

Apostle NanoFlex 800

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Micro-Spectrophotometer

THANK YOU

Thank you for purchasing the Apostle NanoFlex 800 Micro-Spectrophotometer. This manual is provided as a guide to operating and troubleshooting the instrument. Read the instructions carefully and save this manual for future reference.

Please check the instrument and packing list to ensure all the listed components are present. If anything is missing or damaged, please contact the vendor.

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Safety Warnings and Guidelines

- To ensure safe operation, please read this manual carefully before using the instrument.
- The operation, maintenance, and repair of this instrument should comply with the guidelines and warnings below. Failure to follow these instructions may affect the life of the instrument and warranty.
- This instrument is for indoor use only.
- Unauthorized repairs or opening of the instrument will void the warranty and could result in injury. Please contact Apostle for repairs.
- Immediately stop use and unplug the instrument in the following cases:
 - Liquid has spilled inside the instrument,
 - The instrument is sparking, smoking, or on fire,
 - Abnormal sounds or smells are coming from the instrument,
 - The instrument was dropped or the outer shell was damaged,
 - Basic functions are not working.

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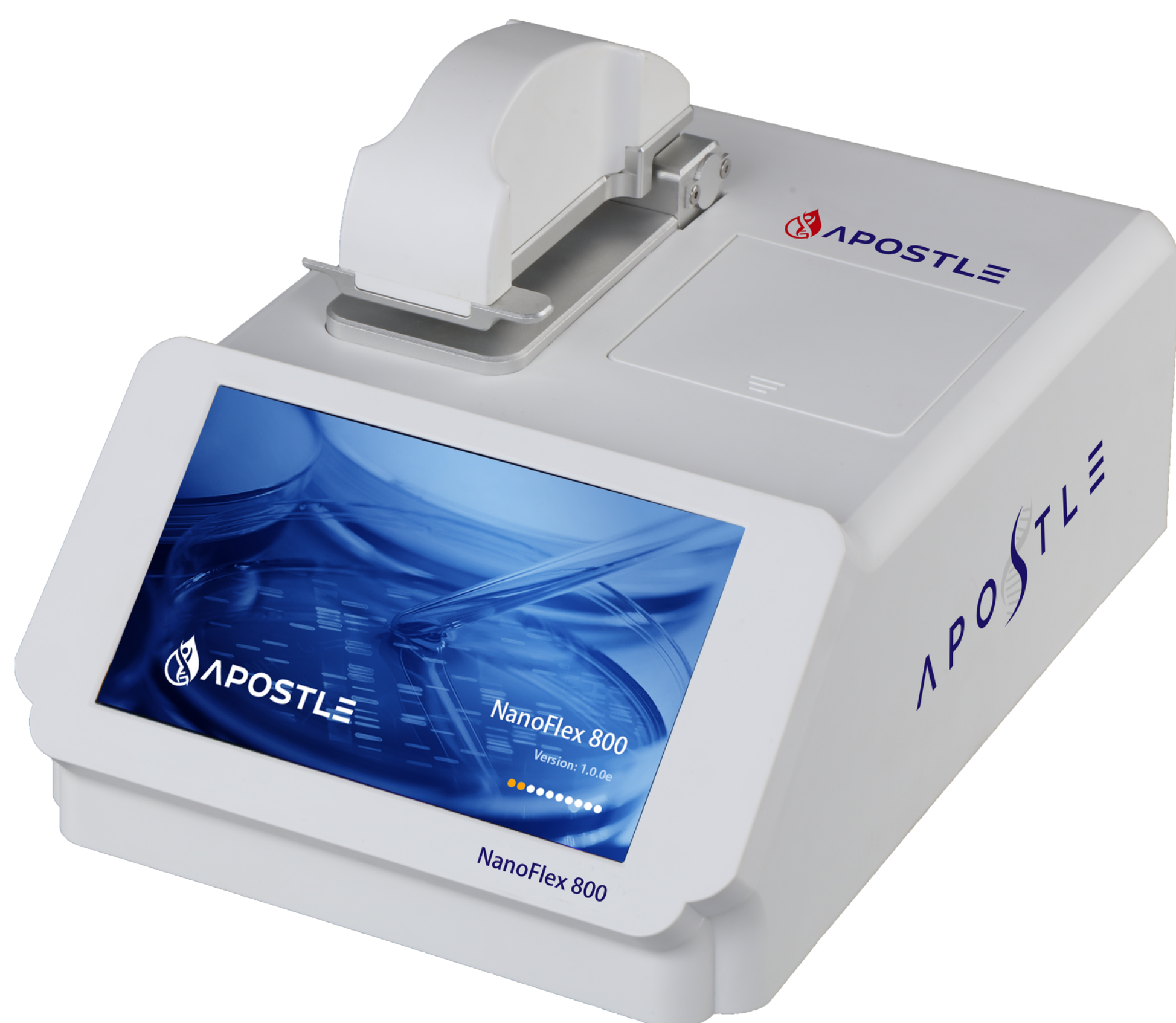
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TROUBLESHOOTING

About Apostle NanoFlex 800

The NanoFlex 800 is a spectrophotometer that measures 0.5 to 2 μL samples with high accuracy and reproducibility. Sample pedestals hold the sample droplet in place with surface tension, forming a column. During measurement, light goes through the sample column.

The NanoFlex 800 can measure highly concentrated samples without dilution, up to 100 times more concentrated than samples measured in a standard cuvette.



2.1 | Normal operating conditions

- Ambient temperature 5–35°C
- Relative humidity less than 70%
- Power supply: 24 V DC, 2A

2.2 | Maintenance

- Clean the pedestal of the spectrophotometer with a lint-free wipe and pure water.
- Clean the outside of the instrument with a lint-free wipe and alcohol.

2.3 | Parameters

Model	NanoFlex 800
Power supply	24 V DC, 2A
Power usage	25 W
Dimensions	208×320×186 mm
Weight	3.6 kg
Minium sample size	0.5 μ L (2 μ L is recommended)
Path length	0.05, 0.2, or 1 mm
Light source	Xenon flash lamp

Specifications

Light source life	> 10 ⁹ flashes		
Detector type	2048-element linear silicon CCD array		
Wavelength range	200–800 nm		
Wavelength accuracy	± 1 nm		
Spectral resolution	≤ 3 nm (FWHM@Hg 253.7 nm)		
Absorbance precision	0.003 Abs (1 mm path length)		
Absorbance accuracy	± 1% (7.332 Abs, at 260 nm)		
Absorbance range	0.04-300 (10 mm equivalent at 260nm)		
Detection range	2–15,000 ng/μL (dsDNA)		
Detection time	< 6 s		
OD600 range	0–4.000 Abs		
OD600 stability	≤ 0.5% (0–3 Abs)	≤ 1% (3–4 Abs)	
OD600 repeatability	≤ 0.5% (0–3 Abs)	≤ 1% (3–4 Abs)	
OD600 precision	≤ 0.005 Abs (0–2 Abs)	≤ 1% (2–3 Abs)	≤ 2% (3–4 Abs)

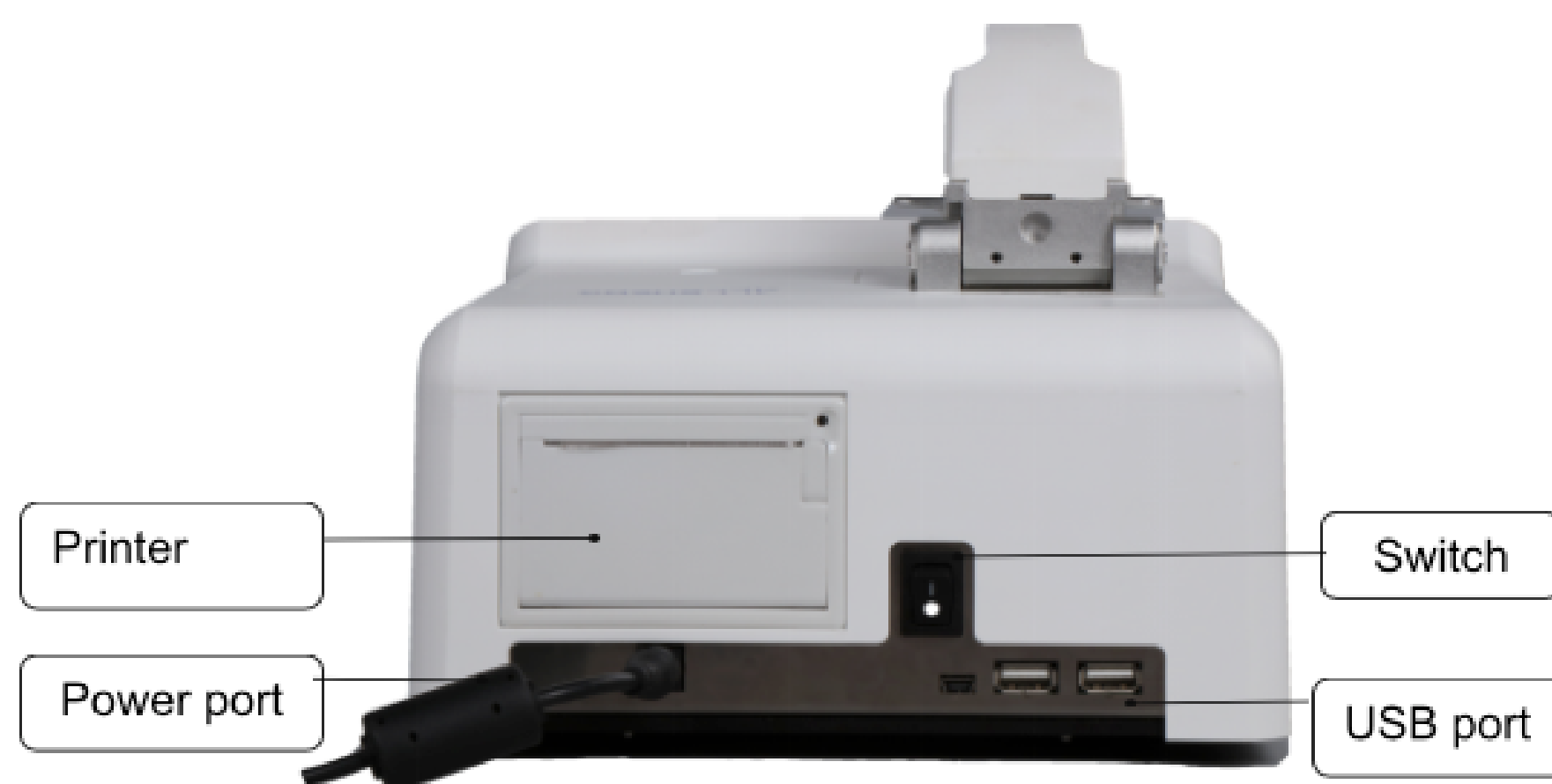
Fluorometer linearity	$R^2 \geq 0.995$
Fluorometer repeatability	$\leq 1.5\%$
Fluorometer stability	$\leq 1.5\%$
Excitation wavelength	$365 \pm 20 \text{ nm}$
Emission wavelength	420 - 480 nm

3.1 | Instrument

3.1.1 Front



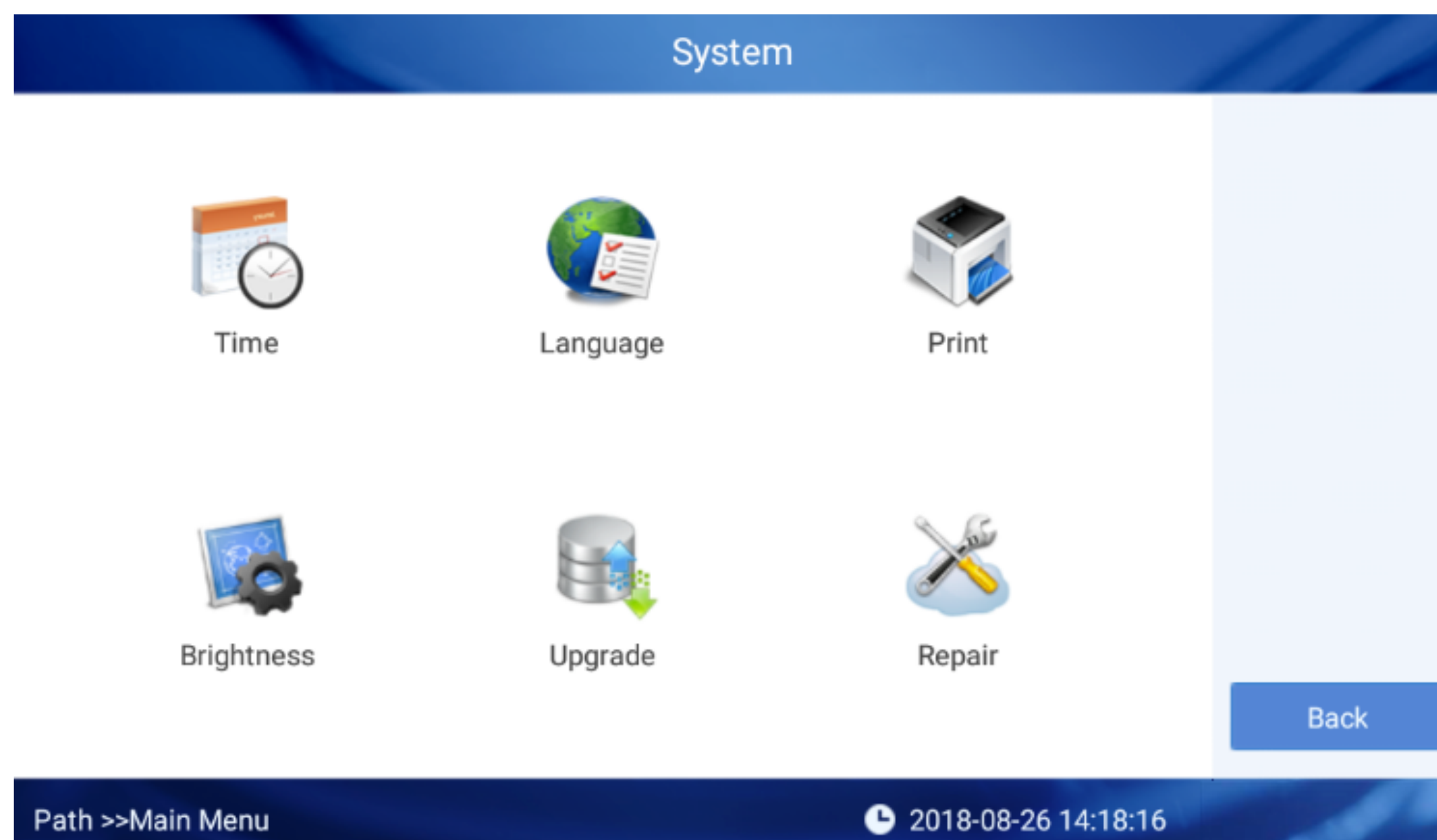
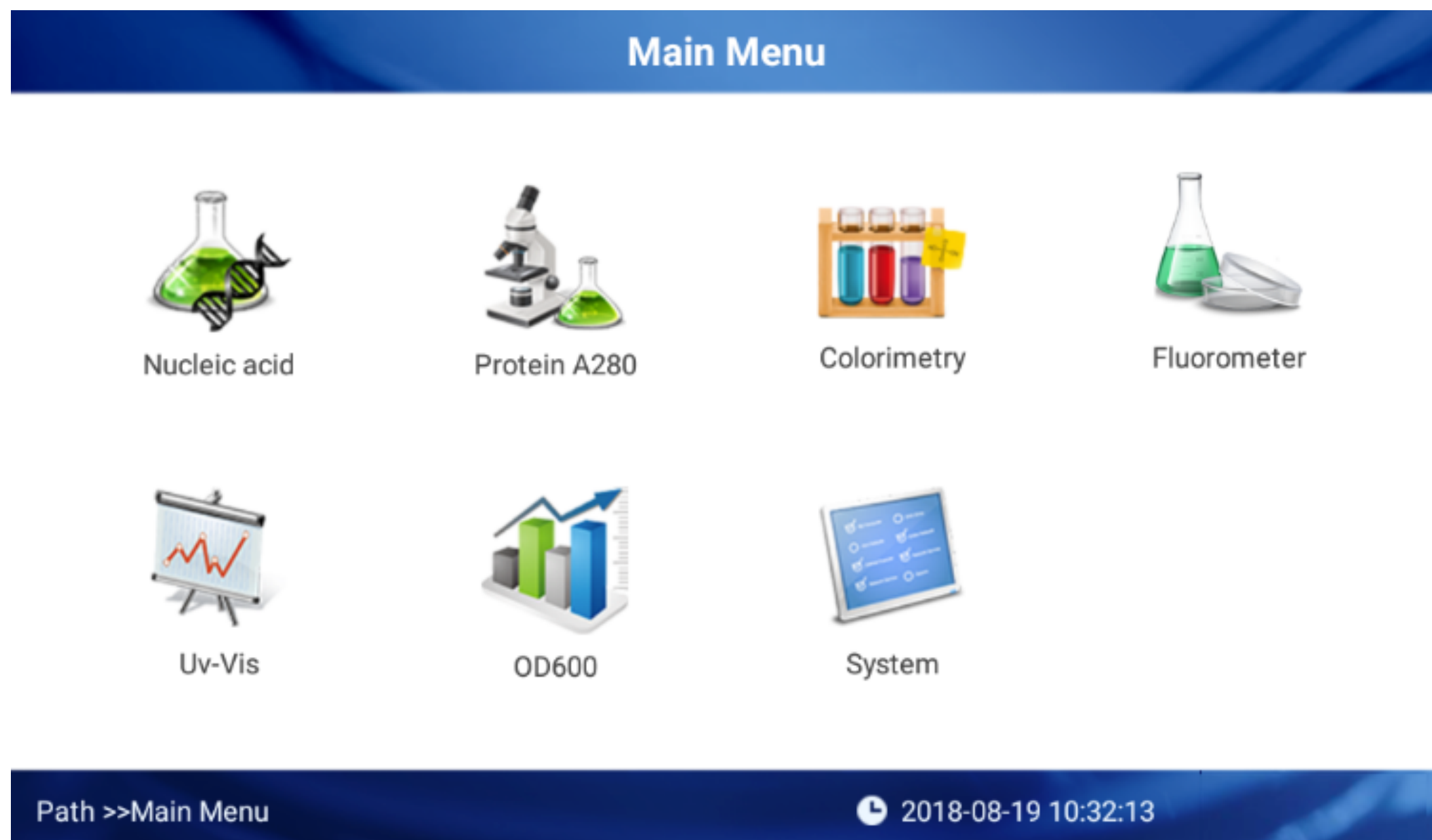
3.1.2 Back



Notes: Make sure the power supply with ground wire.

3.2 | Settings

Press "System" to access system settings, including language, brightness, time and date, 24-hour time format, automatic printing, and software updates.



4.1 | Sample

4.1.1 Sample Size

Although sample size is not critical, it is essential that a complete liquid column is formed between the upper measurement pedestal and lower measurement pedestal. It is best to use a 2- μ L pipettor and maintain consistent volume between samples. A 2 μ L sample is recommended for higher accuracy.

4.1.2 Sample ID

The sample batch ID defaults to the current date and time, e.g., 181212_143114. Users can edit the batch ID. Each ID can store 1000 measurements.

4.2 | Blanking

A blank measurement of the buffer solution is required before measuring samples. The system will automatically blank with the first measurement in each batch ("Auto Blank" can be turned off). Or, press "Blank" to measure a new blank. The accepted range of blank absorbance values is 0.004–0.03 Abs. If the blank is rejected, information will appear under the *i* icon. Blanks are valid for 30 minutes, after which the system will prompt the user to blank again.

4.3 | Baseline Calibration

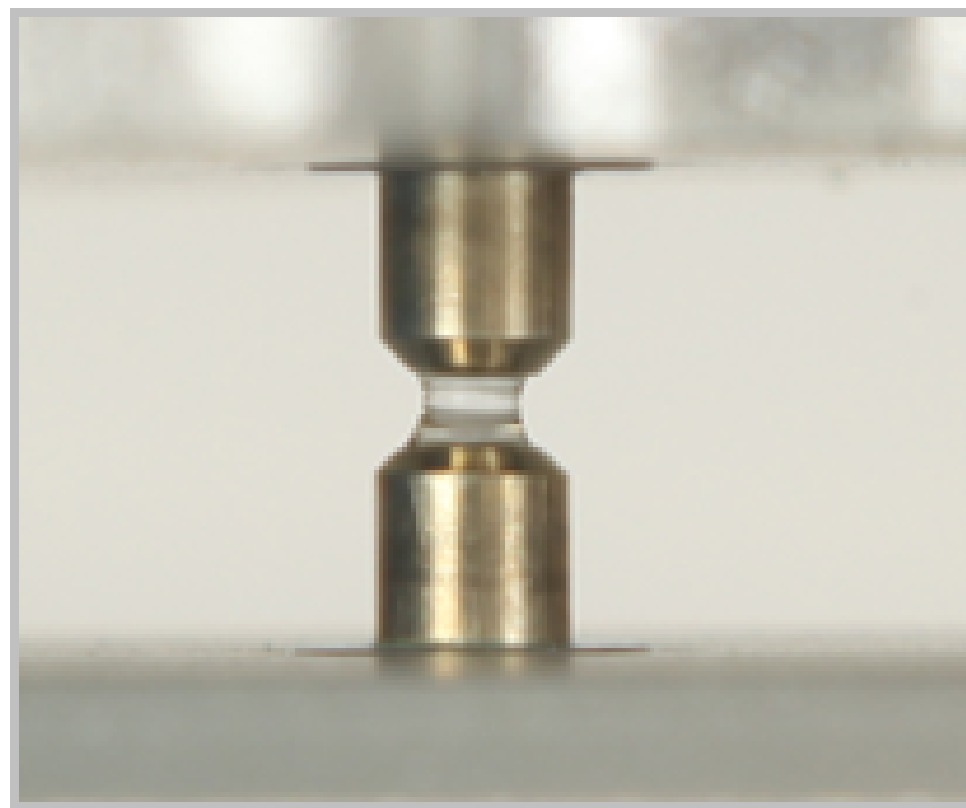
The baseline absorbance value is subtracted from all measurements. The default baseline (340 nm) can be changed, or turned off. A baseline is required for accurate results.

4.4 | Measuring a sample

1. Raise the upper arm of the spectrophotometer and make sure both pedestals are clean.
2. Pipette a 0.5 μL to 2 μL sample onto the center of the lower pedestal. Make sure there are no bubbles, and that the sample forms a tight droplet.



3. Gently lower the arm. The sample should form a bridge between the upper and lower pedestals, held by surface tension. The measurement will initiate automatically (Auto Sample can be turned off).



Liquid column

4. When the measurement is complete, open the upper pedestal and wipe the sample from both the upper and lower pedestals with a soft laboratory wipe. Simple wiping prevents sample carryover in the pedestals.
5. After each use, clean the pedestals with pure water



Wipe the sample

- Press “Data” to see the data from the current batch, and press “Graph” to return to the full spectrum graph for the current sample.
- Press “Spectrum Data” to save the full spectrum absorbance data for a sample. Otherwise, only the select data points will be saved.
- Press the “Report” tab to view and manage all results.
- Press “Enlarge Curve” to choose a point on the spectrum and see its absorbance, or enter a wavelength in the box at the top of the window.

5.1 Introduction

Select Nucleic Acid to measure the concentration of DNA and RNA samples. The Beer-Lambert equation is used to calculate the nucleic acid concentration:

$$C = \frac{A \times \epsilon}{b}$$

C=nucleic acid concentration, ng/μL
A=absorbance, AU
ε=extinction coefficient, ng · cm/μL
b=path length, cm

5.2 Measurement

The spectrophotometer can measure dsDNA concentrations up to 15,000 ng/μL by automatically adjusting the path length in the range of 0.05–1.0 mm. The absorbance value is equivalent to a path length of 1 cm.

Select the sample type and extinction coefficient from the drop-down menu:

- dsDNA – 50 ng · cm/μL
- ssDNA – 33 ng · cm/μL
- RNA – 40 ng · cm/μL
- Other – input a value for ε

5.3 Results and Interpretation

Nucleic acid is measured at 230, 260, and 280 nm.

A260/A280: This absorbance ratio can be used to judge the purity of DNA or RNA. Pure DNA will be around 1.8, while pure RNA will be around 2.0. If the ratio is lower, it means the sample contains protein, phenol, or other contaminants.

A260/A230: This absorbance ratio should be in the range of 1.8–2.2. If the ratio is lower, it means the sample is contaminated.

5.4 Report

Click “Report” to check results, choose one ID No. You can read all the results of this ID.

6.1 Introduction

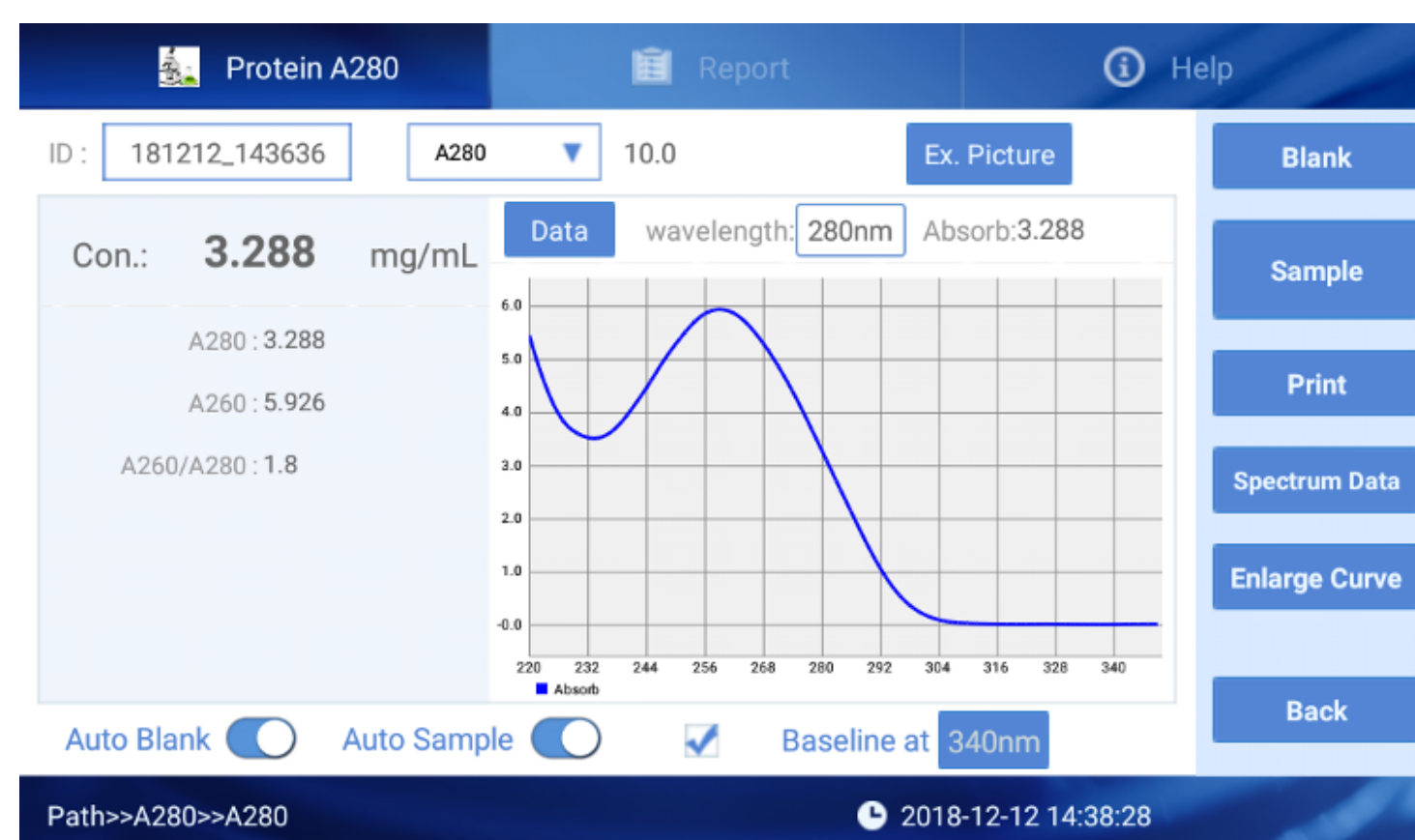
The protein A280 method is applicable to purified proteins containing Trp, Tyr, or Cys-Cys disulfide residues, which exhibit absorbance at 280 nm. It does not require generation of a standard curve. The software calculates the protein concentration in mg/mL directly after measuring the absorbance value. The full UV spectrum is measured at 10 mm equivalent path length.

The spectrophotometer will accurately measure protein samples up to 90 mg/mL (BSA) without dilution. If the sample is too concentrated, the software will inform the user to choose a shorter path length to ensure the precision of the measurement.

The user can input a different extinction coefficient in the drop-down menu under "other."

6.2 I Result

A260/A280: The absorption ratio at 260 and 280 nm is a measure of nucleic acid contamination. A value below 0.60 is ideal.



UV-Vis full-spectrum scanning

For general spectrophotometry, the full ultraviolet-visible spectrum function measures from 200 to 800 nm. Choose up to five individual wavelengths to save in the data report. The instrument will automatically adjust the path length, allowing samples up to 300 Abs to be measured.

The screenshot shows the main data entry screen of the UV-Vis instrument software. At the top, there are tabs for 'Uv-Vis', 'Report', and 'Help'. Below the tabs, the 'ID' field contains '181212_150735'. There are buttons for 'Save', 'Blank data', 'Sample data', and 'Ex. Picture'. A table with five rows is visible, each with a 'No.' column (1-5), a 'Wave' column (all '000'), and an 'Absorb' column (all '0.000'). To the right of the table is a 'Data' section with 'wavelength: 000nm' and 'Absorb: 0.000'. Below this is a graph area with a grid. At the bottom, there are toggle switches for 'Auto Blank' and 'Auto Sample', and a 'Baseline at 450nm' field. On the right side, there are buttons for 'Blank', 'Sample', 'Print', 'Spectrum Data', 'Enlarge Curve', and 'Back'. The bottom status bar shows 'Path=>Uv-Vis=>Uv-Vis' and the timestamp '2018-12-12 15:07:45'.

Press "Blank data" or "Sample data" to see the raw absorption intensity data for the blank or sample.

The screenshot shows the 'Report' tab of the UV-Vis instrument software. It displays a table with the following columns: 'ID', a checkbox, 'No.', 'W1', 'W2', 'W3', 'W4', 'W5', and 'Time'. The first row is selected and has a checkmark in the checkbox column. The data in the first row is: ID: 190403_151546, No.: 1, W1: 0/0.0, W2: 0/0.0, W3: 0/0.0, W4: 0/0.0, W5: 0/0.0, Time: 2018-12-12 14:25:56. Other rows are listed but not selected. On the right side, there are buttons for 'Print', 'Spectrum Data', 'Export Data', 'Delete Data', 'Delete file', and 'Export File'. The bottom status bar shows 'Path=>Uv-Vis=>Report' and the timestamp '2018-12-12 15:08:06'.

8.1 Introduction

The colorimetry function supports three of the most common methods for measuring the concentration of impure protein solutions - the BCA, Lowry, and Bradford assays. Select an assay from the drop-down menu.

1. BCA (bicinchoninic acid) assay: measures the absorbance of the purple-red copper-BCA chelate at 562 nm, standardized to the baseline absorbance at 750 nm.
2. Lowry assay: measures the absorbance of the heteropolymolybdenum blue compound at 750 nm.
3. Bradford assay: measures the absorbance of the protein complex with Coomassie Bright Blue G-250 at 595 nm, standardized to the baseline absorbance at 750 nm.

8.2 | Constructing a standard curve

A standard curve covering the sample range must be constructed before measuring samples.

1. Select the "Curve" tab.
2. Press "New Curve" and enter a name.
3. Choose units of measure from the drop-down menu.
4. Input the concentrations of the standards to measure. The order does not matter.
5. Select one standard, make a blank measurement, and measure the standard up to five times.
6. To delete erroneous values, select a single value or press and hold a whole row.
7. After measuring all samples, press "Save Curve." Curves can be viewed, but not edited after saving.

The screenshot displays the 'Curve' tab of the Colorimetry software. At the top, there are navigation tabs for 'Colorimetry', 'Curve', 'Report', and 'Help'. Below the tabs, a dropdown menu shows 'BCA-562' and a 'Curve' dropdown shows 'bca'. There are buttons for 'New Curve' and 'Delete Curve'. A table with 8 columns and 8 rows is shown, with the first column being 'Sample name' and the others representing absorbance measurements. All values in the table are 0.000. To the right of the table is a vertical toolbar with buttons: 'Blank', 'Sample', 'Save Curve', 'Display Curve', 'Import Curve', and 'Export Curve'. Below the table are buttons for 'Save concern', 'Delete concern', and 'Import concern'. At the bottom, a status bar shows the path 'Path>>Colorimetry>>Std. Curve', a clock icon, and the timestamp '2018-08-26 13:38:19'. The APOSTLE logo is in the bottom right corner.

Sample name	g/mL	Absorb mean	Absorb one	Absorb two	Absorb three	Absorb four	Absorb five
Sample1	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Sample2	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Sample3	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Sample4	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Sample5	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Sample6	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Sample7	0.000	0.000	0.000	0.000	0.000	0.000	0.000

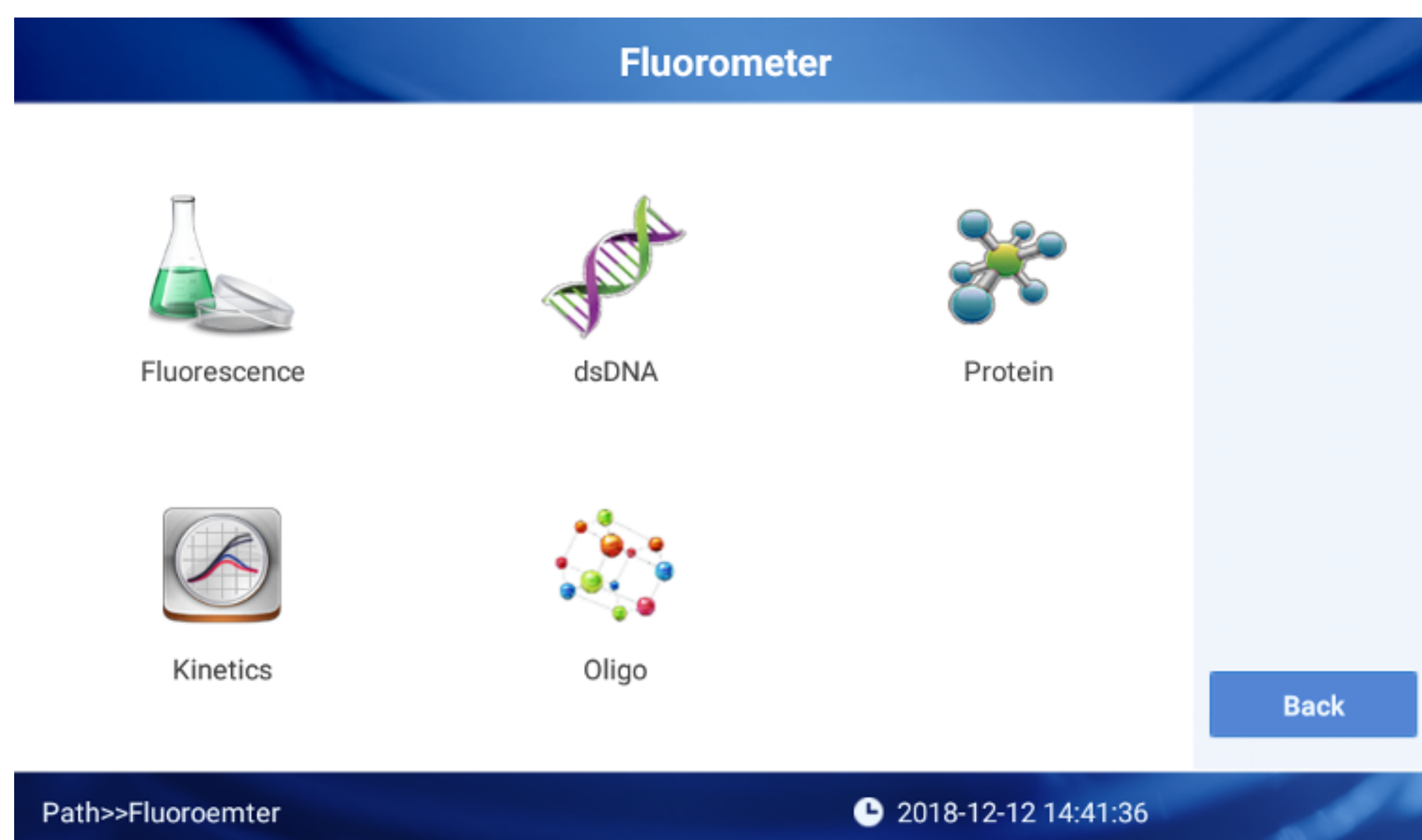
Once a curve is saved, you can select it from the drop-down menu when taking a measurement.

8.3 | Report

Results are displayed under the Report tab. Select an assay method from the drop-down menu to see all reports of that type.

9.1 | Function

- Fluorescence - direct fluorescence measurement, without a curve or concentration analysis.
- dsDNA, Protein, Oligo - measure samples according to a standard curve.
- Kinetics - measure concentration change over time.



9.2 | Concentration Measurement

1. Add the sample into the 0.5 mL PCR tube and make the total volume 200 μ L.
2. Put the tube in the fluorometer and close the lid.
3. Enter a batch ID, choose a standard curve from the drop-down menu, and input the original sample volume.
4. Measure the sample.

9.3 | Standard Curve

A standard curve needs to be established for the dsDNA, Protein, and Oligo measurement functions. The simplest standard curve can be composed of two points, but in order to ensure the accuracy of the detection, it is recommended to have at least 5 points. The curve should cover the possible range of the samples. Distribute standard points as evenly as possible.

Click "Standard Curve" to enter the standard curve interface, as shown in Figure below. The figure shows the curve that has been built.

NO.	ng/μL	Fluo. mean	Fluo. one	Fluo. two	Fluo. three	Fluo. four	Fluo. five
Sample1	0.000	7407.33	7414.0	7400.0	7408.0	0.000	0.000
Sample2	25.0	14463.3	14478.0	14468.0	14444.0	0.000	0.000
Sample3	50.0	24764.0	24797.0	24746.0	24749.0	0.000	0.000
Sample4	100.0	43970.3	44019.0	43968.0	43924.0	0.000	0.000
Sample5	200.0	75511.3	75619.0	75491.0	75424.0	0.000	0.000
Sample6	300.0	105529.	105670.	105518.	105400.	0.000	0.000
Sample7	400.0	143063.	143243.	143056.	142890.	0.000	0.000

- Select the "Curve" tab.
- Press "New Curve." Choose the type of equation used to model the curve, and enter a name.
- Choose units of measure from the drop-down menu.

- Input the concentrations of the standards to measure. The order does not matter.
- Select one standard, and measure the standard up to five times. There is no blanking.
- To delete erroneous values, select a single value or press and hold a whole row.
- After measuring all samples, press "Save Curve." Curves can be viewed, but not edited after saving.

9.4 | Curve Calibration

An existing standard curve can be calibrated to eliminate error caused by drift in the instrument.

1. From the Curve tab, press "Calibration Curve" to enter the calibration curve interface.
2. Measure two or three standards, in any order.
3. Press "Calibrate" to complete the calibration.

dsDNA Curve Report Help

Curve: 2018

No.	ng/μL	Fluo. mean	Fluo. one	Fluo. two	Fluo. three	Fluo. four	Fluo. five
Sample1	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Sample2	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Sample3	0.000	0.000	0.000	0.000	0.000	0.000	0.000

Measure

Calibration

Cancel

Path>>Fluoroemter>>Curve 2018-08-26 17:13:06

9.5 | Kinetics

The Kinetics function measures the same sample multiple times over a time period. Under "Total," input the duration of the test. Under "Interval," input the interval between measurements. The format is Hours:Minutes:Seconds. A maximum of 99 measurements can be made for each test. Press "Stop" to end the test after the next measurement. The report shows the time each measurement was made.

ID	Cycle	Fluorescence	Excitation	Emission	Time
181212_142344	1	5834	460nm	525-570nm	2018-12-12 14:23:57
	2	5831	460nm	525-570nm	2018-12-12 14:23:57

Path>>Fluorometer>>Report 2018-12-12 15:06:39

10.1 | Introduction

OD600 refers to the optical density (absorbance) of a solution at the 600 nm wavelength. An important application of OD600 is measuring the concentration of bacteria or other cells in a culture solution.

10.2 | Measuring a sample

1. Enter the sample batch number.
2. Blank before taking a measurement. The blank can be performed with the cuvette filled with buffer, an empty cuvette, or nothing at all in the cuvette holder.
3. Add 2 to 3 mL of sample into the cuvette.
4. Measure the sample.
5. View data and other batches under the Report tab.

The screenshot shows the OD600 measurement software interface. At the top, there are three tabs: "OD600", "Report", and "Help". Below the tabs, there is a text input field for "ID:" containing the value "181212_150823". To the right of the ID field, there are two labels: "Dark current" with a value of "000" and "intensity" with a value of "000". Below these labels, there is a large light blue area displaying "OD600 : 0.000". To the right of this area, there is a table with two columns: "No." and "OD600". The table is currently empty. On the right side of the interface, there are four buttons: "Blank", "Sample", "Print", and "Back". At the bottom of the interface, there is a status bar with the text "Path>>OD600>>OD600" on the left and a clock icon followed by the time "2018-12-12 15:08:29" on the right.

Problem	Possible Cause	Solution
Instrument cannot turn on	Power supply, adaptor, or switch is defective	Check the power supply and switch. Contact the vendor
Spectrophotometer measurements are not precise,	Liquid column is not forming correctly, or the pedestal is contaminated	Make sure to pipette a full 2 μ L of sample. Check that the liquid column is connecting both pedestals. Clean the pedestals. Contact the vendor
OD600 module failure	Poor connection between cable and board	Contact the vendor
Insufficient light intensity error	Analysis module is defective, or the optical fiber is broken	Contact the vendor
Touch screen problems	Power supply is not ground	Make sure the power supply is grounded correctly
Communication timeout	Analysis module communication failure	Restart instrument. Contact the vendor