Operation Manual V1.2

SmartDrop™ XF

NS1020

ACCURIS INSTRUMENTS

This Product is for Research Use Only

Thank you for purchasing the SmartDrop™ XF Nano Spectrophotometer. This user manual details the instrument's features, specifications, as well as complete operating instructions; please read it carefully before operation. This product is designed for research use only. Keep this user manual for later use.

Important:

Please keep the box and packaging material for this instrument. If service is required, the box will be needed to ship the instrument to our Service Department.

Initial Inspection

Please inspect the instrument as well as all included accessories when you first open the packaging. If you find anything damaged or missing, please contact Benchmark Scientific or your local distributor immediately.

BENCHMARK SCIENTIFIC / ACCURIS INSTRUMENTS
PO Box 709
Edison, NJ 08818
USA
Phone: 908-769-5555
Website: www.benchmarkscientific.com/ www.accuris-usa.com

Safety Warnings and Guidelines

1. Important information for safe use

Users should understand how to use this instrument before operating. Please read this manual carefully prior to operation.

Any improper operation may cause injury. Please read this manual carefully and operate safely according to the guidelines.

2. Operation and Maintenance

The operation and maintenance of the instrument should comply with the basic guidelines and warnings below. Incorrect operation or maintenance will have detrimental effects on the life, performance, and safety features of the instrument.

The instrument is a normal indoor instrument which conforms to class I of the GB 4793.1 standard.

This instrument is designed for use in a laboratory environment. The device must be operated by skilled laboratory personnel with appropriate training.

To prevent injury or voiding the warranty, the operator should not attempt to repair the instrument without explicit guidance from Accuris Instruments. If service is required, please contact Accuris Instruments or your local distributor for repair.

Before powering on, confirm that the voltage used meets the electrical requirements of the instrument as stated on the rating plate. If the electric cord is damaged, replace it with the same type of cord. Hold the socket firmly before pulling the plug from an outlet. Do not pull the electric cord.

The instrument should be installed in an environment of standard room temperature, low dust, low humidity, and away from direct sunlight, electromagnetic interference, and heat sources. Do not block the vents on the instrument.

Always power off the instrument when you are finished using it. Unplug the power cord and cover the instrument with a cloth or plastic sheet to prevent excessive dust from entering the housing.

Pull the connector plug from the electrical outlet immediately and contact the vendor in the event of:

- Liquid entering the housing.
- Abnormal operation: such as any abnormal sound or smell.
- The instrument is dropped or there is any damage to the housing.
- Any malfunction.

3. Maintenance

The pedestal should be cleaned regularly using a soft cloth dampened with deionized water. The instrument housing should be cleaned regularly using a soft cloth dampened with a small amount of alcohol.

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Chapter 1 Introduction

The SmartDrop™ XF nano spectrophotometer measures 0.5μL – 2.0μL samples with high accuracy and reproducibility. This full spectrum (200nm – 800nm) spectrophotometer employs surface tension to position the sample for measurement. The system includes a cuvette slot for OD600 readings & a built-in printer for printing results. The SmartDrop XF can measure highly concentrated samples without dilution (100X concentration of samples measured by a standard cuvette spectrophotometer).

1. Key Features

- User-Friendly Input & Operation – Touch screen for programming and operation (a mouse can also be connected).
- Multifunctional software for Nucleic Acids, Protein A280, Colorimetry, Fluorometer, UV-Vis & OD600 measurements.
- dsDNA detection range from 2ng/μL – 15,000ng/μL.
- Fast & accurate measurements (< 6 seconds, ± 1%).
- 2 cuvettes included (optical glass) for OD600 measurements.

Chapter 2 Specifications

1. Required Installation Environment

Environmental Temperature: 5°C～35°C

Relative Humidity: ≤ 70%

Input Voltage: DC 24V, 2A (Adapter CSA, UL, CE marked)

2. Specifications

Model			**SmartDrop™ XF (NS1020)**
Minimum Sample Size			0.5μL - 2μL
Path Length			0.05 mm, 0.2 mm, 1.0 mm
Light Source / Life			Xenon flash lamp / >10^9 flashes
Detector Type			2048 element linear silicon CCD array
Wavelength Range			200nm — 800nm
Wavelength Accuracy			± 1 nm
Spectral Resolution			≤ 3nm（FWHM@Hg 253.7nm）
Absorbance Precision			0.003Abs（1mm path length）
Absorbance Accuracy			± 1%（7.332Abs, at 260nm wavelength）
Absorbance Range			0.04 — 300（at 260 wavelength, 10mm equivalent）
Detection Concentration Range			2ng/μL dsDNA - 15,000ng/μL dsDNA
Detection Time			< 6 seconds
OD600	**Abs range**		0~4.000 Abs
	Abs stability		[0,3）≤0.5% [3,4）≤2%
	Abs repeatability		[0,3）≤0.5%, [3,4）≤2%
	Abs Precision		[0,2）≤0.005A, [2,3）≤1%，[3,4）≤2%
Fluorometer		**Linearity**	$R^2 \geq 0.995$
		Repeatability	≤ 1.5%
		Stability	≤ 1.5%

Voltage input	DC 24V, 2A
Power	25W
Dimensions（W×D×H）	20.8cm × 32.0cm ×18.6cm / 8.2in x 12.6in x 7.3in
Weight	3.6 kg / 7.9 lbs

Chapter 3 Instrument Overview

1. Structure

Front

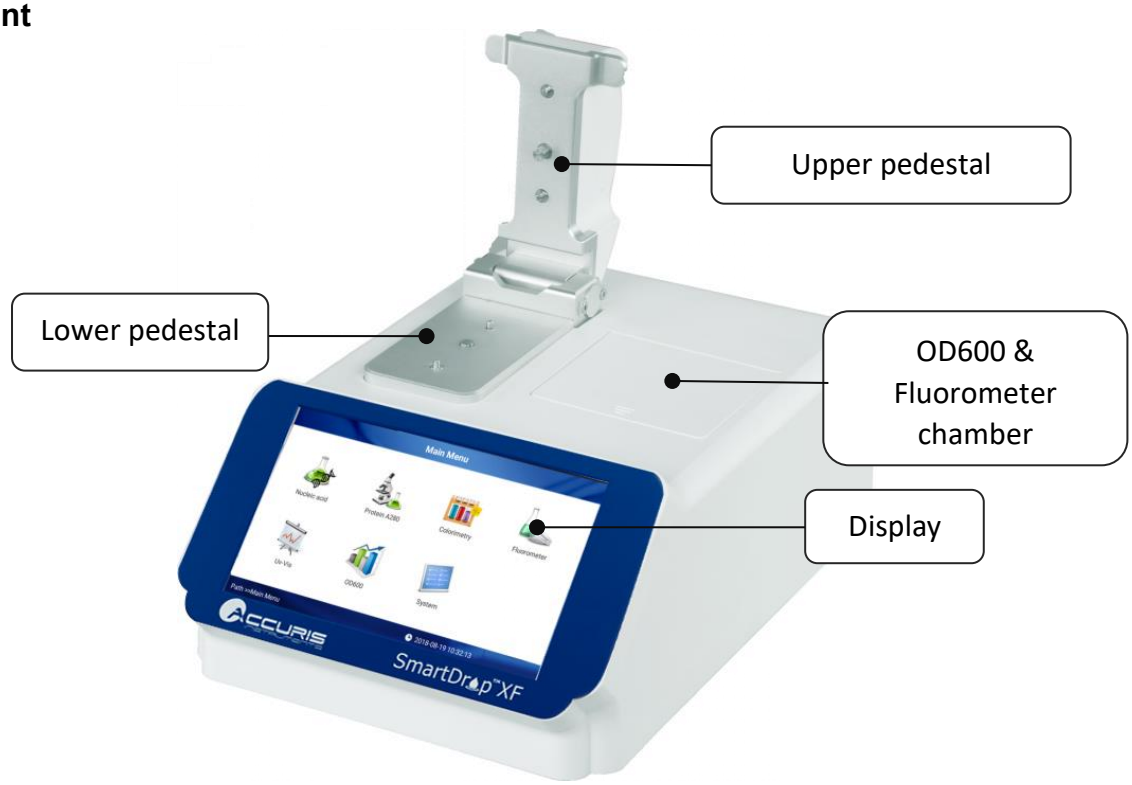


Fig. 1 Front

Back

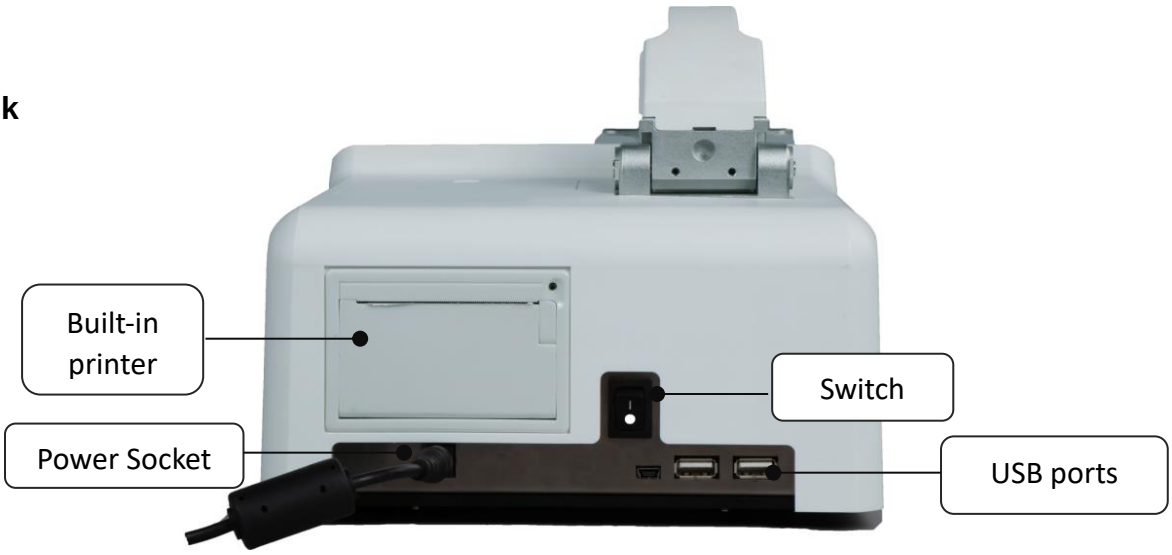


Fig. 2 Back

2. Sample Size Requirements

Surface tension is a critical factor in the formation of the sample column for measurement. The hydrophobic interactions between water molecules in a sample solution is key in creating & maintaining surface tension. The presence of solutes (proteins, DNA, RNA, salt ions, detergent molecules) significantly reduces surface tension and hinders the formation of the sample column. For most samples, a 1µL sample size is enough; however, to ensure accurate and precise measurements, a 2µL sample size is recommended to allow the formation of the sample column for measurement.

To ensure precise and accurate measurements, it is essential that a complete liquid column forms between the upper pedestal and lower pedestal. It is recommended that a precision pipettor (0-2µL) be used to dispense samples.

3. Dispensing Samples onto The Lower Pedestal

Lift the upper pedestal and pipette the sample (0.5µL – 2.0µL) onto the lower pedestal (**Fig. 3**).

Fig. 3 Dispense Sample

Fig. 4 Sample Drop

Lower the upper pedestal onto the sample to form the sample column (**Fig. 5**).

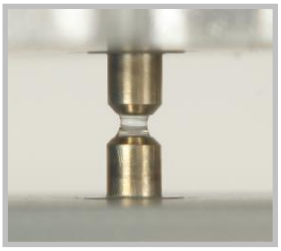


Fig. 5 Sample Column

Note: Please exercise caution when lowering the upper pedestal onto the sample.

To prevent sample carryover, use a soft laboratory wipe and deionized water to clean both pedestals in between sample measurements (**Fig. 6**).

Fig. 6 Clean & Wipe Pedestal

4. OD600 Measurement

The SmartDrop XF includes a cuvette slot for OD600 measurements. Lift the upper pedestal to expose the cuvette slot. Select the OD600 interface on the touch screen. Insert and read a “blank” as required for the experiment. Then add 2~3mL of sample into the cuvette. Place the cuvette into the slot and start the measurement (Fig. 7).

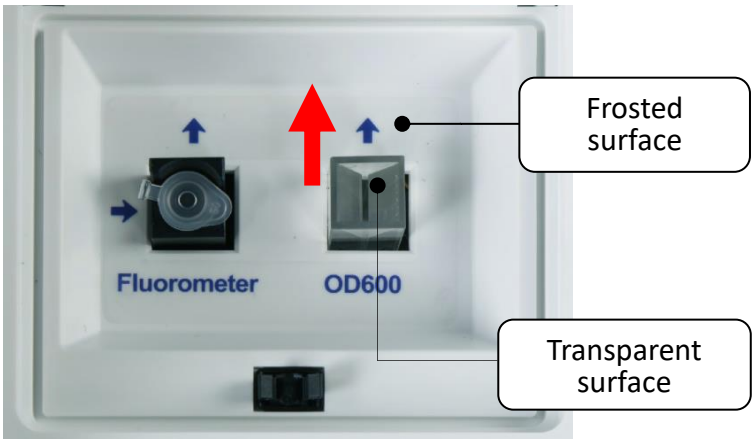


Fig. 7 OD600 & Fluorometer Port

Note： The direction of the light path is shown by the red arrow in the figure above. Please ensure the cuvette is loaded with the correct orientation.

Chapter 4 Programming & Operation

1. Start-up Interface

Upon powering on the instrument, it will perform a self-check, and the start-up screen will be displayed (**Fig. 8)**

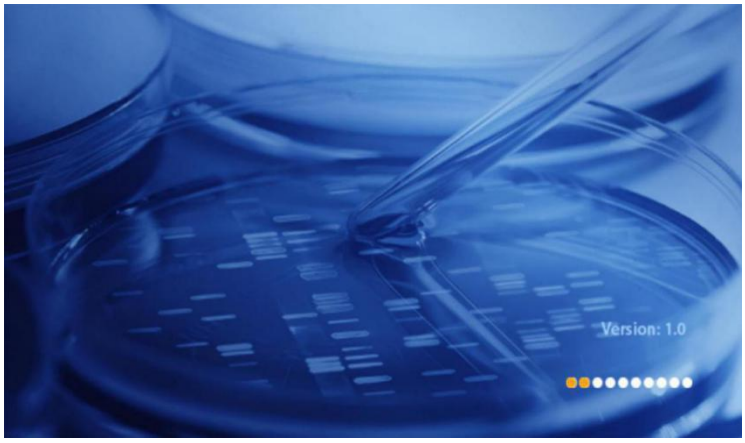


Fig. 8 Start-up Interface

2. Main Menu Interface

Fig. 9 Main Menu Interface

After start-up, the main menu interface will be displayed. There are 7 options: Nucleic Acids, Protein A280, Colorimetry, Fluorometer UV-Vis, OD600, & System Settings

3. Nucleic Acids Interface

Beer-Lambert's Law for DNA/RNA quantitation

The following "Beer—Lambert" equation is used to calculate the concentration of nucleic acids:

$$C = \frac{A * \varepsilon}{b}$$

C＝Sample DNA concentration, unit : ng/μL
A＝Sample absorbance, unit : A
ε＝extinction coefficient, unit: ng-cm/μL
b＝Path Length, unit: cm

Standard DNA/RNA extinction coefficients :
dsDNA：50ng-cm/μL
ssDNA：33ng-cm/μL
RNA：40ng-cm/μL

When the sample column is used, highly concentrated nucleic acid samples can be measured without dilution using a 1.0mm, 0.2mm, or 0.05mm path length. The SmartDrop XF will measure and display sample absorbance values of the 10mm pathlength equivalent of up to 300 A.

The SmartDrop XF will accurately measure dsDNA samples up to 15,000ng/μL without dilution. To do this, the instrument automatically detects highly concentrated samples and adjusts the pathlength to measure the sample absorbance.

Select "Nucleic acid" from the main menu to enter the Nucleic Acids Interface:

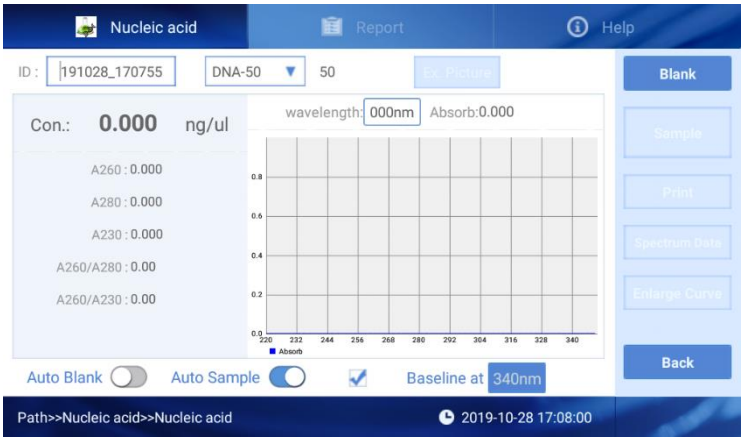


Fig. 10 Nucleic Acids Interface

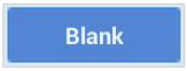
Fig 10; there are three tabs in the Nucleic Acids Interface: Nucleic Acids, Report, and Help.

-

: The sample ID name has a default value of the current date and time. Users can rename the sample ID. One sample ID can contain up to 1000 measurement values.

-

: Select the sample type: DNA-50 for dsDNA, RNA-40 for RNA, ssDNA-33 for ssDNA. For a different nucleic acid type, select “others” and enter the extinction coefficient.

- 

: Perform a blank reading. This step is essential before measurement. Blank absorbance values are typically in the range of 0.004-0.03 Abs and are valid for up to 30 minutes. The instrument will automatically remind the user to perform another blank reading after 30 minutes.

-

: Spectrum normalization; The baseline is automatically set to the absorbance of the sample at 340nm and can be modified. This feature can remove spectroscopic signals from sample measurements by subtracting the measured absorbance at a specified baseline correction wavelength from the absorbance values at all wavelengths of a measured sample.
    - **Note:** If baseline calibration is not performed, the spectroscopic signals will not be separated from interference/background effects and will lead to inaccurate results.

-

: When turned on, the blank measurement starts automatically when the upper pedestal is lowered.
    - **Note:** The automatic blank only takes effect when no blank readings have been made in a current run.

-

: When turned on, the sample measurement starts automatically when the upper pedestal is lowered.
    - **Note:** Automatic sample detection only takes effect after a blank reading has been performed.

- The icon appears in the upper right corner to indicate an error in reading blank/sample volumes. Please clean and wipe the pedestal and perform another blank reading. If the problem persists, contact Accuris Instruments.

Operation:

1. Set the Sample ID.
2. Clean the upper and lower pedestals with a lint-free wipe, add 2μL buffer solution to perform a blank reading.
3. Clean the buffer solution on the pedestals with a wipe.
4. Measure a 2μL sample volume and click “Measure” to detect the sample.
   Note: A blank reading must be performed prior to sample measurements. The sample volume must be equivalent to the volume used to set the blank reading.
5. Clean and dry the pedestal between measurements.

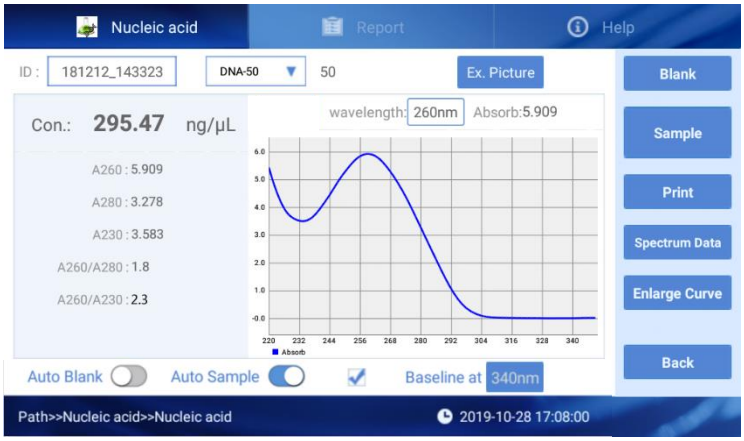


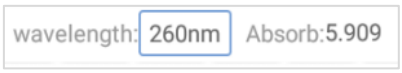
Fig. 11 Nucleic Acid Sample Results

The sample concentration and absorbance ratios will display on the left side of the interface **(Fig. 12)**.

Fig. 12 Sample Concentration & Absorbance Ratios

Conc.：Calculated nucleic acid concentration.
A260: The sample absorbance at 260nm (10mm pathlength equivalent).
A280: The sample absorbance at 280nm (10mm pathlength equivalent).
A230: The sample absorbance at 230nm (10mm pathlength equivalent).
A260/A280: The ratio of corrected absorbance values at 260nm to corrected absorbance values at 280nm. An A260/A280 ratio of ~1.8 is generally accepted as pure for DNA (~2.0 for RNA). Acidic solutions will under-represent the A260/A280 ratio by 0.2 – 0.3 units, whereas basic solutions will over-represent the A260/280 ratio by 0.2 – 0.3 units.

A260/A230： The ratio of corrected absorbance values at 260nm to the corrected absorbance values at 230nm.This ratio can be used as a secondary measure of nucleic acid purity. An A260/A230 ratio within the range of ~1.8 – 2.2 is considered as pure for nucleic acids. Lower ratio values indicate the presence of contaminants that absorb strongly at or near 230nm.



: Input a wavelength to view the corresponding sample absorbance value **(Fig. 13)**.

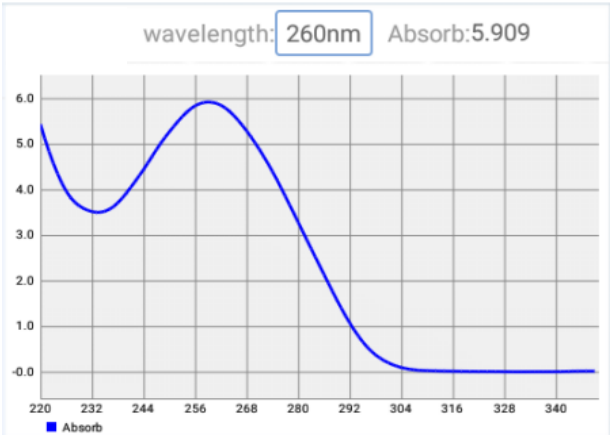


Fig. 13 Nucleic Acid Sample Absorbance Curve (220nm – 350nm)

Ex. Picture :Export the graph (PNG file) and full spectrum absorbance data (1nm steps) to a USB flash drive.

Measure : Begin sample measurement.

Print : Print the calculated data.

Spectrum Data : Save the full spectrum absorbance data in 1nm steps.

Enlarge Curve : Zoom into the sample absorbance curve.

Back : Return to the main menu interface.

Nucleic Acid Report Interface

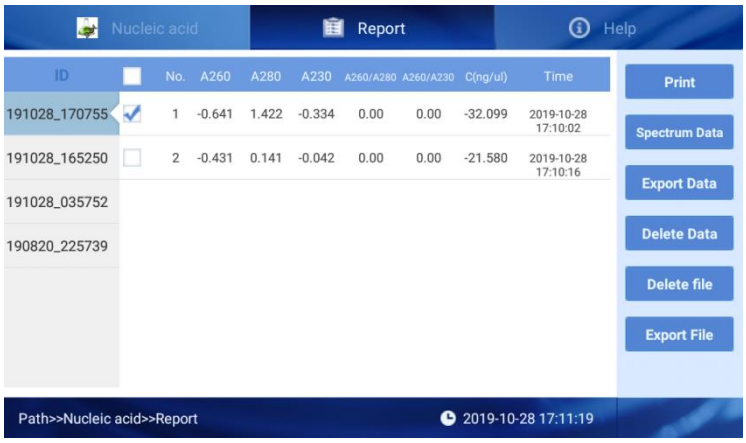


Fig. 14 Nucleic Acid Report Interface

Select the “Report” tab at the top of the Nucleic Acid Interface (**Fig. 14**).

Users can select previously saved results by the file name.

Print : Print the selected data from the built-in printer.

Spectrum Data : To view sample absorbances at a specific wavelength, input a wavelength and the red coordinate line will display the corresponding absorbance value (**Fig. 15**).

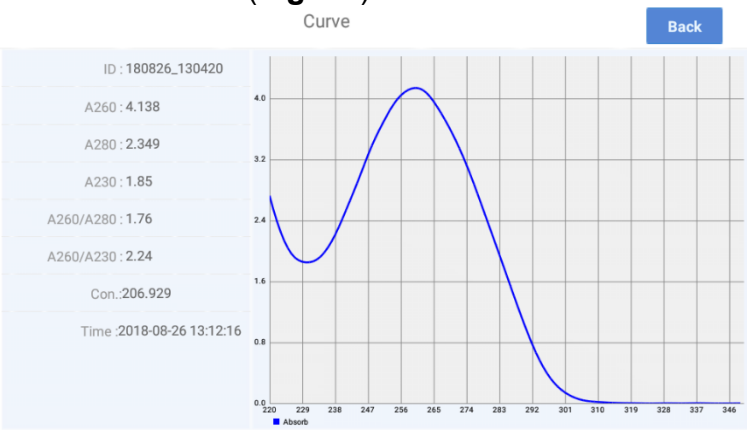


Fig. 15 Nucleic Acid Sample Absorbance Curve (220 – 350nm).

Export Data : Export the result to a USB flash drive.

Delete Data : Delete the selected results.

Delete file : Delete the selected files

Export File : Export the selected files to a flash drive.

4. Protein A280 Interface

Introduction

The Protein A280 interface can be used to quantify purified proteins that contain amino acids such as tryptophan, tyrosine, or cys-cys disulfide bonds. These amino acids exhibit peak absorbance at 280nm. The following sample types can be selected: “A280”, “BSA”, “IgG”, “Lysozyme”, & “Others”.

This interface does not require the generation of a standard curve. Sample absorbance values (260nm & 280nm) and A260/A280 ratios can be measured and displayed. A baseline correction can be used for normalization. Like the Nucleic Acids interface, the Protein A280 interface automatically switches the pathlength to 0.2mm when a highly concentrated protein sample is detected and displays 10mm pathlength equivalent data.

Protein A280 Interface

Select “Protein A280” from the main menu interface.

Fig. 16 Protein A280 Interface

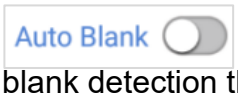
Fig. 16; There are three options at the top of the screen, Protein A280, Report, and Help.

- ID : 191028_171239 : The sample ID name has a default value of the current date and time. Users can rename the sample ID. One sample ID can contain up to 1000 measurement values.
- A280 : Select the sample type: A280, BSA, IgG, Lysozyme. Select “others” and type in the extinction coefficient.
- Blank : Perform a blank reading. This step is essential before

measurement. Blank absorbance values are typically in the range of 0.004-0.03 Abs and are valid for up to 30 minutes. The instrument will automatically remind the user to perform another blank reading.

-

: Spectrum normalization; The baseline is automatically set to the absorbance of the sample at 340nm and can be modified. This feature can remove spectroscopic signals from sample measurements by subtracting the measured absorbance at a specified baseline correction wavelength from the absorbance values at all wavelengths of a measured sample.
Note: If baseline calibration is not performed, the spectroscopic signals will not be separated from interference/background effects and will lead to inaccurate results.

- 

: When turned on, the instrument will automatically perform a blank detection the first time the pedestal is lifted and closed
Note: The automatic blank only takes effect when no blank readings have been made in a current run.

-

: When turned on, the instrument will automatically perform sample measurements once the sample column has formed.
Note: Automatic sample detection only takes effect after a blank reading has been performed.

- The icon appears in the upper right corner to indicate an error in reading blank/sample volumes. Please clean and wipe the pedestal and perform another blank reading. If the problem persists, contact Accuris Instruments.

Operation:

1. Set the Sample ID.
2. Clean the upper and lower pedestals with a lint-free wipe, add 2μL buffer solution to perform a blank reading.
3. Clean the buffer solution on the pedestals with a wipe.
4. Measure a 2μL sample volume and click “Measure” to detect the sample.
   Note: A blank reading must be performed prior to sample measurements. The sample volume must be equivalent to the volume used to set the blank reading.
5. Clean and dry the pedestal between measurements.

Fig. 17 Protein Sample Results

The sample concentration and absorbance ratios will display on the left side of the interface **(Fig. 18)**.

Fig. 18 Sample Concentration & Absorbance Ratios

Conc.: Calculated protein concentration.
A260: The sample absorbance under 260nm (10mm pathlength equivalent).
A280: The sample absorbance under 280nm (10mm pathlength equivalent).
A260/A280: The ratio of corrected absorbance values at 260nm to the corrected absorbance values at 280nm.This ratio can be used as a secondary measure of nucleic acid purity. An A260/A280 ratio within the range of ~1.8 – 2.2 as pure for nucleic acids. Lower ratio values indicate the presence of contaminants that absorb strongly at or near 280nm.

: Input a wavelength to view sample absorbance values **(Fig. 19)**.

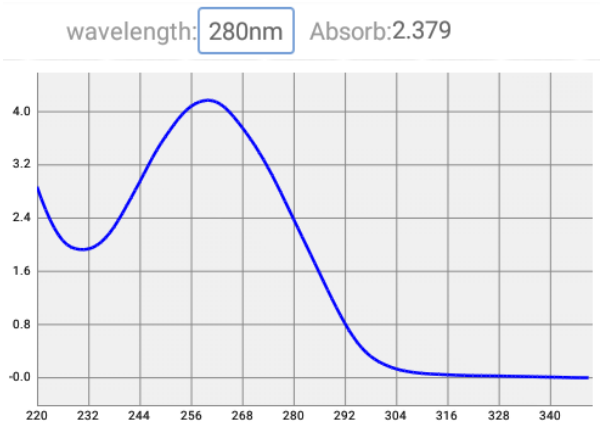


Fig. 19 Protein Sample Absorbance Curve (220nm – 350nm)

Protein A280 Report Interface

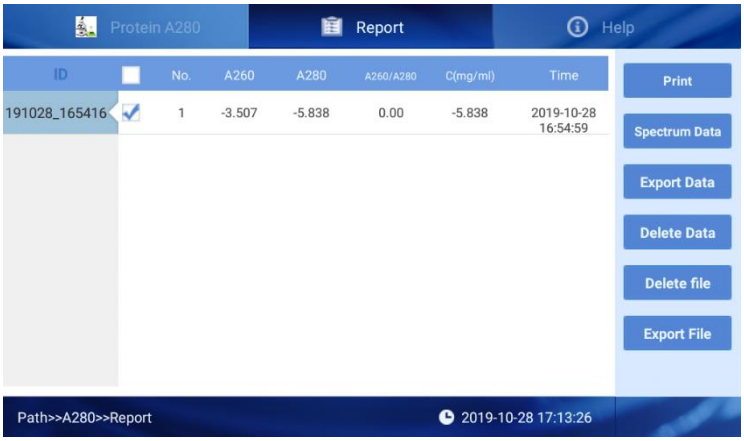


Fig. 20 Protein Report Interface

Note: This interface is similar to the Nucleic Acids detection interface (**see section 3**).

Spectrum Data : To view sample absorbances at a specific wavelength, input a and the red coordinate line will display the corresponding absorbance value (**Fig. 21**).

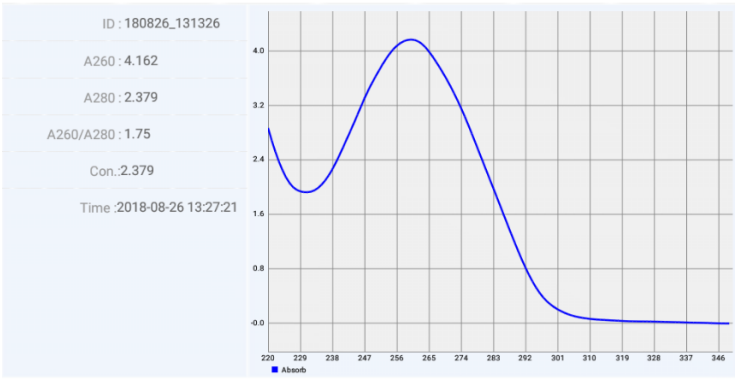


Fig. 21 Protein Sample Absorbance Curve (220 – 350nm)

5. Colorimetry Interface

Introduction
BCA, Lowry, & Bradford protein assays are measured using colorimetric methods, which requires the generation of a standard curve.

BCA Protein Assay:
The BCA Assay is an alternative method for determining protein concentration. It utilizes bicinchoninic acid as a detection reagent to measure protein concentrations in crude samples. This assay measures protein solutions at 562nm and uses a standard curve to calculate the concentration. A baseline-correction can be used for normalization. Bicinchoninic acid is used to detect Cu^{+1}, which forms when Cu^{+2} is exposed to an alkaline environment. A purple chelate is formed when two BCA molecules react with 1 Cu^{+1}. The Cu-BCA chelate is measured at 562nm and baseline-corrected using a 750nm absorbance value.

Lowry Assay:
Folin-Ciocalteu is used as the detection reagent to measure protein concentrations in unpurified protein samples. This assay measures the absorbance of protein solutions at 650nm and uses a standard curve to calculate the concentration. A baseline-correction can be used for normalization. When protein solutions are exposed to cupric sulfate in an alkaline environment, tetradentate copper protein complexes form. Folin-Ciocalteu is reduced in proportion to the chelated copper-complexes which results in the formation of a water-soluble blue product that is measured at 650nm and baseline-corrected using a 405nm absorbance value.

Bradford Assay:
The Bradford Assay is an alternative method commonly utilized for determining protein concentration. It is often used for more dilute protein solutions where lower detection sensitivity is needed. Like the BCA and Lowry Assays, the Bradford Assay requires a standard curve before each run. The Bradford uses the protein-induced absorbance shift of Coomassie Blue dye at 595nm to measure protein concentration. The bound protein-dye complex is measured at 595nm and baseline-corrected using a 750nm absorbance value.

Note: Please perform measurements quickly. Coomasie dye-dye & dye-protein aggregates can form the longer it sits, which will result in fluctuations in absorbance readings.

Colorimetry Interface

A standard curve must be generated prior to sample measurement.

Fig. 22 Colorimetry Interface

BCA-562 : Select the assay type: BCA-562, Bradford-595, Lowry-650.

Curve uuuuu : Select the curve.

Operation:

1. Set the colorimetry and curve type.
2. Ensure that the upper and lower pedestals have been wiped clean. Pipette 0.5μL-2μL of buffer solution to perform a blank reading.
3. Wipe the buffer solution off the pedestals with a laboratory wipe.
4. Measure a 0.5μL-2μL sample. Select “Sample” to perform the reading. The sample volume must be equivalent to the volume used to set the blank reading.

Note: A blank reading must be performed prior to sample measurements.

5. Clean and wipe the pedestals between each sample measurement.

Curve

To generate a standard curve, at least 5 standard sample concentrations are needed. The concentration range of the standards should cover all unknown sample concentrations.

Colorimetry Curve Interface:

Click the “Curve” tab to build a standard curve **(Fig.23)**.

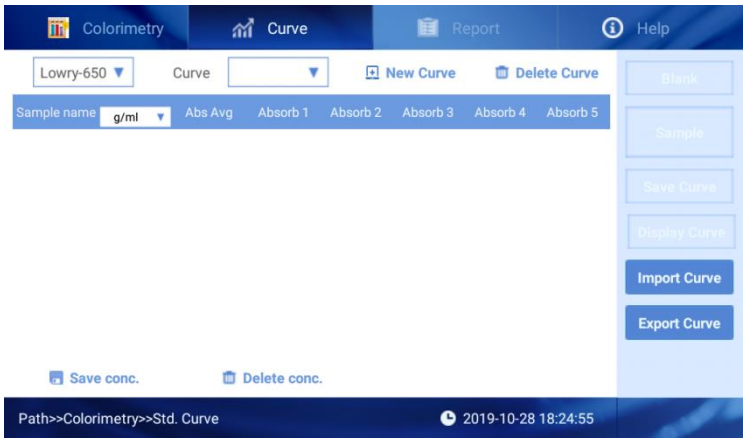


Fig. 23 Colorimetry Curve Interface

Standard Curve Generation:

Click New Curve . Input the curve name and click “Confirm”. The standard curve table will display.

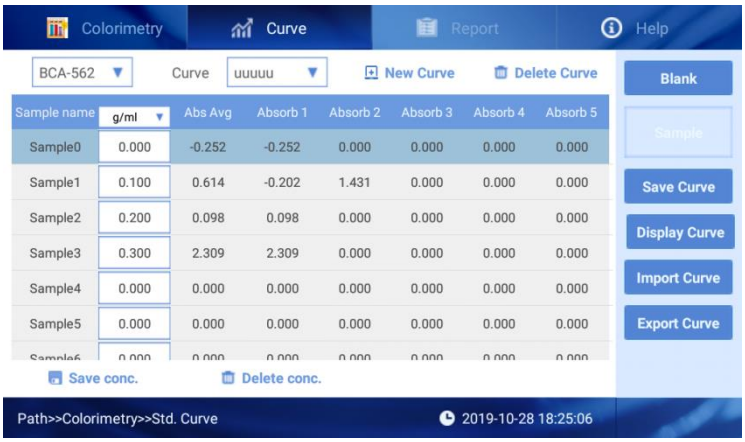


Fig. 24 Standard Curve Interface

Click g/ml to choose the unit for samples and Sample0 20 to input the concentration.

Select a standard sample and then click “Blank” to perform a blank reading. Then, click “Measure” to measure the absorbance of the standard sample.

Each standard sample can be measured up to 5 times, and the average value can be used to build the standard curve. Users can delete the standard sample values or delete single values amongst the 5 measurements of an individual sample.

After measuring all standards, click Save Curve to save the curve.

Note: Please save the curve it prior to further operation.

Display Curve : View the standard curve as below:

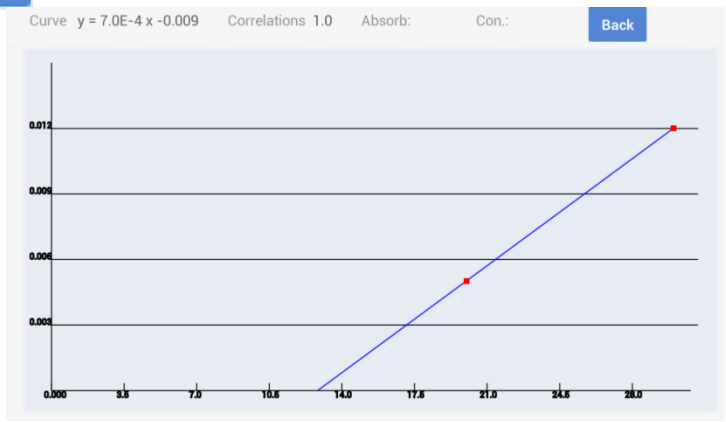


Fig. 25 Standard Curve

Import Curve : Import a standard curve from a USB flash drive.

Export Curve : Export a standard curve to a USB flash drive.

Save conc : Save the inputted standard sample concentration value.

Delete conc : Delete the inputted concentration value.

Colorimetry Report Interface

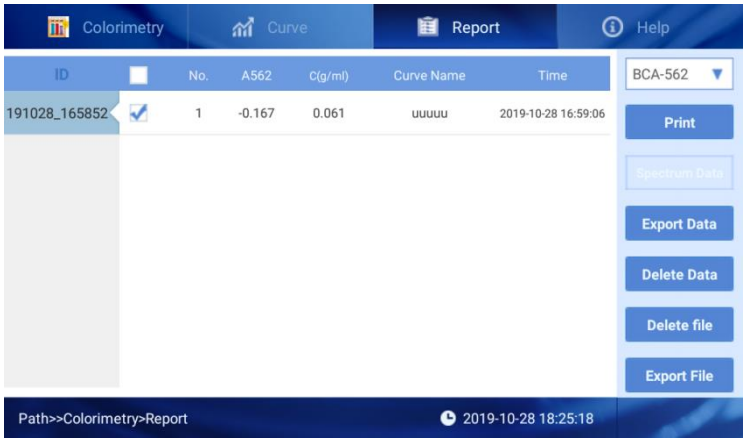


Fig. 26 Colorimetry Report Interface

This interface is similar to the Nucleic Acids detection interface (**see section 3**).

BCA-562 : Choose the assay type and the detection data will be displayed.

6. Fluorometer Interface

Introduction

The Fluorometer interface allows for accurate quantitation of nucleic acids and proteins that have been labeled with a fluorescent dye. The default excitation/emission wavelength for fluorescence readings is set to 460/525nm. Select “Fluorometer” from the main menu interface to enter the fluorometer interface (**Fig. 27**). For direct sample fluorescence measurements, select “Fluorescence” to enter the fluorescence interface. In this interface, no standard curve is required.

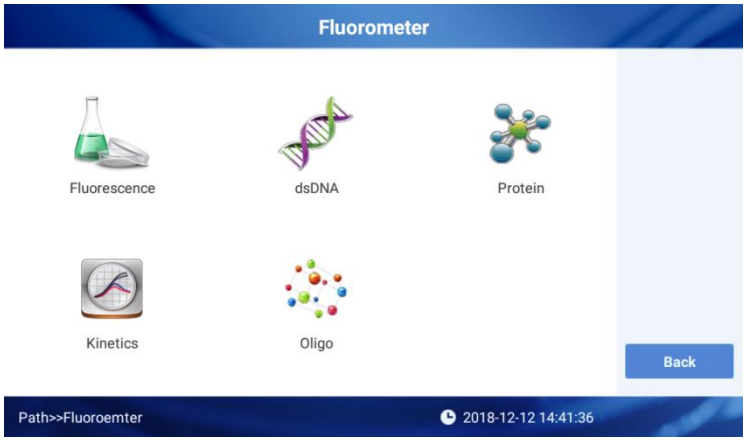


Fig. 27 Fluorometer Interface

Fluorescence Interface

Select “Fluorescence” to enter the fluorescence interface (**Fig. 28**).

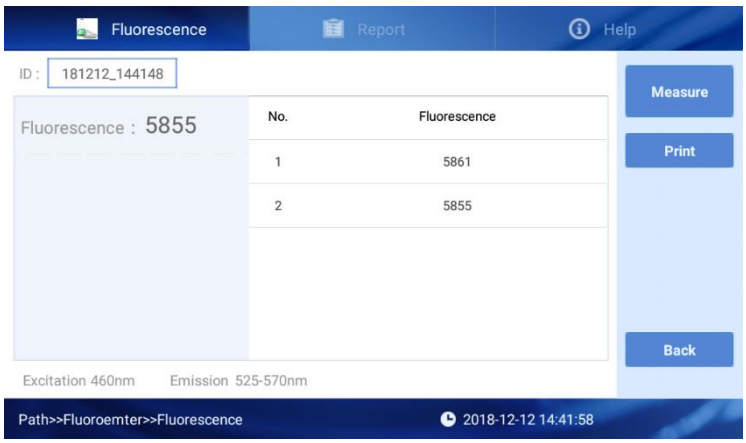


Fig. 28 Fluorescence Interface

Measure : Begin sample measurement.

Print : Print the calculated data.

Excitation 525-570nm Emission 460nm : Current excitation/emission wavelengths.

Operation:

1. Set the sample ID.
2. Put the tube holder into the fluorescence sample port.
3. Add 200μl of sample into a 0.5ml PCR tube and place it into the sample port.
4. Select “Measure” to begin sample measurement; results will be displayed towards the left of the interface.

Fluorescence Report

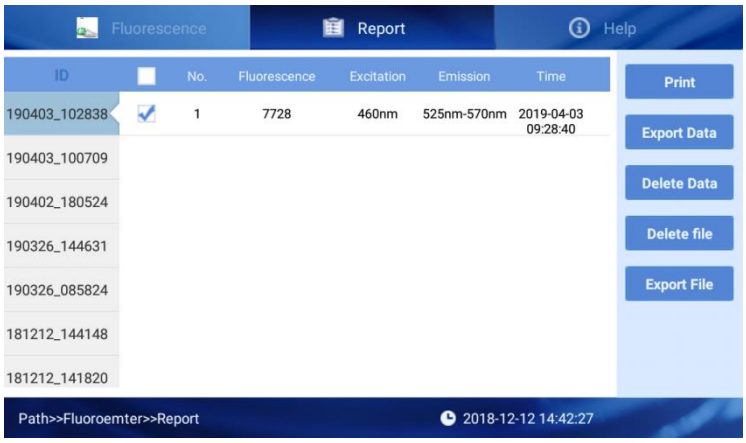


Fig. 29 Fluorescence Report Interface

This interface is similar to the Nucleic Acids detection interface (**see section 3**).

dsDNA, Protein, & Oligo Interfaces

The “dsDNA”, “Protein” or “Oligo” interfaces require the generation of a standard or calibration curve. The dsDNA interface can measure samples concentrations as low as 0.5pg/μl. **Note:** The interfaces for dsDNA, Protein, & Oligo are identical.

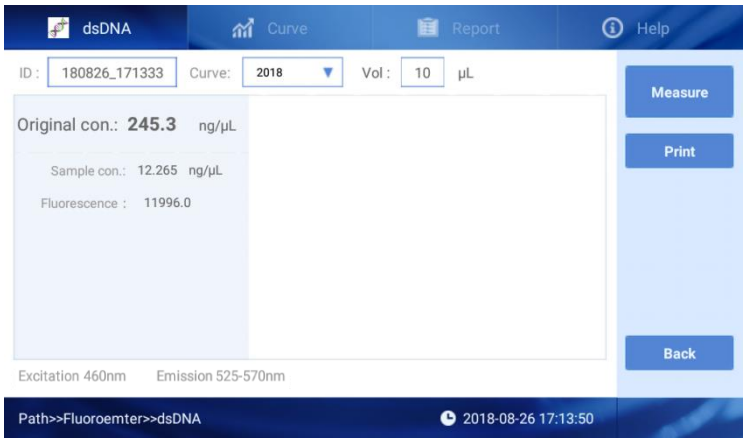


Fig. 30 dsDNA Interface

ID : 180826_171333 : The sample ID name has a default value of the current date and time. Users can rename the sample ID. One sample ID can contain up to 1000 measurement values.

Curve: 2018 : Select a standard curve.

Vol : 10 μL : Input the original sample volume.

Measure : Begin sample measurement.

Print : Print the calculated data.

Fig. 31 dsDNA Sample Results

Original con.: The original sample concentration.
Sample con.: The PCR tube sample concentration.
Fluorescence: The fluorescence value of the measurement.

dsDNA Standard Curve Interface

Select “Curve” to enter the dsDNA standard curve interface (**Fig. 32**).
To generate a standard curve, at least 5 standard sample concentrations are needed. The concentration range of the standards should cover all unknown sample concentrations.

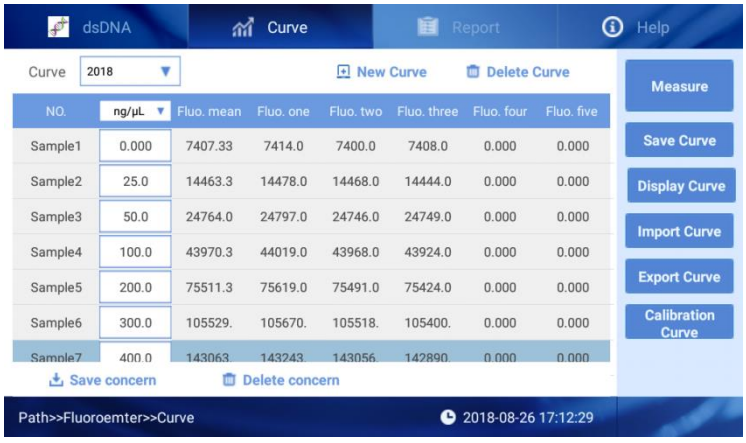


Fig. 32 dsDNA Standard Curve Interface

This interface is similar to the colorimetry curve interface (**see Chapter 4.5**). Please note the following differences:

- A blank is not required for this interface; select “Measure” to begin sample measurement directly.
- Calibration Curve: Calibrate the created standard curve to eliminate potential drift error caused by the instrument.

Standard Curve Generation:

Select New Curve and input the curve name and select the curve type (**Fig. 33**).

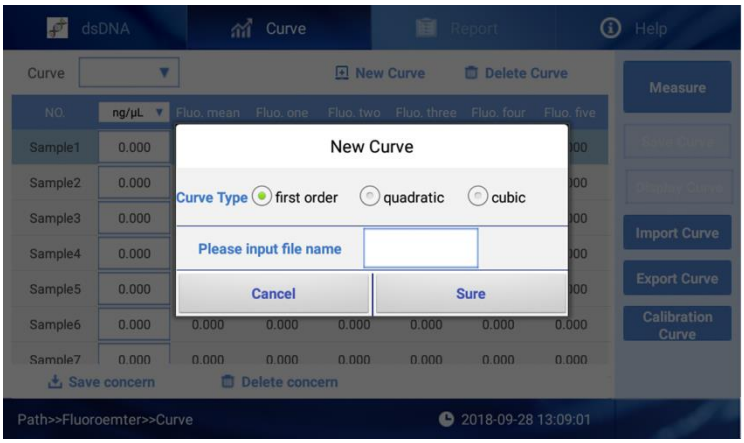


Fig. 33 New Standard Curve

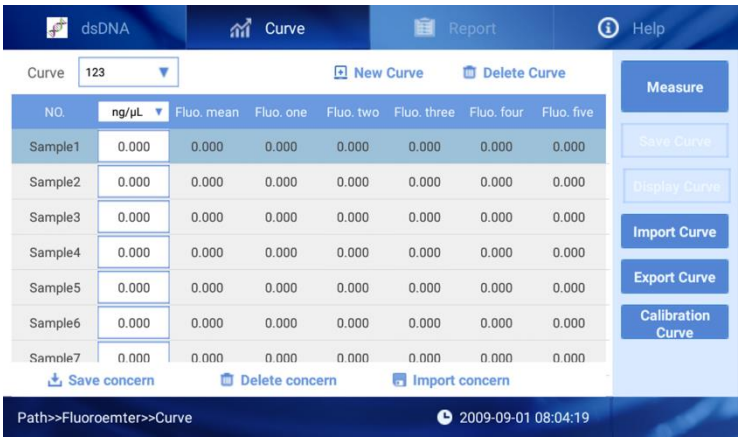


Fig. 34 Standard Curve Interface

Select ng/μL to set the units of standards. To input the concentration of standards, select Sample1 0.000 . Make sure the set concentration is the same as standard sample. There is no requirement of the orders when set the concentrations.

Fig. 34; when a standard sample is selected, the row will be highlighted in blue.

Select “Measure” to begin fluorescence detection. Each standard sample can be measured up to 5 times, and the average value can be used to build the standard curve. Users can delete the standard sample values or delete single values amongst the 5 measurements of an individual sample.

Click Save Curve to save the created standard curve.

Calibration Curve Interface:

Click Calibration Curve to enter the calibration curve interface.

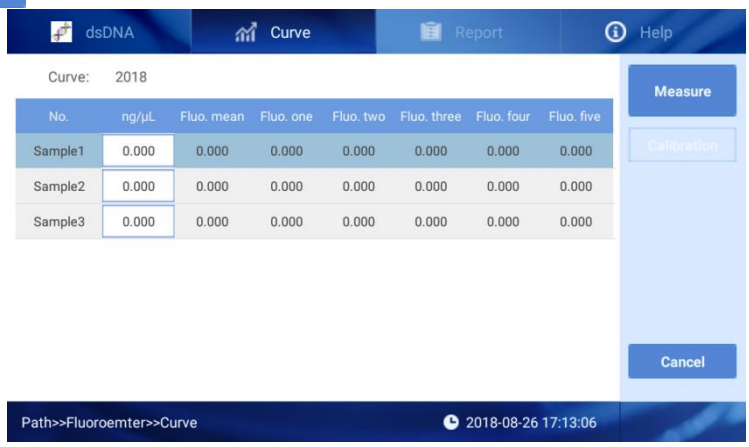


Fig. 35 Calibration Curve Interface

Input the concentration of the samples. Select “Measure” to begin the selected standard fluorescence detection. Select “Calibrate” to complete the calibration.

dsDNA Sample Measurement

After generating a standard/calibration curve, return to the dsDNA interface (**Fig. 30**) for sample measurements.

Operation:

1. Set the sample ID, standard curve, and input the original sample volume.
2. Put the tube holder into the fluorescence sample port.
3. Add 200μl of sample into a 0.5ml PCR tube and place it into the sample port.
4. Select “Measure” to begin sample measurement; results will be displayed towards the left of the interface.

dsDNA Report Interface

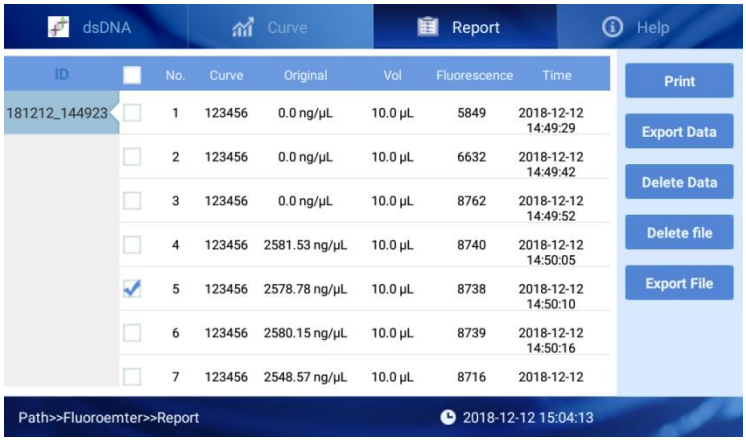


Fig. 36 dsDNA Report Interface

This interface is similar to the Nucleic Acids detection interface (**see section 3**).

Kinetics Interface

In the Fluorometer interface, click “Kinetics” enter the interface (**Fig. 37**). In this interface, kinetic fluorescence readings can be made, and a kinetic curve will be displayed.

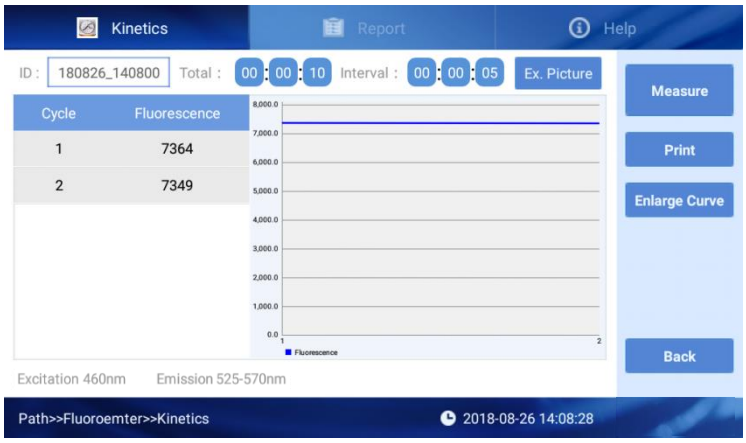


Fig. 37 Kinetics Interface

ID : 180826_140800 : Input the sample ID

Total : 00 : 00 : 10 : Set the total time (Hour: Minute: Second).

Interval : 00 : 00 : 05 : Set the interval between two tests (Hour: Minute: Second).

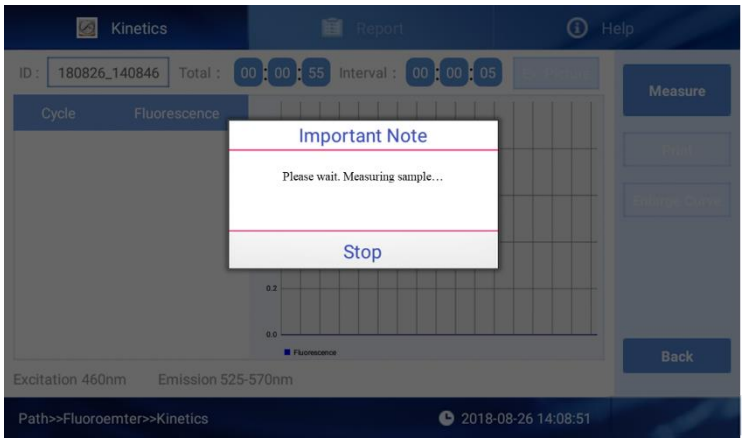


Fig. 38 Kinetics Sample Detection

Ex. Picture :Export the graph (PNG file) and full spectrum absorbance data (1nm steps) to a USB flash drive.

Print : Print the calculated data.

Enlarge Curve : Zoom into the sample absorbance curve.

Operation:

1. Set the sample ID, standard curve, and input the original sample volume.
2. Put the cuvette holder into the fluorescence sample port.
3. Add 200μl of sample into a 0.5ml PCR tube and place it into the sample port.
4. Select “Measure” to begin sample measurement; results will be displayed towards the left of the interface.

Kinetics Report Interface

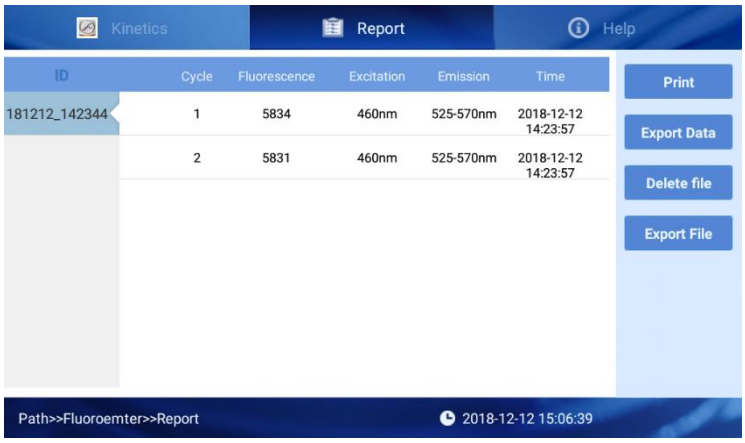


Fig. 39 Kinetics Report Interface

This interface is similar to the Nucleic Acids detection interface (**see section 3**).

7. UV-Vis Interface

Introduction

The UV-Vis module allows the SmartDrop XF to function as a conventional spectrophotometer. Sample absorbances will display from 200nm to 800nm. Samples with high absorbance values (10mm pathlength equivalent of 300A) can be measured directly.

UV-Vis Measurement

Fig. 40 UV-Vis Interface

Click **Blank** to set a blank reading. After setting a blank, click **Blank data** to enter the full wavelength interface of the blank sample.

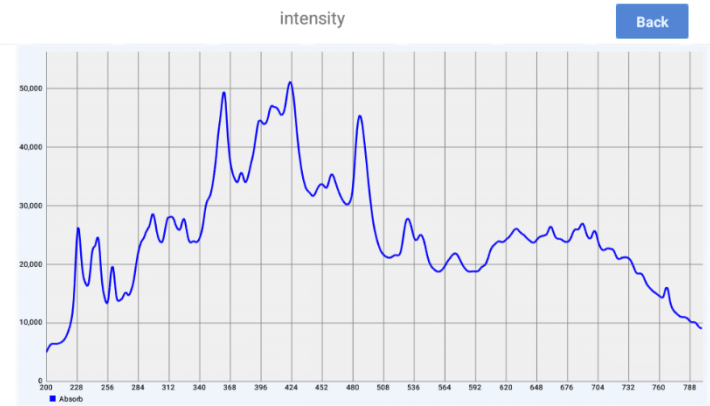


Fig. 41 Blank Full Wavelength Interface (200 - 800nm)

Users can input up to 5 wavelengths before detection and the corresponding absorbance values will be displayed after detection **(Fig. 42)**.

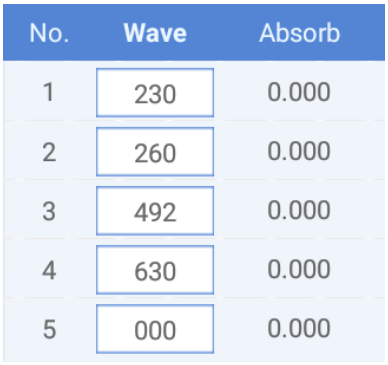


Fig. 42 Select Wavelengths for Measurement

After blank detection, click Measure to perform a sample reading. Click Sample data to enter the full wavelength interface of the sample.

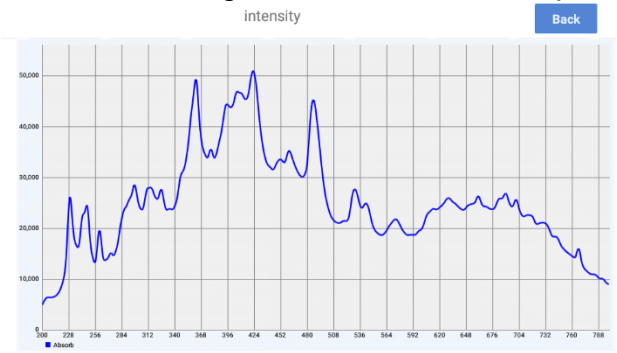


Fig. 43 Sample Full Wavelength Interface

Operation:

1. Set the Sample ID.
2. Clean the upper and lower pedestals with a lint-free wipe, add 2μL buffer solution to perform a blank reading.
3. Clean the buffer solution on the pedestals with a wipe.
4. Measure a 2μL sample volume and click “Measure” to detect the sample.
   Note: A blank reading must be performed prior to sample measurements. The sample volume must be equivalent to the volume used to set the blank reading.
5. Clean and dry the pedestal between measurements.

UV-Vis Report Interface

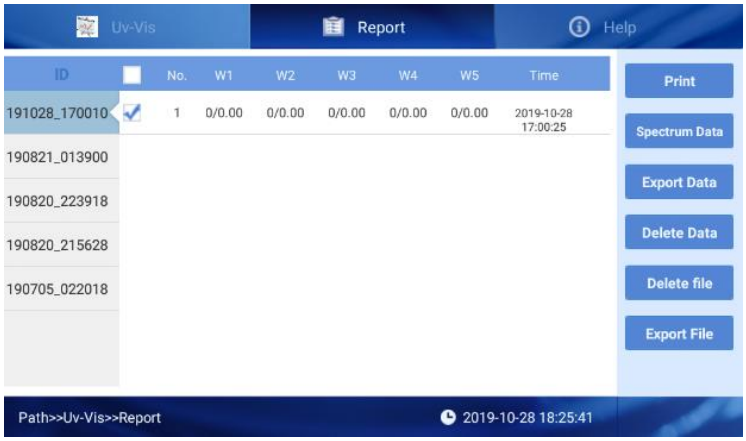


Fig. 44 UV-Vis Report Interface

Spectrum Data : Click to enter the UV-Vis Full Spectrum Interface. Input a wavelength to view the corresponding sample absorbance value **(Fig. 45)**.

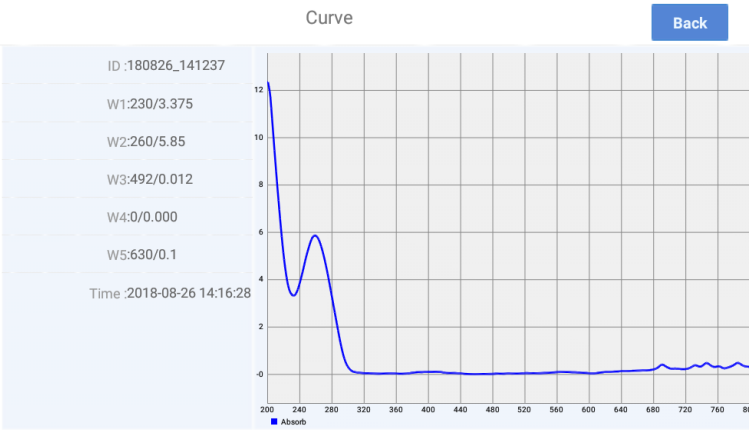


Fig. 45 UV-Vis Full Spectrum Interface

8. OD600 Interface

Introduction

The OD600 function allows for measuring absorbance values at 600nm. It is commonly used for measuring the growth rate of bacterial cell cultures by measuring absorbance of the culture in growth media at 600nm. The Beer-Lamber equation is used to calculate the concentration (**see section 3**). This interface does not require the generation of a standard curve.

OD600 Interface

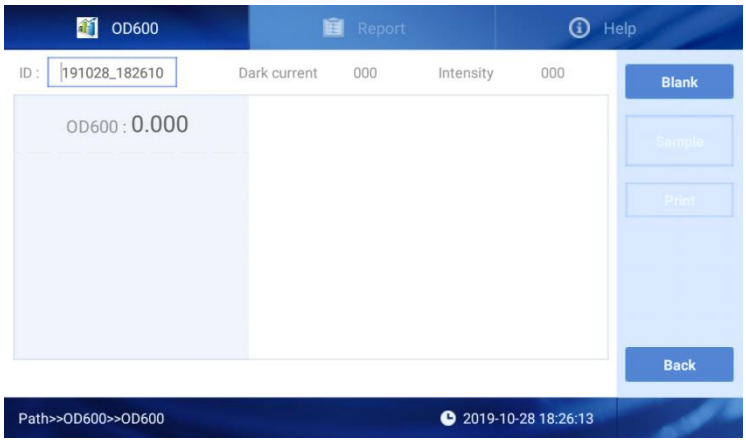


Fig. 46 OD600 Interface

Operation:

1. In the main instrument interface, click OD600 icon.
2. Set the sample ID.
3. Lift the spectrophotometer arm and place a 1.5 mL cuvette containing blanking solution (e.g. media) into the cuvette port.
4. On the instrument screen, select “blank”.
5. Replace the cuvette containing the blank solution with the cuvette containing the sample in the cuvette port and select “Sample” on the screen of the instrument.
6. Repeat the previous step until samples have been read by the instrument.

OD600 Report Interface

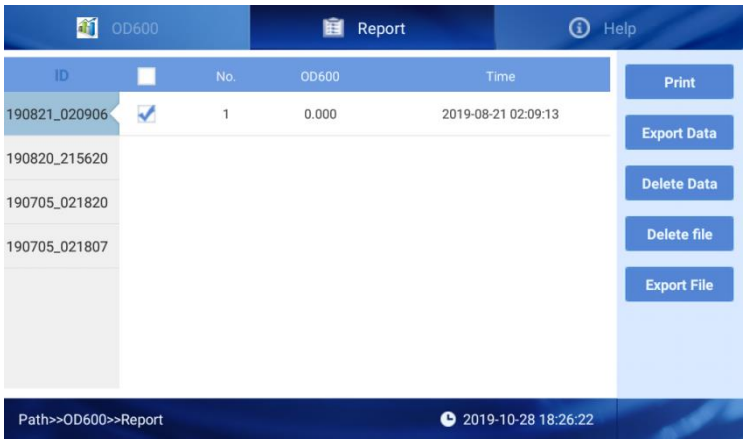


Fig. 47 OD600 Report Interface

This interface is similar to the Nucleic Acids detection interface (**see section 3**).

9. System Settings Interface

Click “System” on the main interface to enter the System Settings Interface **(Fig. 48)**.

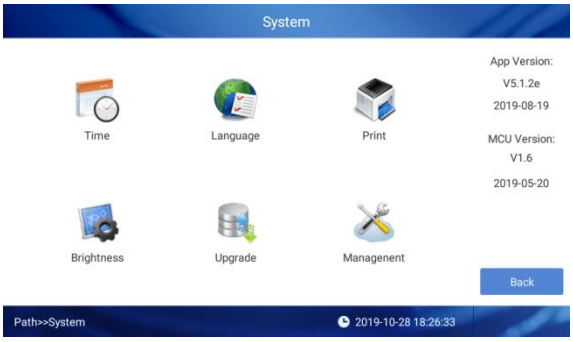


Fig. 48 System Settings Interface

Date & Time Settings Interface

Click the “Time” icon to enter the date and time settings interface.

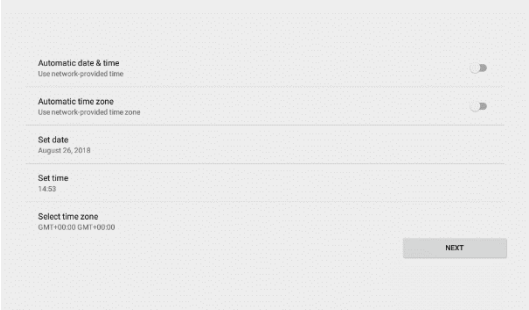


Fig. 49 Date and Time Settings Interface

Click “Set date” to enter the Date Settings Interface **(Fig. 50)**. Click “Set Time” to enter the Time Settings Interface **(Fig. 51)**.

Fig. 50 Date Settings Interface

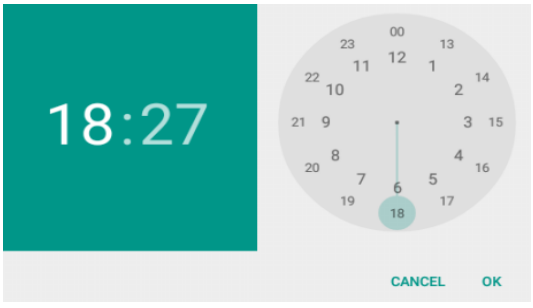


Fig. 51 Time Settings Interface

Print

Click the “Print” icon to set the print mode.

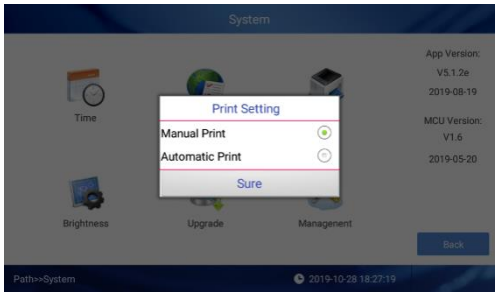


Fig. 52 Print Settings Interface

Brightness

Click the “Brightness” icon to enter the Brightness Settings Interface. Use the slider to adjust the brightness of the display.

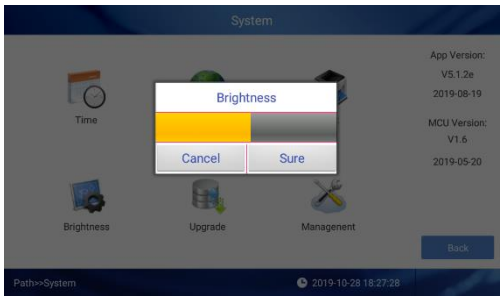


Fig. 53 Brightness Settings Interface

Chapter 5 Troubleshooting

Fault	Analysis	Troubleshooting
Instrument does not power on.	No power supply, Switch defective, Power adapter defective.	Check the power supply, Replace the switch, Contact Accuris Instruments.
Measurement results not precise	Sample column unformed, Pedestal contaminated	Add sample again, make sure the liquid column formed well, Clean the pedestals, Contact Accuris Instruments.
OD600 module failure	Poor connection between cable and board.	Contact Accuris Instruments.
Insufficient light intensity error	Analysis module defective, optical fiber broken.	Contact Accuris Instruments.
Touch screen error	Power supply does not have effective grounding.	Provide effective grounding power supply.
Communication timeout	Analysis module communication failure.	Contact Accuris Instruments.