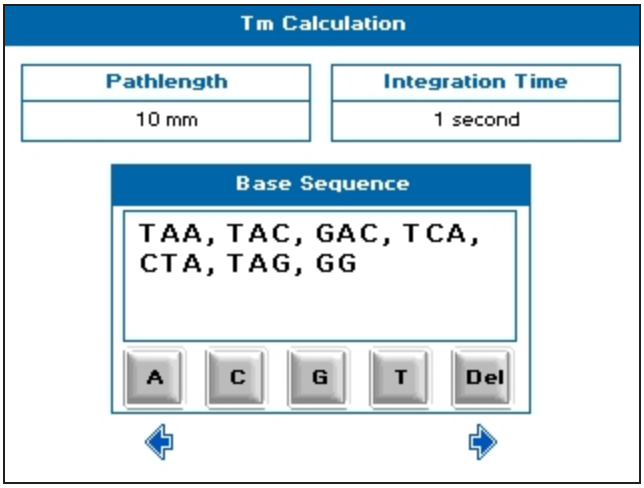
To use Tm Calculation:

1. From the main screen, touch **Life Science**, then touch **Nucleic Acids**, then touch **Tm Calculation**.
2. Set **Base Type** to either **DNA** or **RNA**.
3. Depending on your base, set **Phosphorylated** to **Yes** or **No**.
4. Set **Primer Concentration** as needed in pmoles/ml.
5. Set **Buffer Molarity** as needed.

6. Set **Counter Ion** as needed. Choices include: **Na** (sodium), **K** (potassium), **TEA** (triethylammonium), or **Other** to set the required molecular weight (MW) of the counter ion.

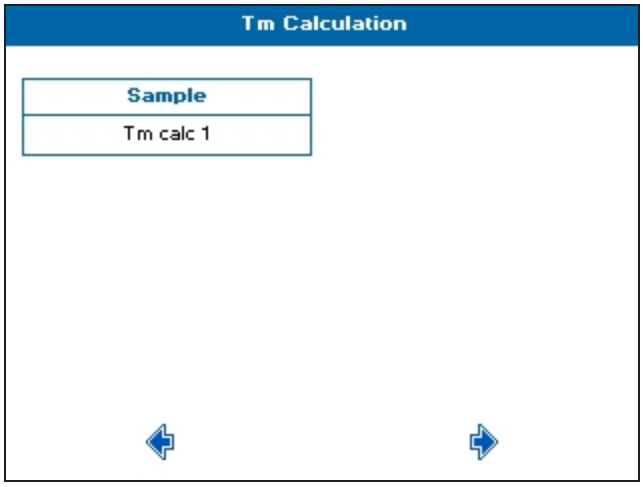


7. When finished setting, touch to go to the next screen.
8. Set **Pathlength** and **Integration Time** as needed.
9. In **Base Sequence**, touch-enter the known base sequence triplets. A comma is automatically added after each triplet.

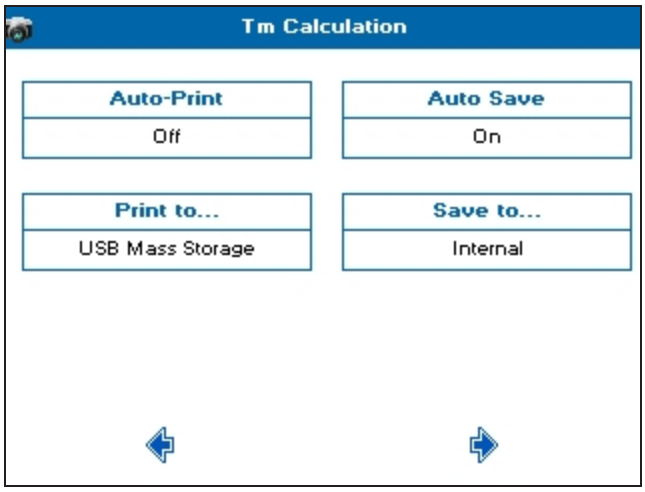


10. When finished setting, touch to go to the next screen.

11. The **Sample Seed** entered under **Sample** becomes the file name of any automatically saved file.

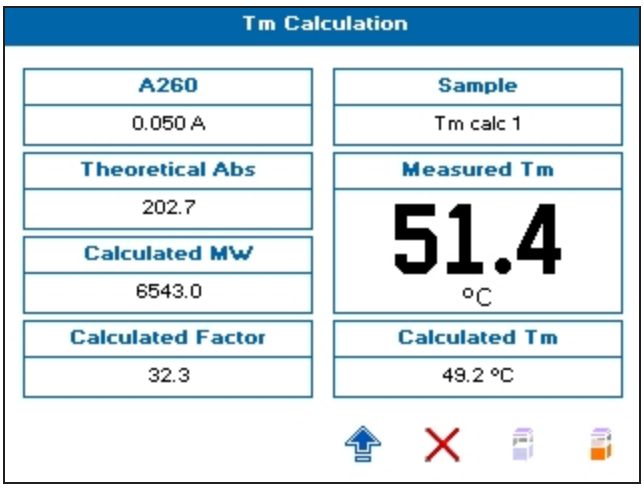


12. When finished setting, touch to go to the next screen.
13. Set the outputs required in your method. For saving methods, see Save and Delete Methods on page 87.



14. Touch to go to the next screen, and take a measurement.

15. See Take Sample Measurements on page 25.



Theoretical Absorbance

The Theoretical Absorbance is based on a calculation as follows:

For each adjacent pair of bases (nearest neighbours) an extinction coefficient weight is accumulated using a 4 × 4 table (one for either DNA or RNA). This total weight is doubled and then for each internal base a counterweight is subtracted using another 1 × 4 table. The end bases are excluded from the latter summation.

Total Extinction Coefficient E = Σ (2 × aTable[base_type][base(n)][base(n+1)])- Σ(tTable[base_type][base(n]])

Conversion Factor

The Conversion Factor is given by = $\frac{\text{Molecular weight}_{ABCDE}}{\Sigma_{EABCDE}}$

where E_{ABCDE} = [2 × (EAB +EBC +ECD +EDE) –EB –EC –ED]

The molecular weight (MW) of a DNA oligonucleotide is calculated from:

MW (g/mole) = [(dA × 312.2) + (dC × 288.2) + (dG × 328.2) + (dT × 303.2.)] + [(MWcounter-ion) × (length of oligo in bases)]

(for RNA oligonucleotide, (dT × 303.2) is replaced by (dU × 298.2)

The MW calculated using this equation must be adjusted for the contribution of the atoms at the 5’ and 3’ ends of the oligo.

For phosphorylated oligos— Add [17 + (2 × MW of the counter-ion)]

For non-phosphorylated oligos— Subtract [61 + (MW of the counter-ion)]

The MW (g/mole) of the most common oligo counter ions are:

- Na (sodium)—23.0
- K (potassium)— 39.1
- TEA (triethylammonium)—102.2
- Other—Defaults to 1.0 (variable 0.1–999.9)

Calculated molecular weight— a weight is added for each base looked up from a table. The weight of the counter ion is added for every base from a small table for the known ions. If phosphorylated, then the system adds 17.0 plus two counter ions otherwise it subtracts 61.0 and one ion.

Theoretical Absorbance— for each adjacent pair of bases (nearest neighbours) a weight is accumulated using a table. For each internal base a weight is subtracted using another table. Separate tables are used for DNA and RNA.

Calculated factor— this is the calculated molecular weight divided by the theoretical absorbance.

Protein Read Types

The instrument provides dedicated methods for both colorimetric protein assays and direct UV measurements.

BCA, Bradford, Lowry and Biuret Protein Assays

The BCA, Bradford, Lowry and Biuret protein assays are well established spectrophotometric methods for determining the amount of protein in a sample. The exact choice of the assay depends upon the concentration of protein being measured and the detergents or reducing agents used in purification. Detailed protocols are supplied with all assay kits and should be followed closely to ensure accurate results. An outline of protein assays in the instrument include:

- **Bradford** method— Quantifies the binding of the dye Coomassie Brilliant Blue to an unknown protein and compares this binding to that of different, known concentrations of a standard protein at 595 nm. The standard protein is usually bovine serum albumin (BSA).
- **Biuret** method— Depends on reaction between Cu^{2+} ions and amino acid residues in an alkali solution. The resulting copper complex absorbs light at 546 nm.
- **BCA** method— Depends on reaction between Cu^{2+} ions and amino acid residues. In addition, this method combines this reaction with the enhancement of Cu^{+} ion detection using bicinchoninic acid (BCA) as a ligand, giving an absorbance maximum at 562 nm. The BCA process is less sensitive to the presence of detergents used to break down cell walls.

- **Lowry** method—Depends on quantifying the color obtained from the reaction of Folin-Ciocalteu phenol reagent with the Tyrosyl residues of an unknown protein and comparing with those derived from a standard curve of a standard protein at 750 nm (usually BSA).

Determine Protein Concentration Using the BCA Protein Assay

The principle of the bicinchoninic acid (BCA) protein assay relies on the formation of a Cu^{2+}-protein complex under alkaline conditions, followed by reduction of the Cu^{2+} to Cu^{+}. The amount of reduction is proportional to the amount of protein present. BCA forms a purple-blue complex with Cu^{+} in alkaline environments, thus providing a basis to monitor the reduction of alkaline Cu^{2+} by proteins. The BCA assay can be used to quantify proteins in the concentration range 0.2 to 1.0 mg/ml. It is compatible with many detergents but not compatible with reducing agents such as dithiothreitol above 1 mM.

Get Started

Prepare the standard in the same buffer as the sample to minimize any interference effects. BCA assays are typically measured at 37 °C. Color development begins immediately and can be accelerated by incubation at higher temperatures. Higher temperatures and/or longer incubation times can be used for increased sensitivity.

Materials Required

- Bicinchoninic Acid Kit for Protein Determination
- Suitable tubes with caps to hold and mix 2.1 ml samples and to heat at up to 60 °C
- Plastic disposable cuvettes
- Standard protein solution of known concentration (1 mg/ml)
- Incubator or block heater to heat sample tubes

Prepare the BCA Working Reagent

BCA reagents A and B are available commercially from a number of different sources. Instructions given here are for the kit supplied by Sigma Aldrich, other methods will be similar. Refer to the manufacturer's instructions.

1. Mix 50 parts of Reagent A (a solution containing bicinchoninic acid, sodium carbonate, sodium tartrate and sodium bicarbonate in 0.1N NaOH, pH 11.25) with 1 part of Reagent B (4% (w/v) $_{CuSO4}.5H_2O$), preparing sufficient reagent for all the standards and samples. 2 ml of working reagent is required for each sample.
2. Mix until the solution is a uniform light green color. The solution is stable for 1 day.

Prepare Standard

1. Prepare a series of protein standards ranging in concentration from 0.2 to 1.0 mg/ml such that the final volume for the assay is 0.1 ml. The instrument can measure up to 9 standards and up to 3 replicates.

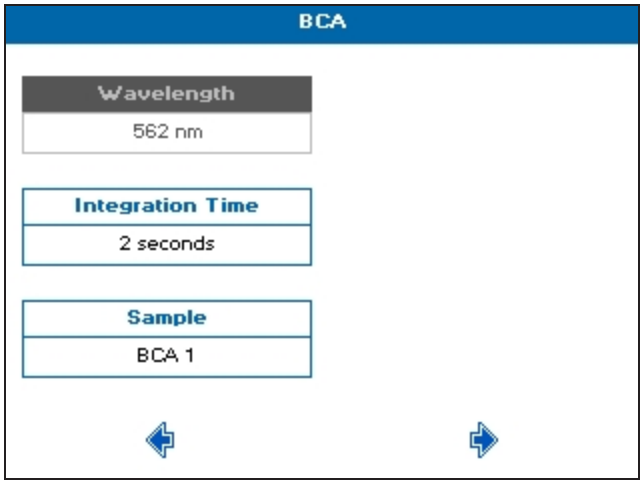
2. Add 2.0 ml of the BCA working reagent to each standard, vortex gently and incubate using one of the following parameters: 60 °C for 15 minutes, 37 °C for 30 minutes or room temperature from 2 hours to overnight.
3. If required, allow the tubes to cool to room temperature.

Prepare Sample

1. Prepare the unknown samples as described above ensuring that the final volume is 0.1 ml.
2. Add 2.0 ml of the BCA working reagent to each sample, vortex gently and incubate using one of the following parameters: 60 °C for 15 minutes, 37 °C for 30 minutes or room temperature from 2 hours to overnight.
3. If required, allow the tubes to cool to room temperature.

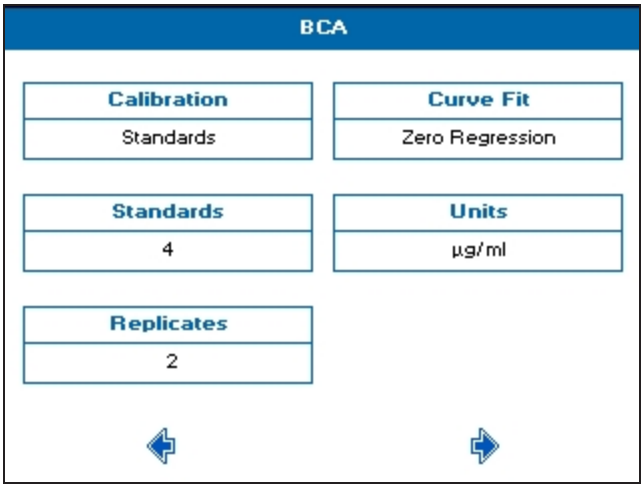
Create Standard Curves

1. From the main screen, touch **Life Science**, then touch **Protein**, then touch **BCA**.
2. **Wavelength** is set to 562 nm. Set **Integration Time** as needed.
3. The **Sample Seed** entered under **Sample** becomes the file name of any saved file.

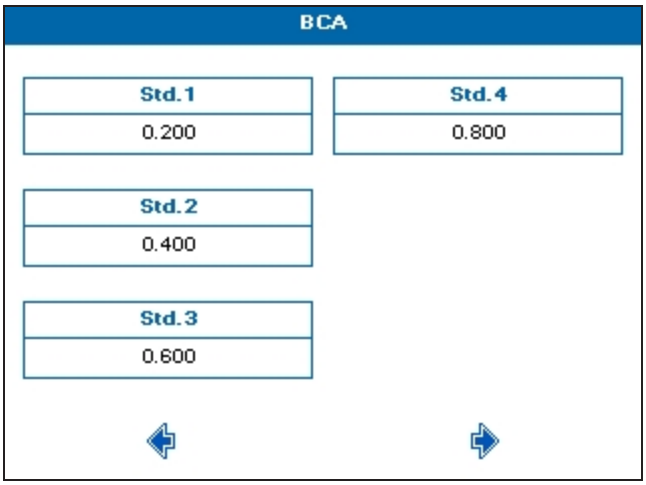


4. When finished setting, touch to go to the next screen.
5. Set **Calibration** to **Standards**. With **Calibration** set to **Manual**, you have to enter both the standard concentrations and the absorbances.
6. Set **Curve Fit** to **Zero Regression**.
7. Set **Units** to **mg/ml**.

8. Set **Standards** and **Replicates** as needed. For optimum accuracy, set the number of standards to 4 or more, and set replicates to more than 1.

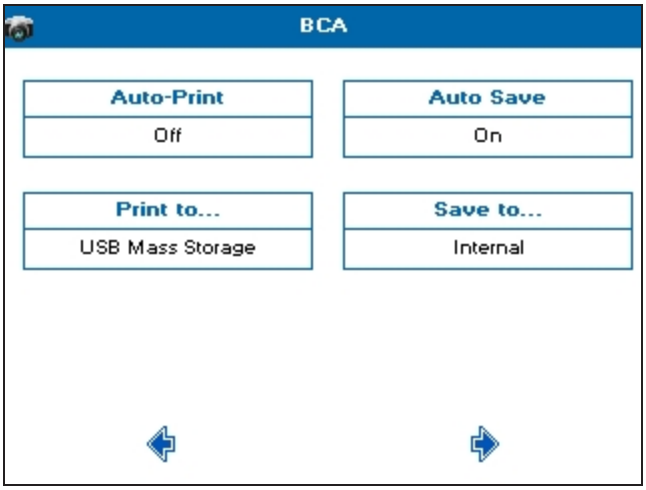


9. When finished setting, touch to go to the next screen.
10. Enter the concentration of your prepared standards.



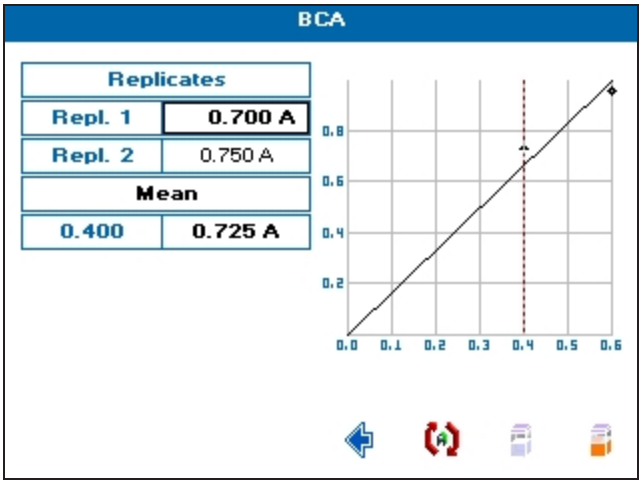
11. When finished setting, touch to go to the next screen.

12. Set the outputs required in your method. For saving methods, see Save and Delete Methods on page 87.



13. When finished setting, touch to go to the next screen.

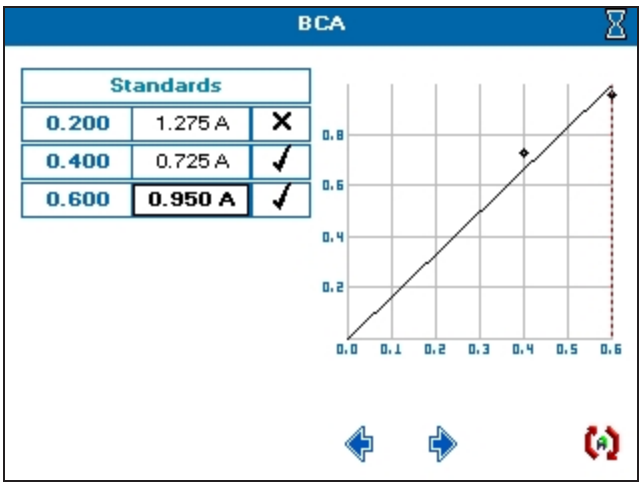
14. To create the standard curve using replicates, touch .



15. To create a standard curve, insert a cuvette containing the reference solution in the cuvette holder, then touch , and wait for the reference measurement to finish.

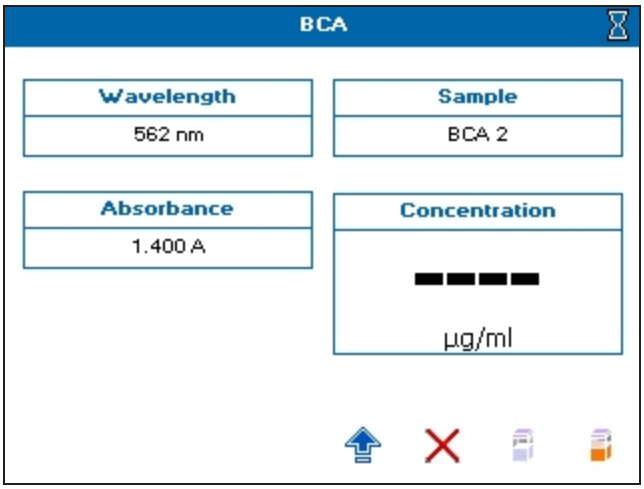
16. Remove the reference cuvette, replace with a cuvette containing the first standard in the replicate series, then touch to take the measurement.

17. Repeat step 16 until the all of the standards in the replicate series are measured.



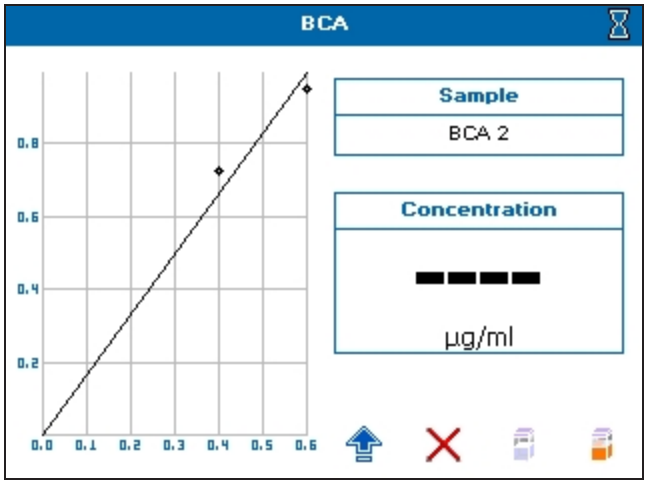
18. To ignore any outlying standard measurements, touch the check mark in the needed row to toggle it to an **X**. Any ignored measurement is automatically removed from the standard curve. Ignored measurements can be reinstated by touching the **X** to toggle it back to a check mark.

19. Touch to go to the next screen, and take a measurement.



20. See Take Sample Measurements on page 25.

21. To see the standard curve on the sample measurement screen, touch to open the Options menu, then touch



22. To save the method and the standard curve, from the sample measurement screen , touch to open the Options menu, then touch . Recalling a method with method parameters and standard curve lets you measure samples directly.

Determine Protein Concentration Using Direct UV Methods

The direct UV method of protein determination has a number of advantages over traditional colorimetric assays in that it does not rely on an external protein standard and the sample is not consumed in the assay. However the presence of nucleic acid in the protein solution can have a significant effect due to strong nucleotide absorbance at 280 nm. This can be compensated by measuring A260 and applying the Warburg and Christian equationfor the protein crystalline yeast enolase (Equation 1).

Protein concentration (mg/ml) = (1.55 × Abs280) – (0.76 × Abs260) **1**

Protein concentration = (Factor 1 × Abs280) - (Factor 2 × Abs260) **2**

The instrument uses default A260 and A280 factors of 0.76 and 1.55, respectively. These factors can be edited so that the equation can be applied to other proteins (Equation 2). Compensation for background, dilution and pathlength can also be entered.

To customize Equation 2 for a particular protein, the A260 and A280 values should be determined at known protein concentrations to generate simple simultaneous equations, which, when solved provides the two coefficients. In cases where Factor 2 is found to be negative, it should be set to zero since it means there is no contribution to the protein concentration due to absorbance at 260 nm.

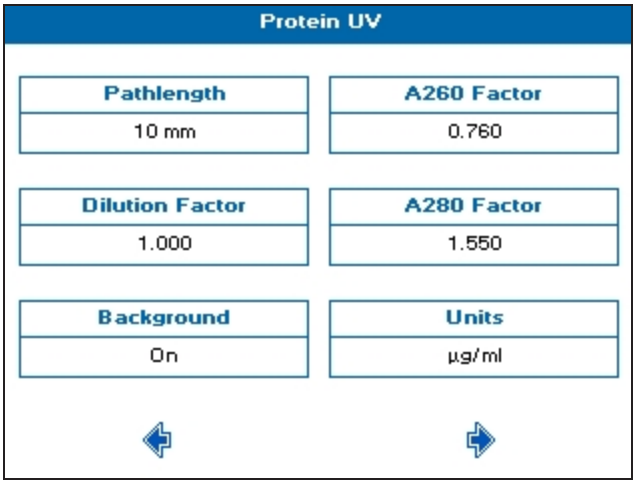
The A260/A280 ratio also gives an indication of protein purity; a ratio of 0.57 can be expected for pure protein samples.

Background Correction

- To compensate for the effects of background absorbance caused by turbidity, high absorbance buffer solutions and the use of reduced aperture cuvettes the instrument can use background correction at a 320 nm.
- When used A320 is subtracted from A260 and A280 prior to use so that:
  Protein concentration = [Factor 1 ×(Abs 280 - Abs 320)] - [Factor 2 ×(Abs 260 - Abs 320)]
  Ratio = (Abs 260 - Abs 320) / (Abs 280 - Abs 320)
- The use of background correction can remove variability due to handling effects of low-volume disposable cuvettes.

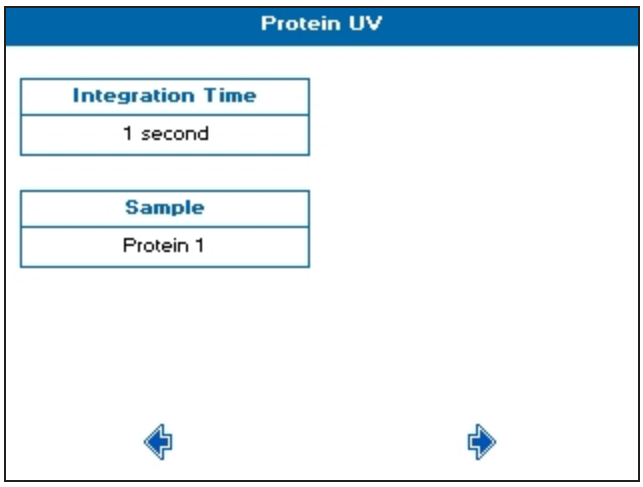
Create Protein UV Measurements

1. From the main screen, touch **Life Science**, then touch **Protein**, then touch **Protein UV**.
2. Set **Pathlength** and **Dilution Factor** as needed.
3. If needed, set **Background Correction** to **On**.
4. The default value for **A260 Factor** is 0.760, and the default value for **A280 Factor** is 1.550. Change these values as needed.
5. Set **Units** to the expected concentration of your samples.

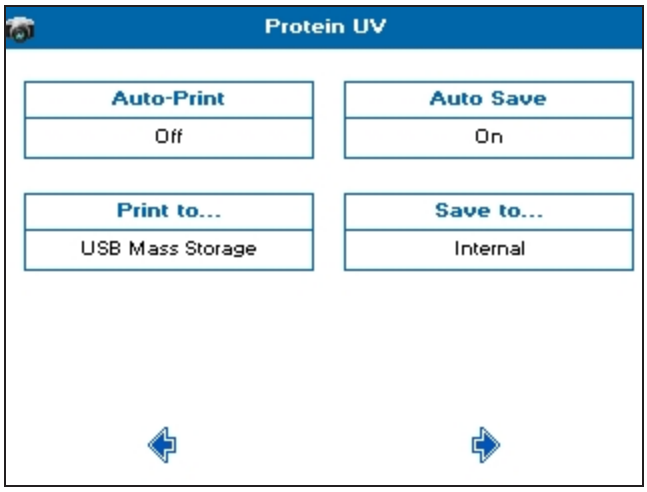


6. When finished setting, touch to go to the next screen.
7. Set **Integration Time** as needed.

8. The **Sample Seed** entered under **Sample** becomes the file name of any saved file.

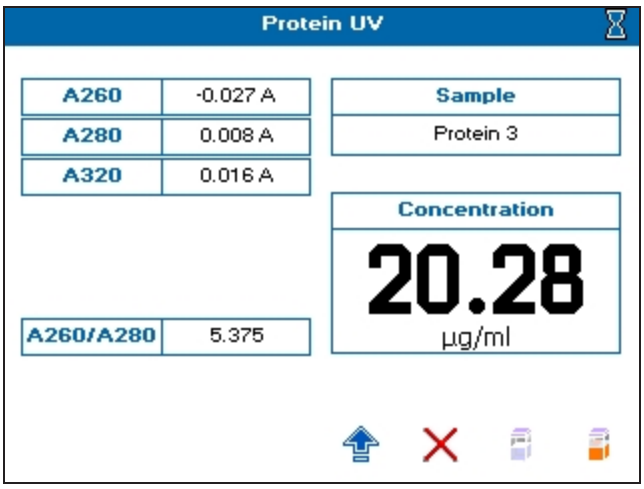


9. When finished setting, touch to go to the next screen.
10. Set the outputs required in your method. For saving methods, see Save and Delete Methods on page 87.



11. Touch to go to the next screen, and take a measurement.

12. See Take Sample Measurements on page 25.

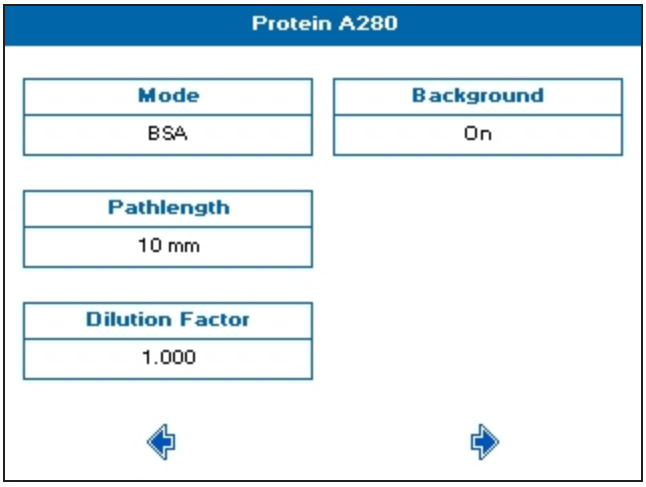


If the **Background** parameter is set to **On**, the A320 result is included in the left results column, and automatically subtracted from the displayed A230, A260, A280, A260/A230, A260/A280 results.

Protein A280

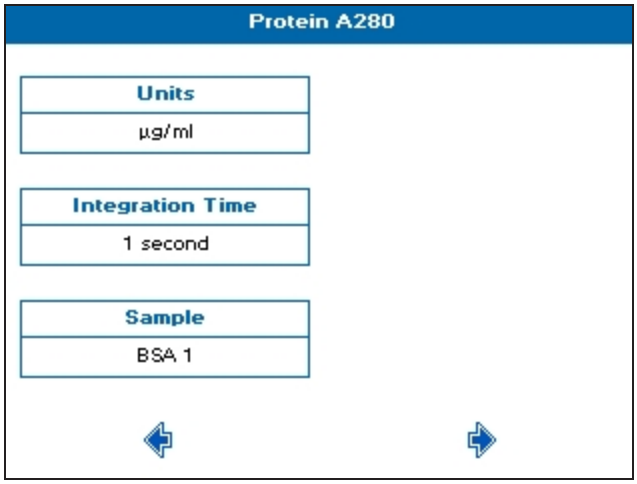
To create a Protein A280 measurement:

1. From the main screen, touch **Life Science**, then touch **Protein**, then touch **Protein A280**.
2. Set **Mode** as needed. Choices include: **Christian Warburg**, **BSA**, **IgG**, **Lysozyme**, **Molar Extinction**, **Mass Extinction**, and **E 1%**.
   If you choose **Molar Extinction**, you must also enter the molar extinction coefficient, and molecular weight and atomic units for Mass Extinction.
3. Set **Pathlength** and **Dilution Factor** as needed.
4. If needed, set **Background Correction** to **On**.

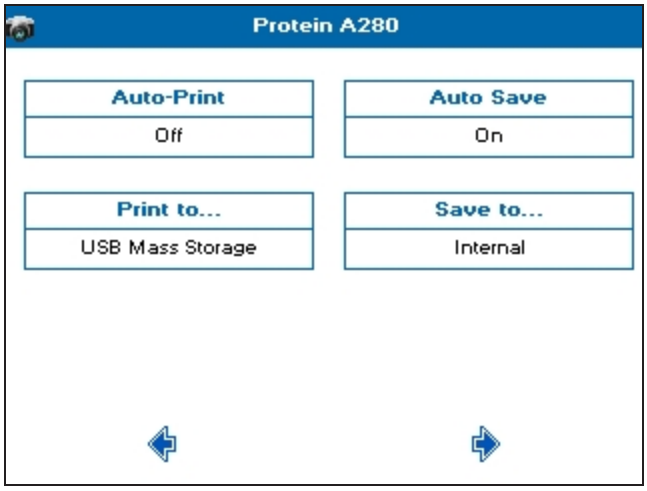


5. When finished setting, touch to go to the next screen.

6. Set **Units** to the expected concentration of your samples.
7. Set **Integration Time** as needed.
8. The **Sample Seed** entered under **Sample** becomes the file name of any saved file.

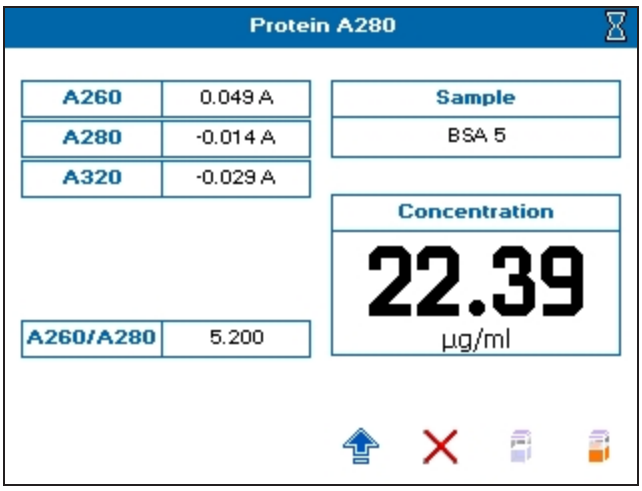


9. When finished setting, touch to go to the next screen.
10. Set the outputs required in your method. For saving methods, see Save and Delete Methods on page 87.

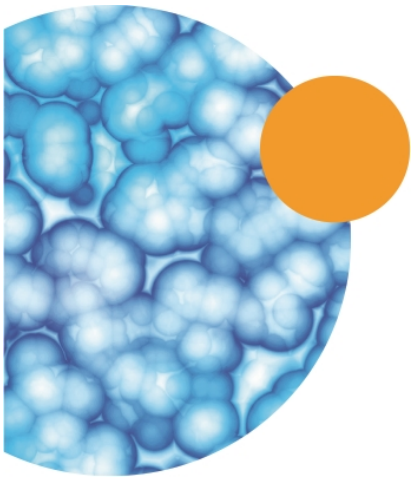


11. Touch to go to the next screen, and take a measurement.

12. See Take Sample Measurements on page 25.



If the **Background** parameter is set to **On**, the A320 result is included in the left results column, and automatically subtracted from the displayed A230, A260, A280, A260/A230, A260/A280 results.

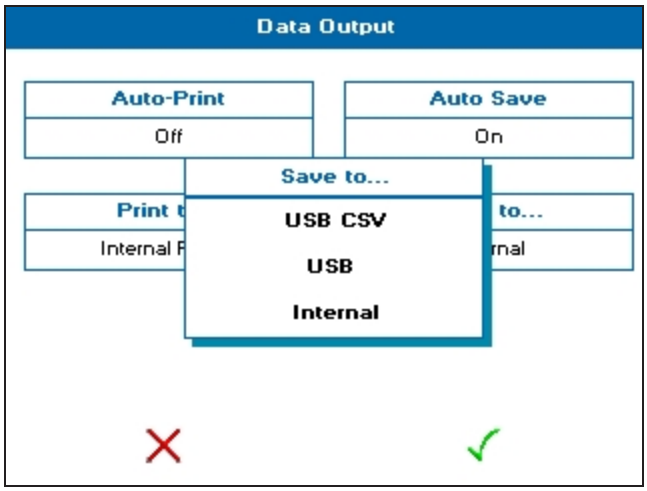


Chapter 6: Save Sample Data

6

The instrument can save sample data either in internal instrument memory or on a USB flash drive. Sample data can be saved within the different read types or globally for all read types from **Data Output** in **Settings**.

In **Settings**, using **Data Output**, you can set up your global sample data saving preference that sets the sample data saving preference for all read types.



You can set **Auto-Save** to be on or off for all read types. You can also set **Save to** preferences for all read types. You can only choose the **USB**, or **USB CSV** preferences if a USB flash drive is plugged in to the USB port on the left side of the instrument, otherwise sample data saves to **Internal** instrument memory by default. Sample data saved on the instrument is saved in the internal instrument memory format that is viewed using the **Sample Manager**. See Sample Manager on page 78.

CAUTION! When data is being written to the USB flash drive the LED above the power button lights. Do not remove the flash drive when the LED is lit because data can get corrupted. If you have finished your set of measurements, exit the read type to close the file on the flash drive.

If you change settings on the **Data Output** screen, touch ✓ to save your changes. To exit the screen without saving changes, touch ✗.

USB CSV

The data is saved to a USB flash drive in comma separated variable (CSV) format allowing it to be opened directly using Microsoft Excel or other similar programs. Files in this format cannot be opened using the instrument.

To view the data displayed in the File Created, Date and Time cells in a recognized format, you must format the cells as follows:

File Created— Right-click in the appropriate cell and select **Format Cells** from the list. Select **Custom** *dd/mm/yyyy h:mm* from the list on the right side, then select **OK**.

Date and Time— Right-click in the appropriate cell, and select **Format Cells** from the list. Under **Category**, select **Date** or **Time**, select the format from the list on the right hand side, then select **OK**.

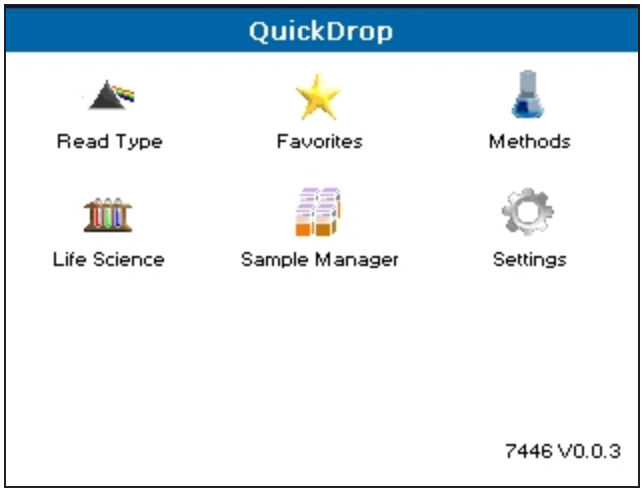
USB

The sample data is saved to a USB flash drive in a format that can be read by the QuickDrop Spectrophotometer only.

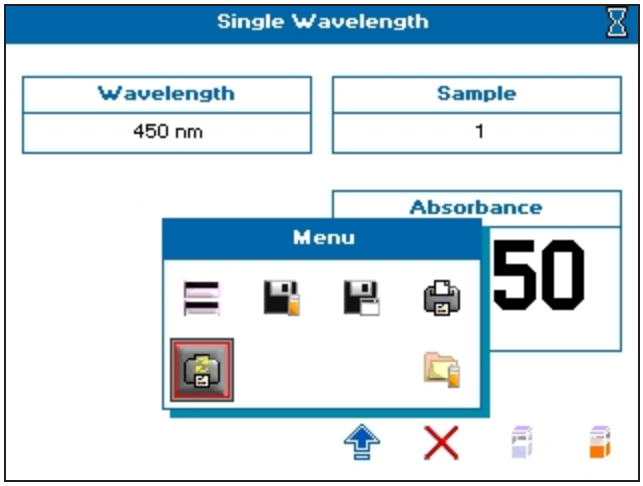
Note: Sample data is saved to the **Samples** directory on the USB flash drive. If this directory has not been created already, it will be created automatically.

Sample Manager

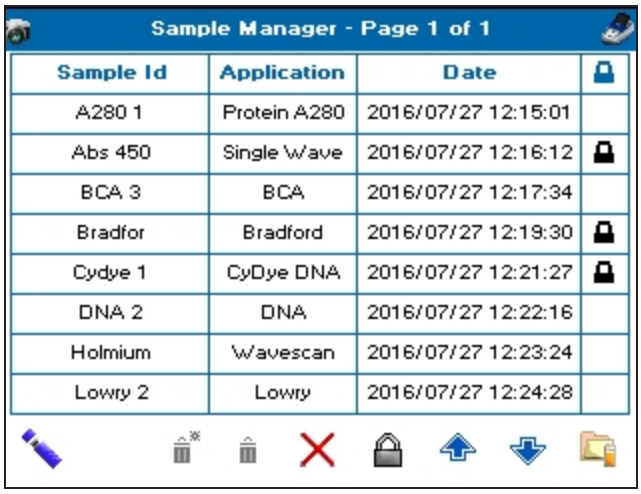
The **Sample Manager** enables you to save and recall sample data from the internal instrument memory and the USB instrument format. Sample Manager can be opened from either the main screen or from within a read type by opening the Options menu and touching the Sample Manager icon.



When you open **Sample Manager** within a read type, only saved sample data for that read type is listed. You can open the saved data files to review them, or from the list screen, you can lock, or unlock, and delete sample data files.



Sample Manager stores 100 sample data files and displays a list of 8 rows per screen. When there is a lot of saved data, to scroll through the list screens, touch the and arrows .The screen title bar indicates the total number of stored pages in the list, and on which page you are looking. You should periodically delete or move, using a USB flash drive, old or unneeded data so that you stay under the 100 file storage limit. The icon on the top right corner of the screen indicates where the data is saved, either on a USB flash drive, or instrument internal memory.



Sort Saved Data

To find a saved data file from a long list, you can sort the files names in ascending or descending order by touching the column title. You can sort by **Sample Id**, **Read Type**, or **Date**. Depending on the column content, the sort is either alphabetical or numeric.

Open Saved Data

To open a saved sample data file, from the list, touch anywhere in the row to highlight and select the line, then touch . To deselect a highlighted row, touch anywhere in the row again.

Lock and Unlock Saved Data

You can lock files saved to the internal instrument memory to prevent accidental file deleting. The lock function is only available in Sample Manager when it is opened from the main screen.

To lock a file, from the saved files list, touch anywhere in the row to highlight and select the line, then touch . To unlock a file and make it available for deleting, from the list, touch anywhere in the row to highlight and select the line, then touch .

Recall Saved Files

When recalled, sample data files display the first sample recorded in a measurement. To access all sample data within a recalled file, touch the **Sample** box to display a list of all samples contained within the file. Touching a listed file populates the boxes on the sample measurement screen with the saved data. Choosing to measure another sample with an old sample data file displayed updates the sample measurement screen and the appropriate boxes.

Note: Wavescan and Kinetics read type sample data is recalled using **Trace Manager**. For details see Trace Manager - Overlay and Manipulate Wavescan and Kinetic Files on page 81.

Delete Saved Files

To ensure that the internal instrument memory stays with the 100 saved sample data files limit, you have to delete unwanted sample data files. Use **Sample Manager** to delete sample data files. The deleting functions are only available in Sample Manager when it is opened from the main screen. You can delete files in one of three ways:

- Delete a single file—Touch anywhere in the row of a file in the list to highlight and select the file for deletion, then touch . When prompted, touch to confirm and continue the deleting.
- Delete multiple files—Touch anywhere in the row for multiple files in the list to highlight and select the files for deletion, then touch . When prompted, touch to confirm and continue the deleting.
- Delete all files—Touch . When prompted, touch to confirm and continue the deleting.

To delete locked files, you must first unlock the files. To unlock a file and make it available for deleting, from the list, touch anywhere in the row to highlight and select the line, then touch .

Note: Sample data files saved on a USB flash drive cannot be locked or deleted with Sample Manager. You can delete saved files on a USB flash drive using a computer.

To exit **Sample Manager**, touch .

Trace Manager - Overlay and Manipulate Wavescan and Kinetic Files

Trace Manager is the mode used by the instrument to overlay and manipulate Wavescan and Kinetics read type files.

Load sample data into Trace Manager using either Sample Manager or from within the read type.

Load Sample Data Using Sample Manager

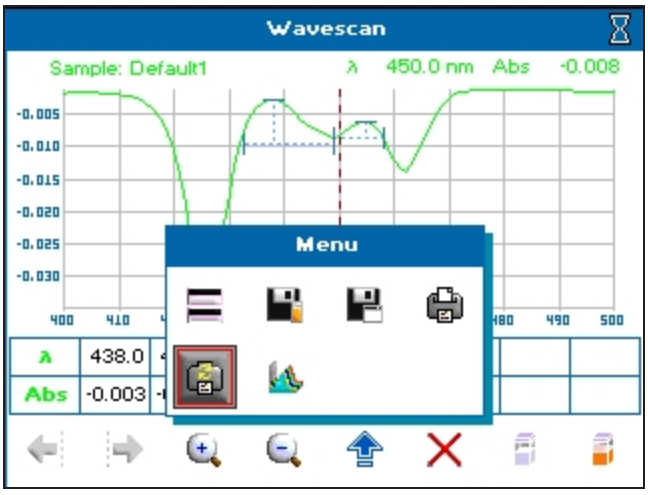
Wavescan and Kinetics read type sample data files can be loaded directly into Trace Manager by selecting the required files from Sample Manager from the main screen.

To load sample data using Sample Manager:

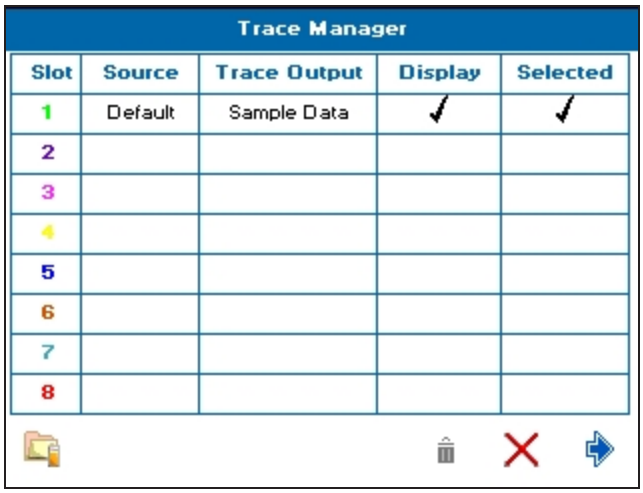
1. From the main screen, touch **Sample Manager**.
2. From the list, locate the Kinetics or Wavescan Read Type sample data you need.
3. Touch anywhere in the row to highlight and select the line, then touch . You can highlight and select more than one line at a time by touching other unselected lines.

   Note: If a USB flash drive is installed, you can toggle between files stored on the internal and USB memories using the icon in the left bottom corner. The icon in the top right corner of the screen displays the memory that is active.

4. Touch to open the options menu.



5. Touch to open **Trace Manager**.



   All recalled files are displayed on the Trace Manager screen, up to 8. The color of the **Slot** number is the color of the trace when it is displayed on the screen.

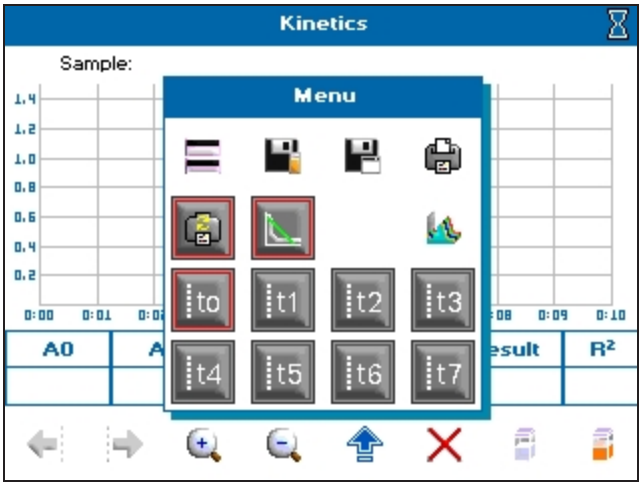
6. To toggle which files are displayed on the measurement screen, from the list, touch in the **Display** box of the needed Slot, up to 8 files can be displayed.
7. To specify which data file displayed on the measurement screen is selected, touch in the appropriate **Selected** box. Only one file can be selected.
8. Touch to view the overlaid data.
9. To save the sample data, touch to open the options menu, then touch .
10. To return to Trace manager, touch to open the options menu, then touch .
11. To exit without saving, touch .
12. To do post scan manipulations, see Post Scan Manipulation on page 84.

Load Sample Data From Within a Wavescan or Kinetics Read Type

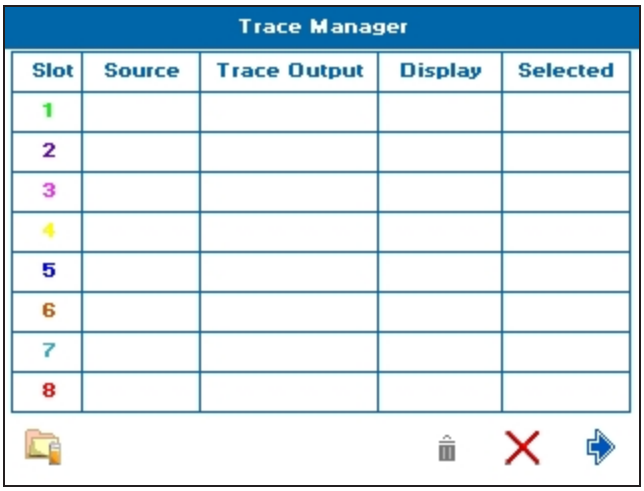
Trace Manager can be accessed from within the Wavescan or Kinetics read type to overlay saved files with a live trace displayed. This procedure is required for Limited users because Sample Manager on the main screen is unavailable to them. See User Access Control Settings on page 20.

To load sample data from with Within a Wavescan or Kinetics read type:

1. From the main screen, touch **Read Types**, then touch either **Wavescan** or **Kinetics**.
2. Touch to open the options menu.



3. Touch to open **Trace Manager**.



Trace manager is empty when opened without overlays displayed.

4. To add sample data to an empty Trace Manager screen, touch to open Sample Manager. Only saved data for your active read type is displayed for selection.

5. From the list, touch anywhere in the row of the sample data that you want to select to highlight and select the line, then touch . You can highlight and select more than one line at a time by touching other unselected lines.

   Note: If a USB flash drive is installed, you can toggle between files stored on the internal and USB memories using the icon in the left bottom corner. The icon in the top right corner of the screen displays the memory that is active.

   All recalled files are displayed on the Trace Manager screen, up to 8. The color of the **Slot** number is the color of the trace when it is displayed on the screen.

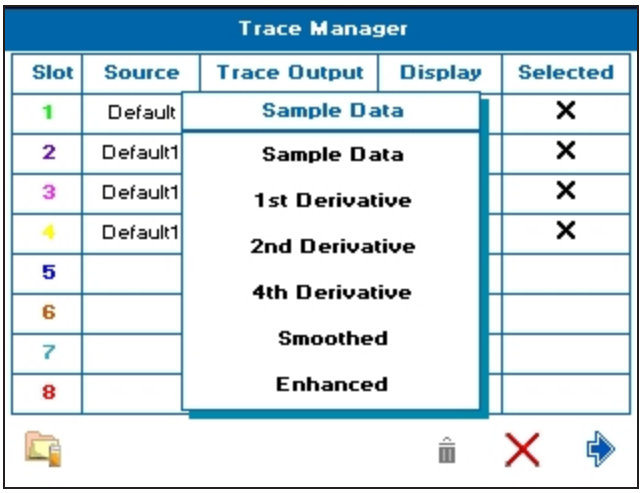
6. To toggle which files are displayed on the measurement screen, from the list, touch in the **Display** box of the needed Slot, up to 8 files can be displayed.
7. To specify which data file displayed on the measurement screen is selected, touch in the appropriate **Selected** box. Only one file can be selected.
8. Touch to view the overlaid data.
9. To return to Trace Manager, touch to open the options menu, then touch .
10. To exit without saving, touch .
11. To do post scan manipulations, see Post Scan Manipulation on page 84.

Post Scan Manipulation

Trace Manager enables you to manipulate recalled Wavescan and Kinetics read type sample data.

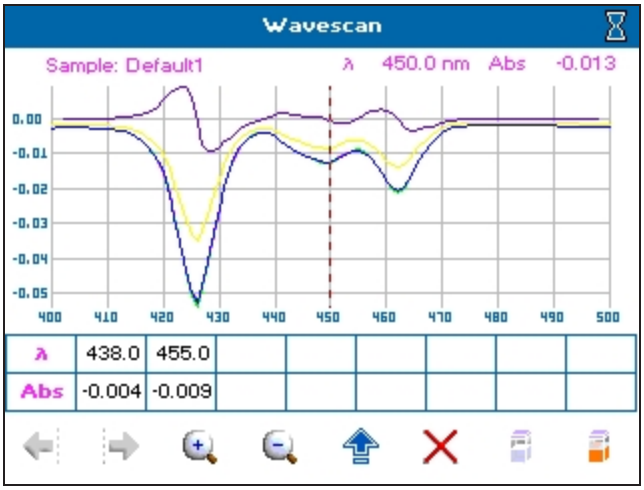
To do post scan manipulations in Trace Manager:

1. With the needed sample data files loaded into Trace Manager, touch the needed **Trace Output** box to display the manipulation choices.



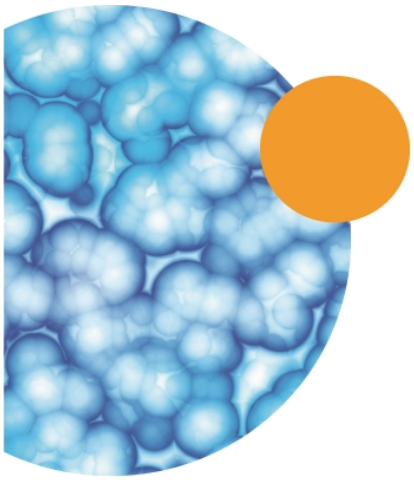
2. From the list, touch a manipulation choice to assign to the Slot. Manipulation choices include:
   Wavescan post scan manipulations
   - **Sample Data**— Displays the raw wavescan data. This is the default setting.
   - **1st Derivative** through **4th Derivative**— Displays the derivative data to the desired order.
   - **Smoothed**— Uses the Savitzky-Golay algorithm to reduce noise and smooth the data.
   - **Enhanced**—Sharpens peaks and valleys.

   Kinetics post scan manipulations
   - **Sample Data**— Displays the raw kinetics data. This is the default setting.
   - **Low**— Applies a low level of smoothing to the data.
   - **Medium**— Applies a medium level of smoothing to the data.
   - **High**— Applies a high level of smoothing to the data.
3. After the Trace Output manipulations and Display options have been set as needed, touch to view the overlaid and manipulated sample data.



Note: For Wavescan and Serial Kinetic measurements with overlays set to 1 or more, and Parallel Kinetic measurements, data is automatically saved into the internal instrument memory and is displayed in Trace Manager.

To ensure the optimum performance of the instrument, delete unwanted files from the internal instrument memory at regular intervals. See Delete Saved Files on page 80



Chapter 7: Save and Delete Methods

7

The instrument can save methods either in internal memory or on a USB flash drive. A total of 90 methods can be saved in internal instrument memory. You can save 9 methods in the **Favorites** folder, and you can save 9 methods in each of the 9 **Methods** folders. If you use a USB flash drive, only 9 saved methods display.

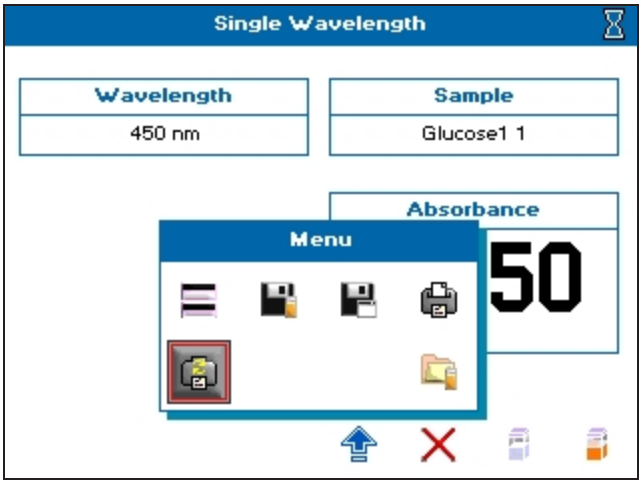
Methods are saved from within the read types after you set the required method parameters.

Methods can be locked or unlocked, and deleted. Method folders can be renamed, locked or unlocked, and backed up or restored using a USB flash drive. See Lock and Unlock Methods on page 91, Rename Methods Folders on page 94, and Back up and Restore Backed up Methods Folders on page 96.

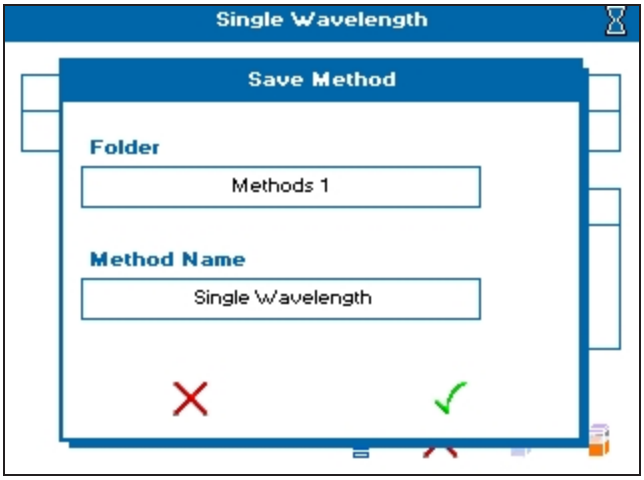
Save Methods

To save methods:

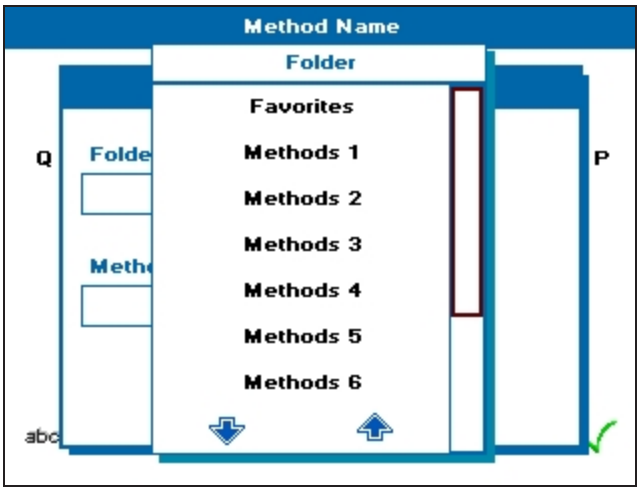
1. Start a read type, then set the required method parameters.
2. When the last screen is displayed, touch to open the Options menu.



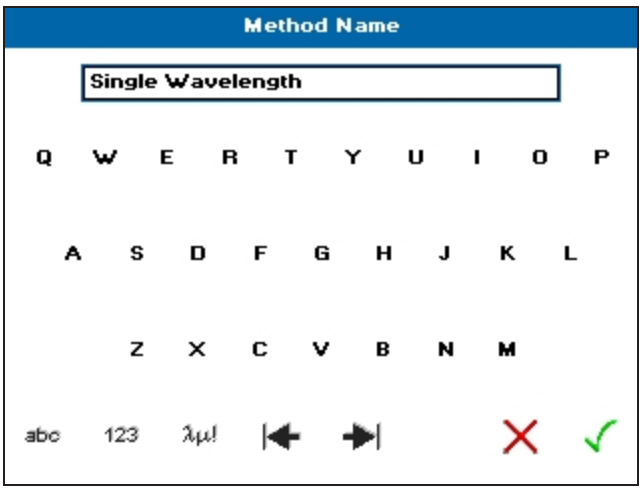
3. Touch to open the **Save Method** dialog.



4. Touch the **Folder** box, then from the list box, touch either **Favorites**, a **Methods** folder, numbered 1 though 9, or **USB Methods**. A USB flash drive must be in the USB port on the left side of the instrument to use the **USB Methods** folder option.



5. Touch the **Method Name** box, then touch-enter a name.



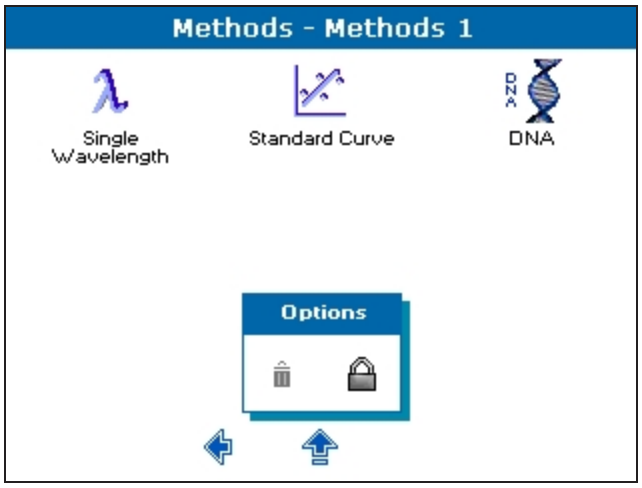
6. Touch ✓ to save the name and close the dialog. To close the dialog without saving, touch ✗.
7. Touch ✓ to finish the **Save Method** and close the dialog. To close the dialog without saving, touch ✗.
8. You can now either run your read type, by taking a reference measurement and then taking a sample measurement, or close the read type screen by touching ✗.

Delete Methods

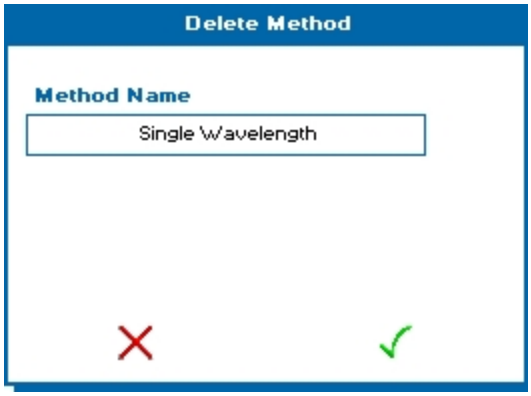
Note: Only methods within the **Methods** folders and **Favorites** folder can be deleted from internal instrument memory, and only when unlocked. See Lock and Unlock Methods on page 91.

To delete a method:

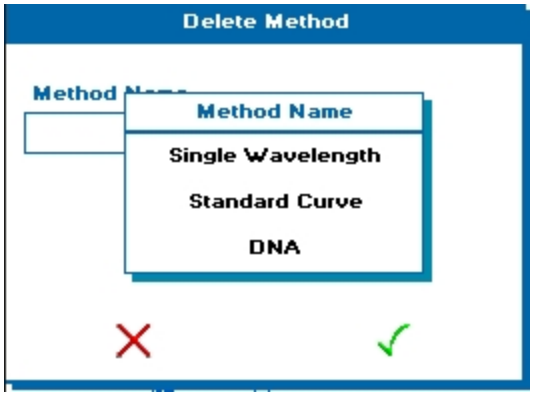
1. From the main screen, open either **Favorites** or **Methods**.
2. From **Favorites**, touch to open the Options menu. From **Methods**, open the methods folder containing the method you want to delete by touching the folder, then touch to open the Options menu.



3. Touch to open the **Delete Method** dialog.



4. Touch the **Method Name** box, then from the list, touch the method name you want to delete.



5. Touch ✓ to finish the **Delete Method** and close the dialog. To close the dialog without saving, touch ✗.
6. Touch ← to return to the main menu.

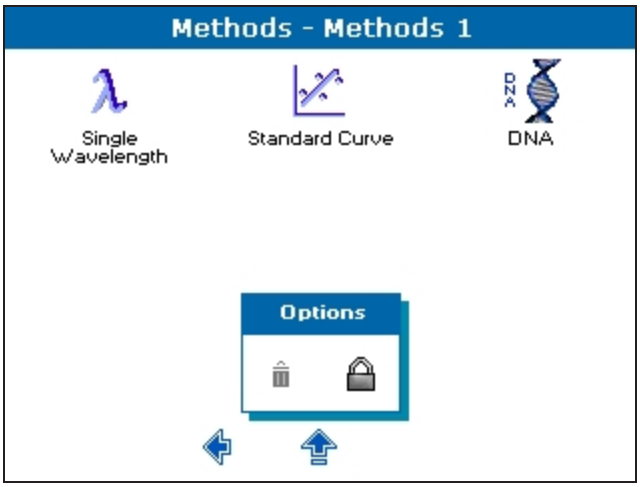
Lock and Unlock Methods

Locking Method folders or methods within folders prevents method folders from being renamed, and methods from being deleted. Methods folders can be pass code locked or unlocked and methods saved within Methods folders can be pass code locked or unlocked. Methods within the Favorites folder can also be pass code locked or unlocked.

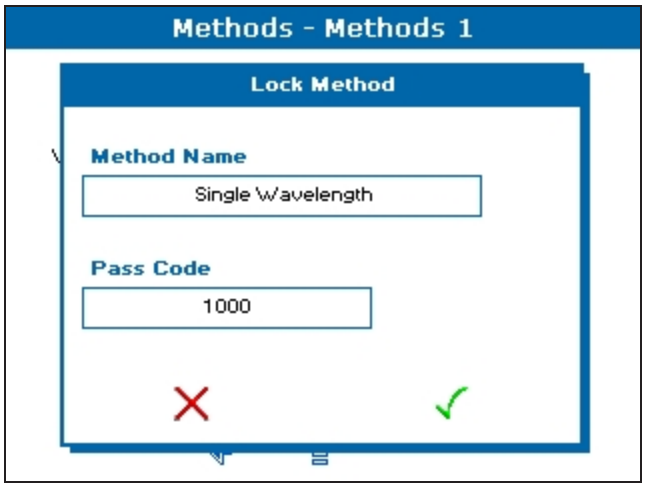
Lock Methods

To lock methods:

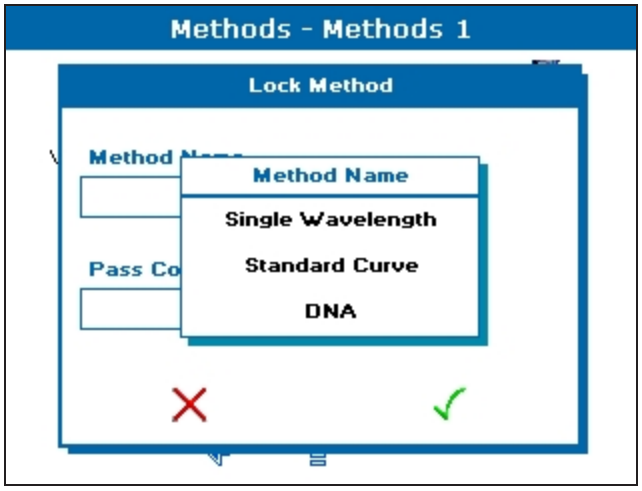
1. From the main screen, open either **Favorites** or **Methods**.
2. From **Favorites**, touch ↑ to open the Options menu. From **Methods**, open the methods folder containing the method you want to lock by touching the folder, then touch ↑ to open the Options menu.



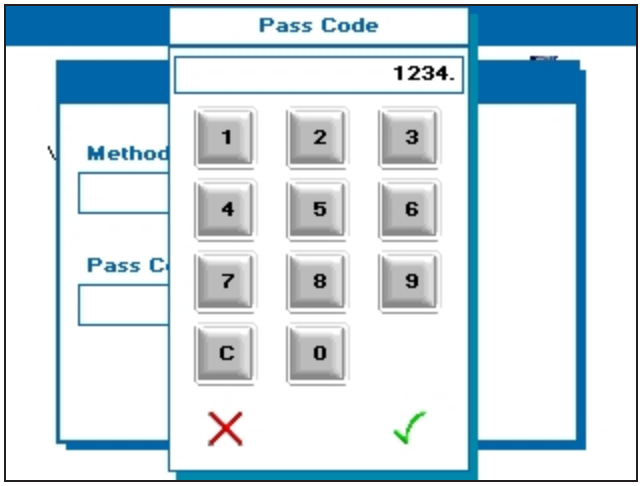
3. Touch to open the **Lock Method** dialog.



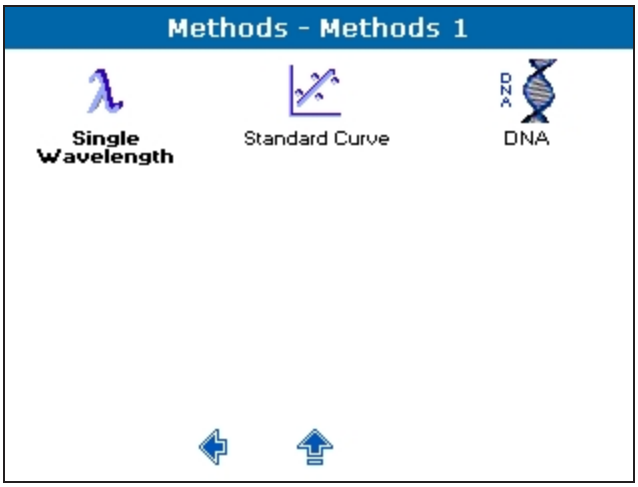
4. Touch **Method Name**, then from the list, touch the method you want to lock.



5. Touch **Pass Code**, then touch-enter a 4-digit pass code.



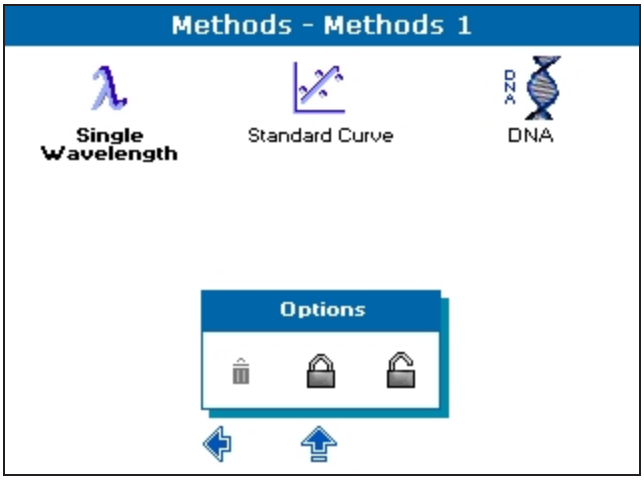
6. Touch ✓ to save the pass code entry and close the dialog. To close the dialog without saving, touch ✗. Keep track of your method lock pass codes so you can unlock them later, as needed.
7. Touch ✓ to finish the **Lock Method** and close the dialog. To close the dialog without saving, touch ✗. The locked method is displayed with bold.



Unlock Methods

To unlock methods:

1. From the main screen, open either **Favorites** or **Methods**.
2. From **Favorites**, touch to open the Options menu. From **Methods**, open the methods folder containing the method you want to lock by touching the folder, then touch to open the Options menu.



3. Touch to open the **Unlock Method** dialog.
4. Touch **Method Name**, then from the list, touch the method you want to unlock. Only the locked methods are displayed.

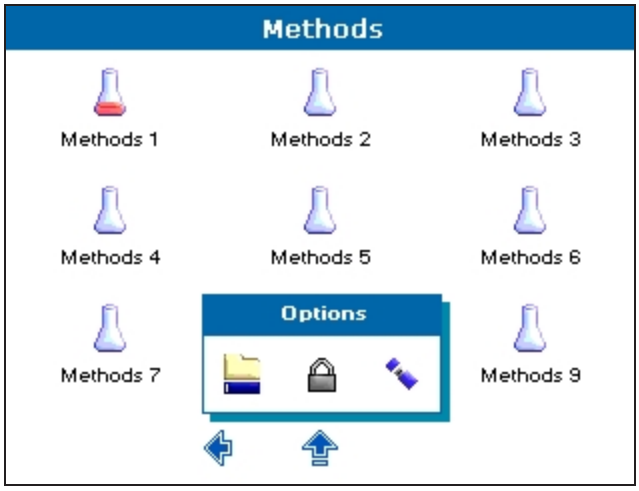
5. Touch **Pass Code**, then touch-enter the 4-digit pass code you set when locking the method.
6. Touch ✓ to save the pass code entry and close the dialog. To close the dialog without saving, touch ✗.
7. Touch ✓ to finish the **Unlock Method** and close the dialog. To close the dialog without saving, touch ✗. The bold is removed from the method name indicating that the method is unlocked and can be deleted. See Save and Delete Methods on page 87.

Rename Methods Folders

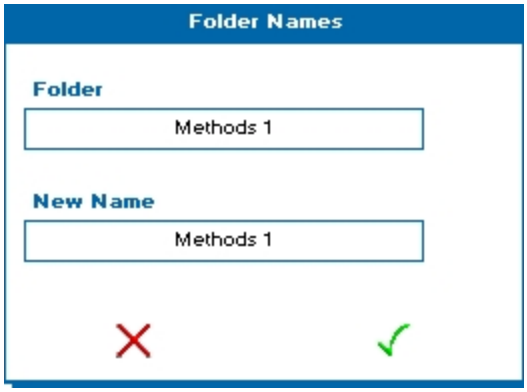
All 9 of the Methods folders can be renamed. By default they are named **Methods 1** through **Methods 9**.

To rename a Methods folder:

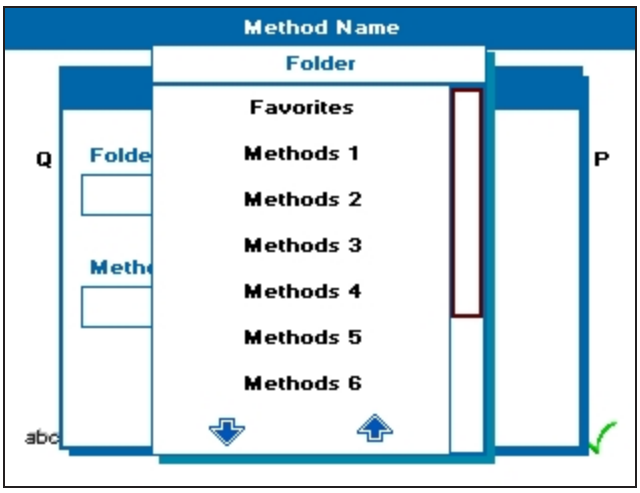
1. From the main screen, touch **Methods**.
2. Touch ⬆ to open the Options menu.



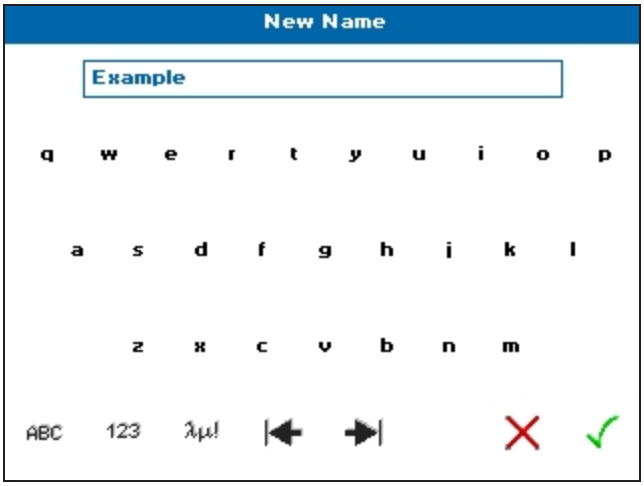
3. Touch 📁 to open the **Folder Names** dialog.



4. Touch **Folder**, then from the list, touch the folder name you want to change.



5. Touch **New Name**, and touch the backspace delete arrow enough times to delete the current name, then touch-enter a new folder name.



6. Touch ✓ to save the new name entry and close the dialog. To close the dialog without saving, touch ✗.
7. Touch ✓ to finish the **Rename** and close the dialog. To close the dialog without saving, touch ✗.

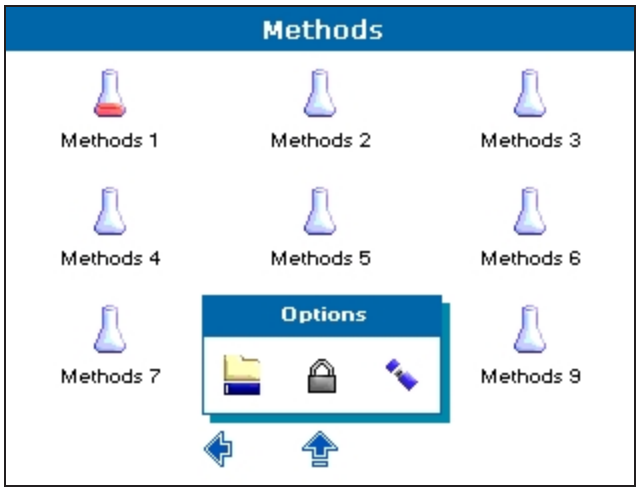
Back up and Restore Backed up Methods Folders

You back up or restore previously backed up Methods folders using a USB flash drive.

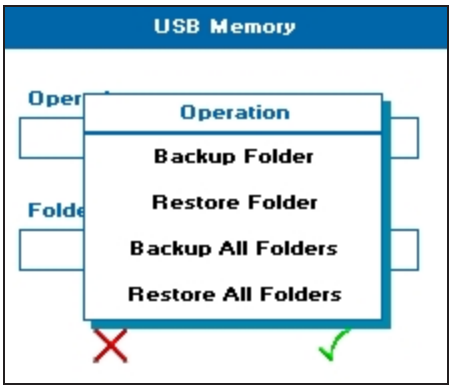
CAUTION! When data is being written to the USB flash drive the LED above the power button lights. Do not remove the flash drive when the LED is lit because data can get corrupted.

To back up or restore Methods folders using a USB flash drive:

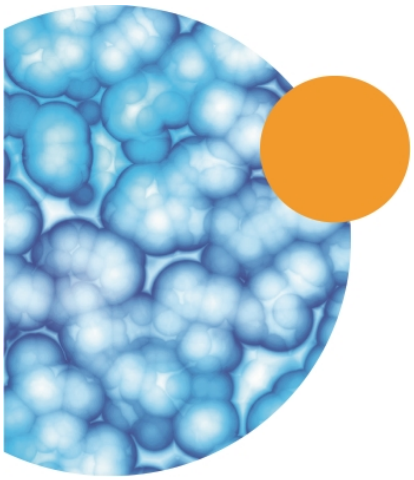
1. Insert a USB flash drive into the USB port on the left side of the instrument.
2. From the main screen, touch **Methods**.
3. Touch to open the **Options** menu.



4. Touch to open the **USB Memory** dialog, then touch **Operation** to view your choices.



5. From the list, touch a backup or restore choice. Choices include:
   - **Backup Folder**—Copies all methods from a specified folder to a USB flash drive.
   - **Restore Folder**—Copies a backed up method folder from the USB flash drive to the internal instrument memory.
   - **Backup All Folders**—Copies all method folders from the internal memory to a USB flash drive.
   - **Restore All Folders**—Copies all backed up method folders from the USB flash drive to the internal instrument memory.
6. Touch ✓ to accept your choice selection and close the dialog. To close the dialog without saving, touch ✗.
7. Touch ✓ to finish the **USB Memory** backup or restore and close the dialog. To close the dialog without saving, touch ✗.



Chapter 8: Print

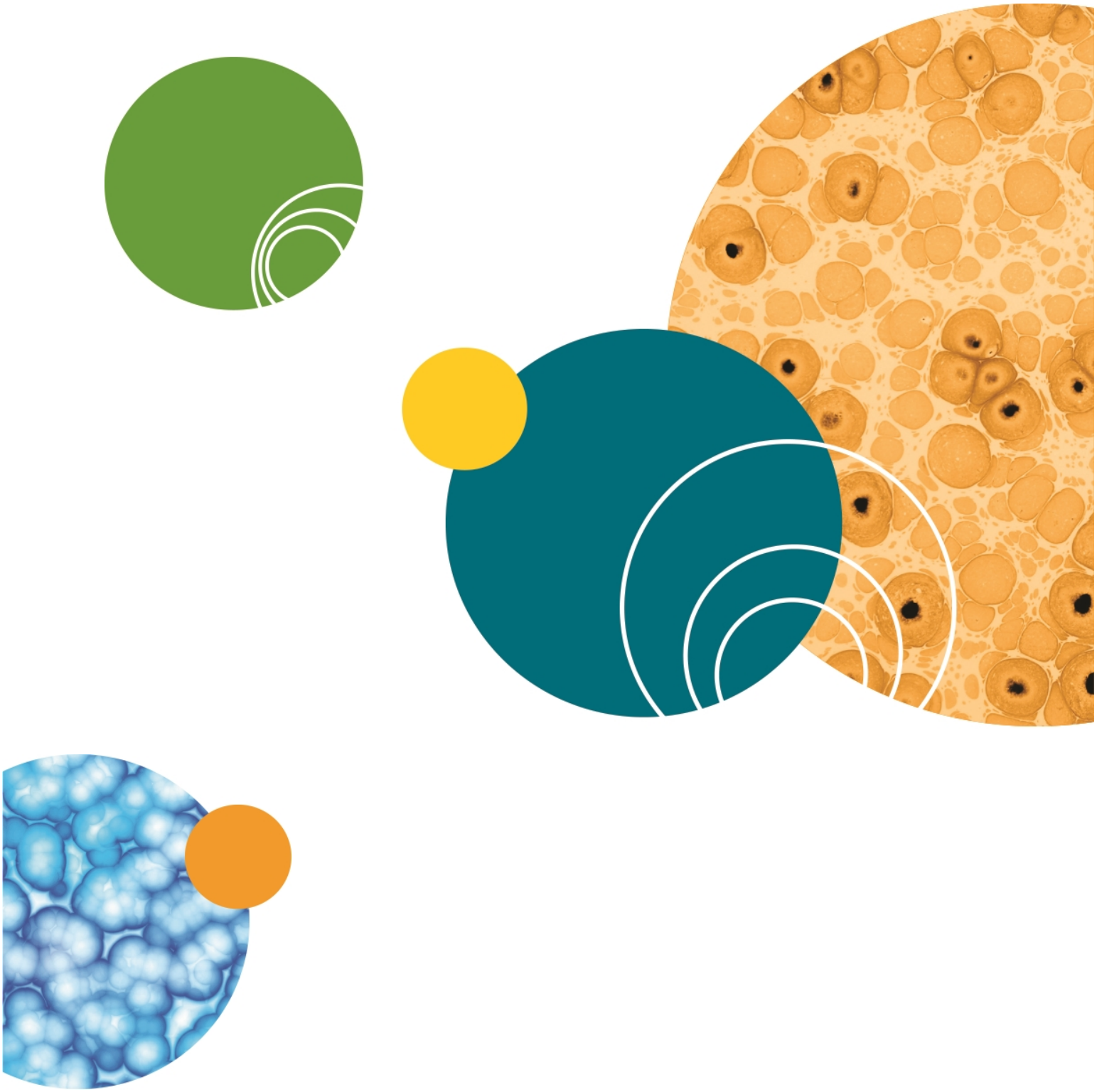
8

The instrument has print functionality, but it requires separate Windows-based Print Via Computer (PVC) software that Molecular Devices does not support. The **Data Output Settings** options to toggle **Auto-Print** on and off, and choose where to **Print to** are available, however, Molecular Devices does not support these functions and recommends **Auto-Print** be set to **Off**.

If you must print, the PVC software installation and operating instructions are on the Molecular Devices Knowledge Base at www.moleculardevices.com/support.

If you have the PVC software installed on your computer, from **Settings > Data Output > Print to**, select one of the following options:

- **PC Via USB** — Requires connecting from the back of the QuickDrop Spectrophotometer using a USB printer cable to a PC. See Back Connections on page 7. Using the PVC software, the data can be printed or saved in a variety of formats, including graphics and text formats or as a CSV file.
- **USB Mass Storage** — Requires a USB flash drive to be installed in the side port before the option is available for selection. The printed data saves on your USB flash drive as a .pvc file that can only be viewed on your PVC software.



Appendix A: Table of Icons

Table A-1: Descriptions of Icons Functions

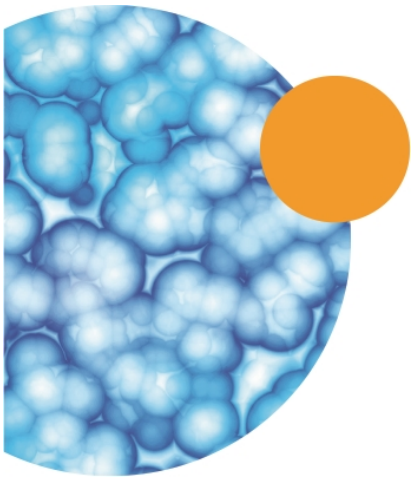
Icon	Name	Function
	Back arrow	Navigates back to the previous screen in a sequence.
	Forward arrow	Navigates to the next screen in a sequence.
	Open Options menu	Displays the relevant Options menu, the exact content of the menu depends on which screen it is available.
	Page down	Navigates to the next page.
	Page up	Navigates to the previous page.
	Cursor left	Use in the Wavescan and Kinetics read types to move the cursor left. The position of the cursor and the corresponding x and y values are displayed above the scan.
	Cursor right	Used in the Wavescan and Kinetics read types to move cursor right. The position of the cursor and the corresponding x and y values are displayed above the scan.
	Toggle data viewed / Reset	When used in the Cydye DNA read type this toggles the data displayed between DNA and dye data. Under Instrument Settings this resets a value.
	Delete all	Deletes all saved data or methods. Delete all is a two stage process.
	Delete	Deletes the highlighted data or method. Delete is a two stage process.
	Thresholds	Use in the Equation Editor. Adds thresholds (pass or fail) limits to their results.
	OK / Accept	Use to confirm or accept any changes. Saves and exits.
	Exit	Exits from a read type or screen. If exit is selected without saving, any changes are lost.
	Lock	Locks sample data file or method folder from accidental deletion.
	Unlock	Unlocks a locked method folder.
	Screen Capture	Use to save a bitmap image of the screen to a USB flash drive The USB flash drive must be installed for the icon to be displayed.

Table A-1: Descriptions of Icons Functions (continued)

Icon	Name	Function
	Instrument	Use in the Sample Manager to access sample data files stored on the internal instrument memory or to indicate that the data being displayed is from the internal instrument memory.
	Add linear section	Use in the Kinetics read type to view a line of best fit on the scan. Toggles on or off.
	Section	Use in the Kinetics read type to view data in a specific section. It is possible to add t0 through to t7. Each toggles on or off.
	Method folder	Methods saved internally can be stored in one of nine method folders. Each method folder can store up to nine individual methods.
	Rename method folder	Accessed via the options menu on the methods screen. Use to rename a method folder.
	Toggle view scan on or off	Used in the Nucleic Acid read types DNA, RNA and Oligo. Use to view a survey scan of the last sample run (in the region 220 - 320 nm). Toggles on or off.
	View method parameters	Accessed via the Open Options menu on the sample measurement screen. Returns to the method parameters.
	Save method parameters	Accessed via the Open Options menu on the sample measurement screen. Use to specify a save location for a method.
	Save sample data	Accessed via the Open Options menu on the sample measurement screen. Use to specify a save location for sample data.
	Sample Manager	Accessed via the Open Options menu on the sample measurement screen. Displays the sample data held in the either the internal memory or on a USB memory stick.
	Instrument Information	Accessed via Instrument Settings. Displays instrument information such as product name, and serial number.
	Instrument Settings	Accessed via Instrument Settings. Use to set the default bandwidth, save new baselines, and view the date of the last service.
	Lamp Settings	Accessed via Instrument Settings.
	Save instrument options	Accessed via Instrument Settings. Saves the instrument options.
	Xenon lamp failed	Displayed on the status bar. Indicates a xenon lamp failure.
	Instrument busy	Displayed on the status bar. Indicates that the instrument is performing a measurement.

Table A-1: Descriptions of Icons Functions (continued)

Icon	Name	Function
	Toggle view standard curve	When used in standard curve read type, for example a Lowry protein assay, this toggles the sample measurement screen to display or hide the standard curve.
	Replicates	Use in the Standard Curve read type to collect data from a group of replicates.
	Take sample measurement	Starts a sample measurement. A reference measurement must be taken prior to a sample measurement
	Take reference measurement	Starts a reference measurement.
	Backspace / delete	Use in text entry mode to move the cursor backwards (left) and delete any unwanted characters.
	Forward space	Use in text entry mode to move the cursor forwards (right) and enter a space.
abc	Lowercase	Selects lower case letters when in text entry mode.
λμ!	Symbols	Selects symbols when in text entry mode.
ABC	Uppercase	Selects upper case letters when in text entry mode.
123	Numeric	Selects a numeric entry when in text entry mode.
	Trace Manager	Available in the Wavescan and Kinetics read types. Use to overlay up to 8 samples data files and use to chooses what type of data is displayed, such as. raw data, smoothed data, or 1st derivative.
	USB flash drive	Available on the Sample Manager screen to access data stored on a USB flash drive. Available in the Options menu in the Methods folder. Use to backup methods to a USB flash drive.
	Add user	Displayed under User Access. Anyone with Administrator privileges can add another user to the instrument.
	Delete user	Displayed under User Access. Anyone with Administrator privileges can delete users from the instrument.
	Edit user	Displayed under User Access. Anyone with Administrator privileges can edit currently users' parameters.
	Zoom in	Available in the Wavescan and Kinetics read types. Use to zoom into a specific region of a scan.
	Zoom out	Available in the Wavescan and Kinetics read types. Use to zoom out and return to the original scan.



Appendix B: Glossary of Boxes

B

Table B-1: Explanations of Box Functions

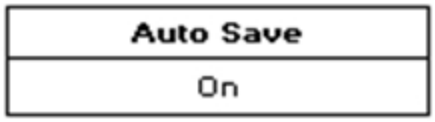
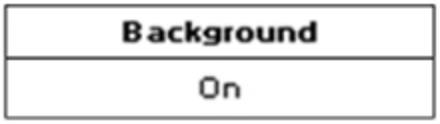
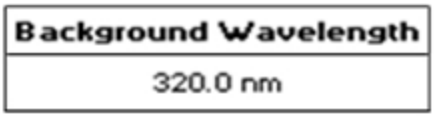
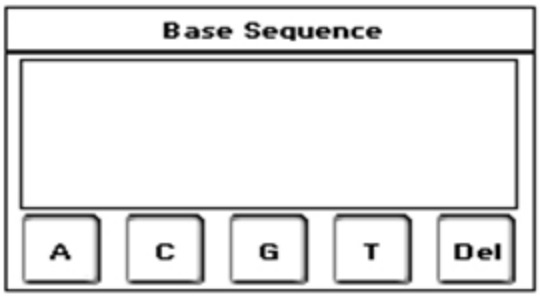
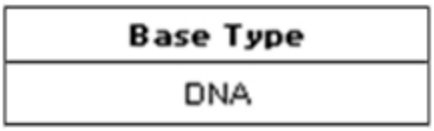
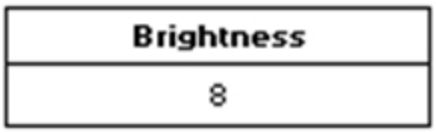
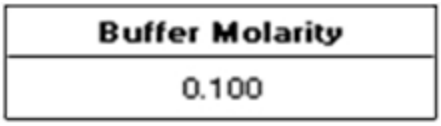
Box	Function
	Toggles between on and off. Use in all applications to set whether sample data is saved automatically or not
	Toggles between on and off. Use in Nucleic Acid and Protein measurements to subtract the absorbance value at 320 nm. This is done to allow for the effects of turbidity, high absorbance buffer solutions and the use of reduced aperture cuvettes.
	Set by numeric entry. Use in Cydye DNA measurements only and enables the user to specify the wavelength of background correction.
	Use in Tm calculation to set the sequence of bases. The bases A, C, G, T can be added in DNA mode and the bases A, C, G, U can be added in RNA mode. Bases are grouped in threes to improve readability.
	Use in Tm calculation to toggle between DNA and RNA base types.
	Use in User Interface in Settings to set the brightness of the screen.
	Numeric entry, use in Tm calculation only. Buffer molarity = buffer molarity + total molarity of salt (moles / L).

Table B-1: Explanations of Box Functions (continued)

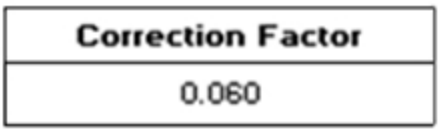
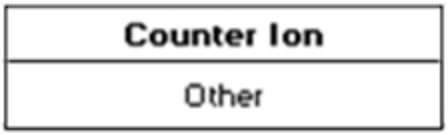
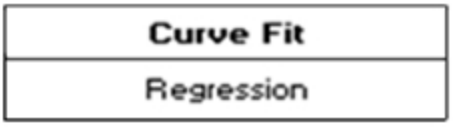
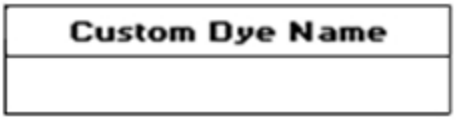
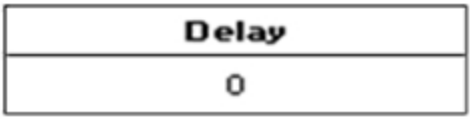
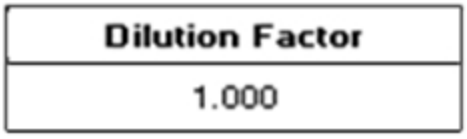
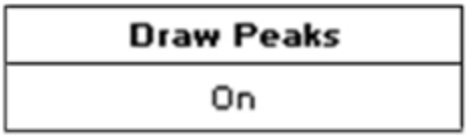
Box	Function
	Use in all Standard Curve applications to set the method used to collect the standard curve. Options are for Standards or Manual.
	Set by numeric entry, use in the Cydye DNA application only. This is the correction factor applied to the absorbance of the dye at a specified wavelength.
	Use in Tm calculation only this allows the user to add the type of counter ion used. The options are sodium (Na), potassium (K), triethylammonium (TEA) or other. If other is selected the molecular weight of this counter ion must be added using Other MW.
	Use in all Standard Curve applications this is the curve fit that will be applied to the standards' absorbance values. Options are Zero Regression, Regression, Interpolation and Cubic Spline.
	Alphanumeric entry for custom dye name, use in Cydye DNA only.
	Numeric entry. This is the delay required before a kinetic measurement starts.
	Numeric entry. Use in Nucleic Acid and Protein applications to compensate for the absorbance of highly concentrated samples.
	Use in Wavescan only, this switches display of peak cursors on and off. Peak cursors show vertical dashed lines displaying the measured peak height and horizontal dashed lines showing the peak width.

Table B-1: Explanations of Box Functions (continued)

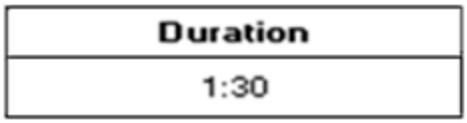
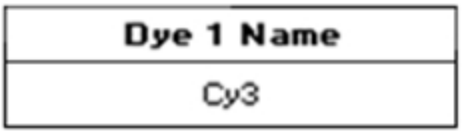
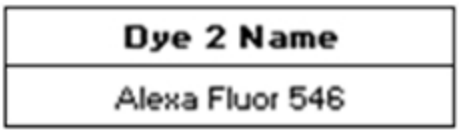
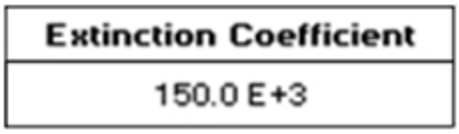
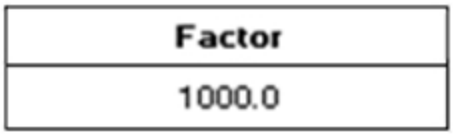
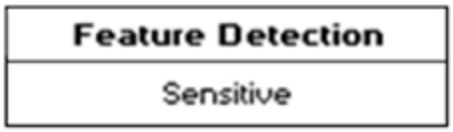
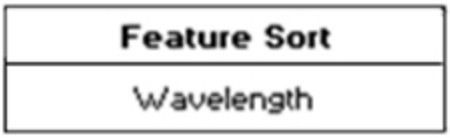
Box	Function
	Numeric entry. This is the duration over which a kinetic measurement isdone.
	Use in Cydye DNA application only. This is the first dye type used in the measurement.
	Use in Cydye DNA application only. This is the second dye type used in the measurement (as needed).
	Numeric entry for Cydye DNA application only. This is the extinction coefficient of the specified dye. These values are not editable and the box name is greyed out, for dyes included in the system software .The values for Custom dyes must be entered.
	Numeric entry to 3 decimal places. In concentration and nucleic acid measurements multiplying absorbance readings by this factor gives the concentration value. In kinetic measurements the result is calculated by multiplying this factor by absorbance, delta absorbance or the slope.
	Use in Wavescan measurements only. This determines the sensitivity of the peak or valley detection, for example, sensitive will detect more peaks or valleys than course. Options include: Off, Coarse, Sensitive or Custom (when Custom is selected the minimum peak height and width must be entered).
	Toggles between wavelength and absorbance, use in Wavescan measurements only. This determines how features are ordered in the peak/valley table below the scan.

Table B-1: Explanations of Box Functions (continued)

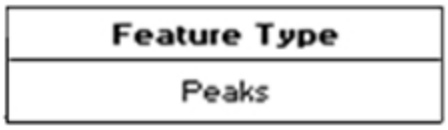
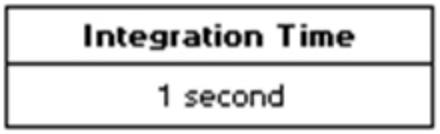
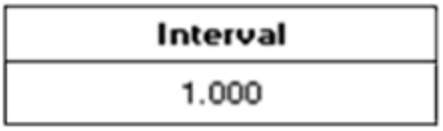
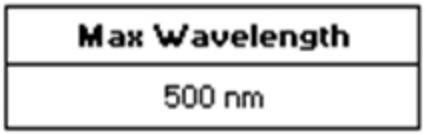
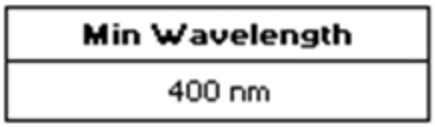
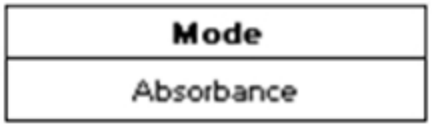
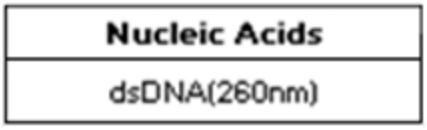
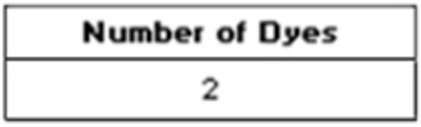
Box	Function
	Toggles between peaks and valleys, used in Wavescan measurements only. This determines what feature type is detected.
	Use in User Access to set the group a user belongs to and what access they are given.
	Use in all applications. This is the duration the instrument takes a reading at an individual wavelength. The longer the integration time, the greater the signal to noise ratio and the greater the accuracy.
	Numeric entry. This is the interval at which serial kinetics readings are taken.
	Numeric entry. This is the upper limit of a wavescan measurement.
	Numeric entry. This is the lower limit of a wavescan measurement.
	Use in the Single Wavelength, Kinetics and Protein A280 applications to set the required measurement mode.
	Use in Cydye DNA application only to set the nucleic acid used in the measurement.
	Toggles between 1 and 2. Available in Cydye DNA application only to set the number of dyes used in the measurement.

Table B-1: Explanations of Box Functions (continued)

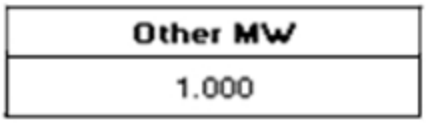
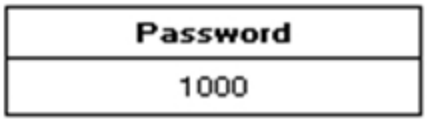
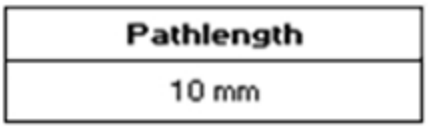
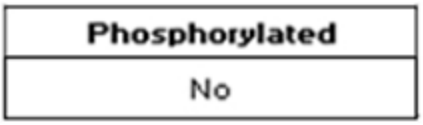
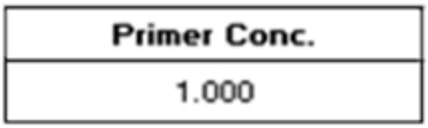
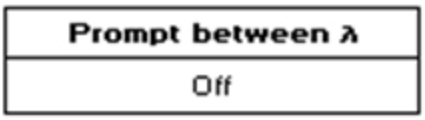
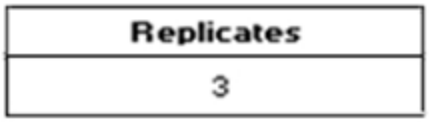
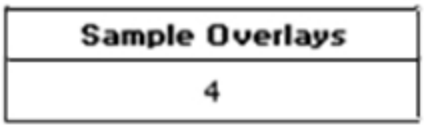
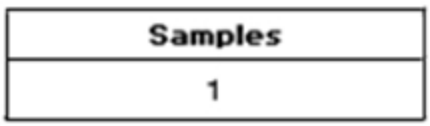
Box	Function
	Numeric entry. This option is only used if the counter ion type in the Tm calculation is set to Other.
	Use in User Access to set a password for new users.
	Use in the Nucleic Acid applications, Protein A280 and Protein UV. This is the pathlength of the cuvette used in the measurement. Options include: 10mm, 5mm, 2mm, 1mm, and µLite 0.5 mm.
	Toggles between yes and no. Use in Tm calculation to set if the sample to be measured is phosphorylated or not.
	Numeric entry to 3 decimal places. Use in Tm calculation to sets the primer concentration in pmole/mL.
	Toggles between on and off. Use in Equation Editor only. With Prompt on the measurement continues as follows: measure wavelength 1, prompt for sample, measure wavelength 2, prompt for sample.
	Use in all standard curve applications. This is the number of times a standard measurement is repeated before the mean of these values is plotted on the standard curve. Options include: off (1 measurement), 2 or 3.
	Use in Wavescan measurements, this determines how many samples are overlaid on the graph. Options include: off, 2 to 8.
	Use in Kinetic measurements to set the number of samples that are measured during the method. Options include: 1, 2 or 3.

Table B-1: Explanations of Box Functions (continued)

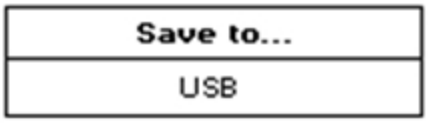
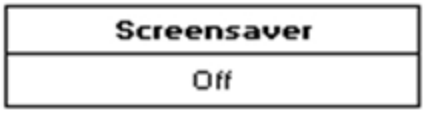
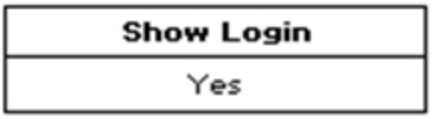
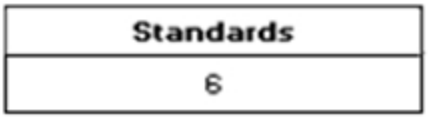
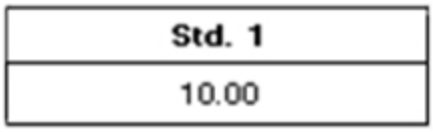
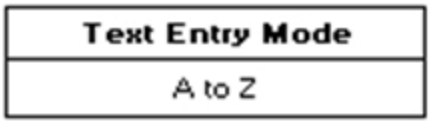
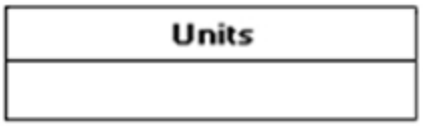
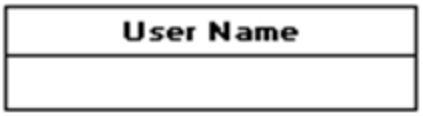
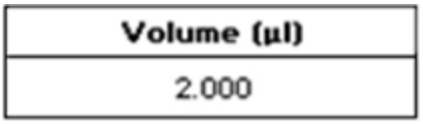
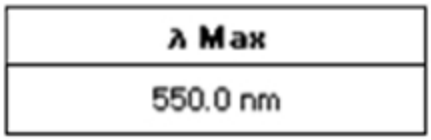
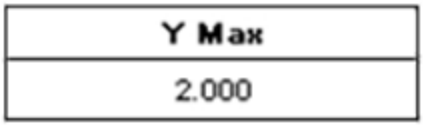
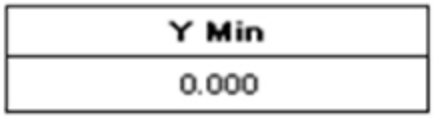
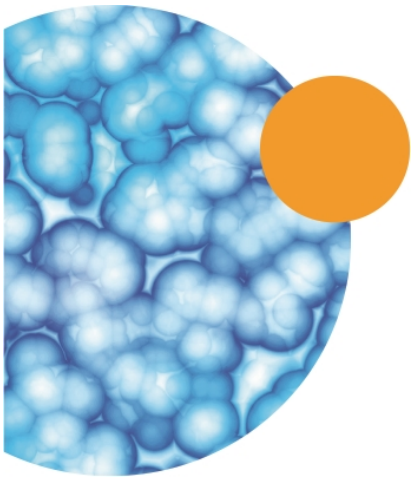
Box	Function
	Use in all applications to set the preferred save location. Only available locations are displayed.
	Use in User Interface in Settings to set the time before the screensaver is displayed
	Use by the Default Administrator in User Access to set if user login is displayed or not.
	Use in all Standard Curve applications. This is the number of standards that are used to create the standard curve; options include: 1 through 9.
	Numeric entry to 2 decimal places. Use in all Standard Curve applications this is the concentration of the standard.
	Use in User Interface in Settings to set the text entry mode used for alphanumeric text entry.
	Use in applications where a concentration is the end result. Enter units using either alphanumeric entry or from a list of options.
	Use in User Access to create a new user.
	Numeric entry to 3 decimal places. Use in the Cydye DNA application for the volume of the probe in µL.

Table B-1: Explanations of Box Functions (continued)

Box	Function
	Numeric entry to 1 decimal place and is used in all fixed wavelength applications to determine the wavelength at which the measurement is done.
	Numeric entry to 1 decimal place. Use in the Cydye DNA application for the wavelength at which the absorbance of the dye is measured. These values are not editable and the box name is greyed out, for dyes included in the system software .The values for Custom dyes must be entered.
	Numeric entry to 3 decimal places. This is the maximum value of the Y axis shown during a kinetics measurement. The graph automatically rescales at the end of the measurement to give the optimum Y max.
	Numeric entry to 3 decimal places. This is the minimum value of the Y axis shown during a kinetics measurement. The graph automatically rescales at the end of the measurement to give the optimum Y min.



Appendix C: Instrument Specifications

C

The following table lists the instrument specifications of the QuickDrop Spectrophotometer.

Table C-1: Physical Specifications of the Instrument

Item	Description
Display	5.7” colour display with capacitive touch panel
Configuration	Split Beam
Lamp	Pulsed Xenon lamp with 3 year warranty
Wavelength range	190 nm to 1100 nm
Wavelength accuracy	±2 nm
Wavelength reproducibility	±1 nm
Spectral bandwidth	5 nm
Stray light	< 0.5%T at 220 nm and 340 nm Using $NaNO_2$
Photometric range	-0.3 A to 2.5 A, 0 to 199%T
Photometric accuracy	±0.005 A or 1% of the reading, whichever is greater at 546 nm
Photometric reproducibility	±0.003 A (0 to 0.5 A), ±0.007 A (0.5 to 1.0 A)
Noise	0.005 A peak to peak, 0.002 A RMS
Power input	Mains power adapter: 100 to 240 V AC~ 50/60 Hz Instrument: 18 V DC ⎓, 50 VA max
Dimensions	H 190 mm x W 290 mm x D 410 mm
Weight	<4 kg
Operating environment	Indoor use only
Ambient operating temperatures	5°C to 40°C
Humidity restrictions	Maximum relative humidity 90% up to 31°C decreasing linearly to 50% at 40°C
Minimum sample concentration for detection	10 mm pathlength standard cuvette port is 0.5 ng/µL (dsDNA) Micro-volume sample port is 1 ng/µL (dsDNA)
Languages	English, German, French, Spanish, and Simplified Chinese

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