Operation Manual

V1.0

Nano-500
Micro-Spectrophotometer

Foreword

Thank you for purchasing a Micro-Spectrophotometer. This manual provided as operational and easy troubleshooting guide. Please read this instruction carefully before operation and save for future reference.

Opening Check

Please check the instrument and Appendix with the packing list when you first open the package. If there is anything don’t match, please contact with the vendor.

File No.:AS169SM

File version No.:1st version , 2018 Dec.

Safety Warnings and Guidelines

1 Warning

To assure the safe operation, please read carefully this manual before operating.

2 Safety Tips

The operation, maintenance and repair of the instrument should comply with the basic guidelines and the remarked warning below. If you don't comply with them, it will have effect on the scheduled using life of the instrument and the protection provided.

This product is indoor instrument.

Users are not allowed to open or repair the instruments, which will lead injury and loss of warranty, please contact

Power off when you finish your work. Pull off the connector plug when there's long time no use of the instrument and cover it with a cloth or plastic paper to prevent from dust.

Pull the connector plug from the jack at once in the following case, and contact the vendor:

- **There is some liquid flowing into the instrument;**
- **Drenched or fire burned;**
- **Abnormal operation: such as abnormal sound or smell;**
- **Instrument dropping or outer shell damaged;**
- **The function has obviously changed.**

3 The maintenance of instrument

The pedestal should be cleaned by the cloth stained with pure water.

If there are smutches on the instrument, clean them with cloth stained with alcohol.

CONTENTS

Chapter 1 Introduction

The Nano-500 is a spectrophotometer that measures 0.5μL-2μL samples with high accuracy and reproducibility. Sample pedestals apply surface tension to make the sample column, so that hold samples in the pedestal. During measurement, the light goes through the sample column; In addition, the Nano-500 has the capability to measure highly concentrated samples without dilution (100X higher concentration than the samples measured by a standard cuvette)

Chapter 2 Specifications

1. The normal operating condition

Ambient temperature:5°C ~ 35°C

The relative humidity:≤70%

Power Supply:DC24V 2A

2. The basic parameters and performance

Model		Nano-500
Minimum Sample Size		0.5μL-2μL (2μL recommended)
Path Length		0.05 , 0.2mm or 1mm
Light Source / Life		Xenon flash lamp / >10^9 flashes
Detector Type		2048—element linear silicon CCD array
Wavelength Range		200—800nm
Wavelength Accuracy		0.2 nm(TWHM at Hg 253.70nm)
Spectral Resolution		≤2nm(FWHM@Hg 253.7nm)
Absorbance Precision		0.003Abs(1mm path length)
Absorbance Accuracy		±1%(7.332Abs, at 260nm wavelength)
Absorbance Range		0.04—240(at 260 wavelength, 10mm equivalent)
Detection Concentration Range		2ng/μL dsDNA ~12,000ng/μL dsDNA
Detection Time		<10seconds
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%
Fluoro meter	Linearity	R^2≥0.995
	Repeatability	≤1.5%
	Stability	≤1.5%
Voltage input		DC24V 2A
Power		25W
Dimension		208×320×186 mm(W×D×H)
Weight		3.6 kg

3. Models

According to the fluorescence detection wavelength, the 4 models of Nano-500 as below:

Model	Light source	Excitation wavelength	Emission wavelength
Nano-500U	UV LED	365±20nm	420-480nm (60nm)
Nano-500B	Blue LED	460±20nm	525–570nm (45nm)
Nano-500G	Green LED	525±20nm	575–640nm (65nm)
Nano-500R	Red LED	625±20nm	670–725nm (55nm)

Nano-500B is the standard equipped which excitation wavelength is 460nm.

Chapter 3 Preparations

1. Structure description

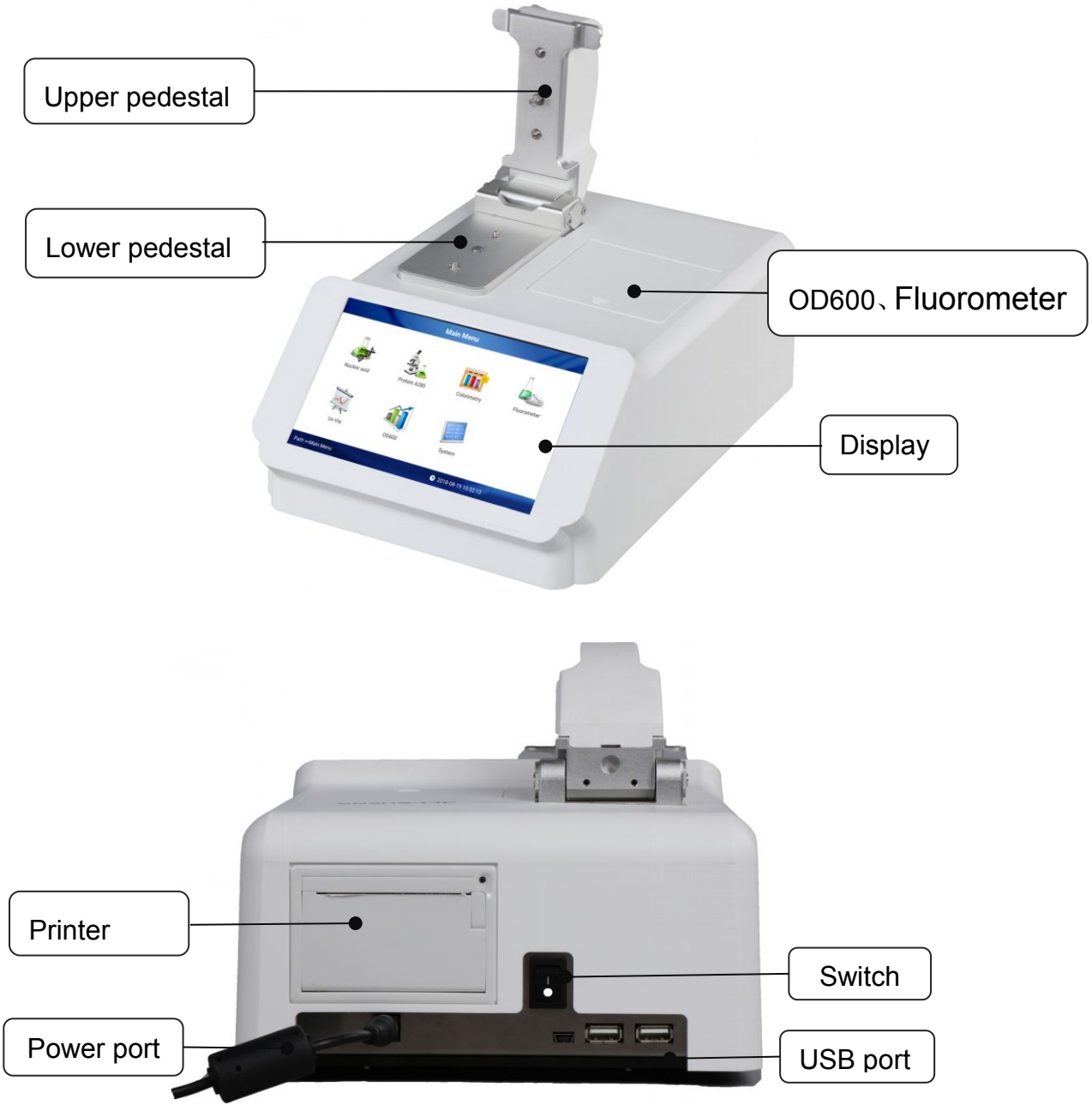


Fig 3.1 Instrument structure

Notes: Make sure the power supply with ground wire.

2. Sample size requirements

Although sample size is not critical, it is essential that the complete liquid column can be formed between the upper measurement pedestal and lower measurement pedestal to make sure the precision of the measurement.

It is best to use a precision pipettor (0-2μL) with precision tips to assure the precision of the sampling. If users are unsure about sample characteristics or pipettor accuracy, a 2μL sample is recommended.

3. Basic use for the pedestal

3.1 With the upper pedestal open, pipette the sample (2μL) onto the lower pedestal.

Fig 3.2 Dropping liquid

3.2 Lower the sampling arm, the sample column is automatically drawn

between the upper and lower measurement pedestals. Then the measurement initiates.

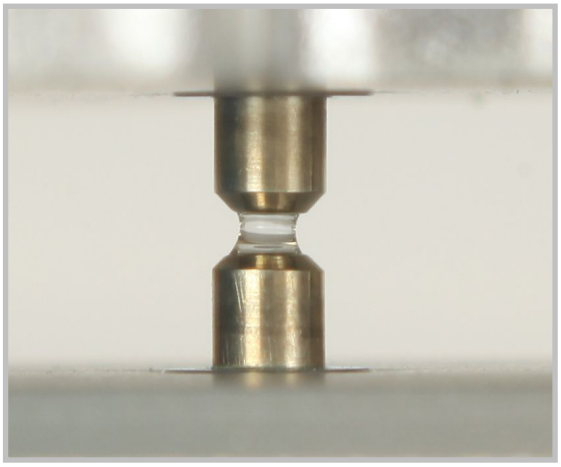


Fig 3.3 Liquid column

3.3 When the measurement is complete, open the upper pedestal and wipe the sample from both the upper and lower pedestals using a soft laboratory wipe. Simple wiping prevents sample carryover in the pedestals.

Fig 3.4 Wipe the sample

Notes: After each measurement, clean the pedestals for 3 times with clean pure water.

4. OD600 measurement

Nano-500 is with measurement of OD600. Lift the upper pedestal, enter into OD600 interface from the touch screen. Make “blank” according to experiments, blank for air, cuvette, or buffer in cuvette. Then add 2~3mL sample into the cuvette, put the cuvette into the slot and start to measure. (As picture below)

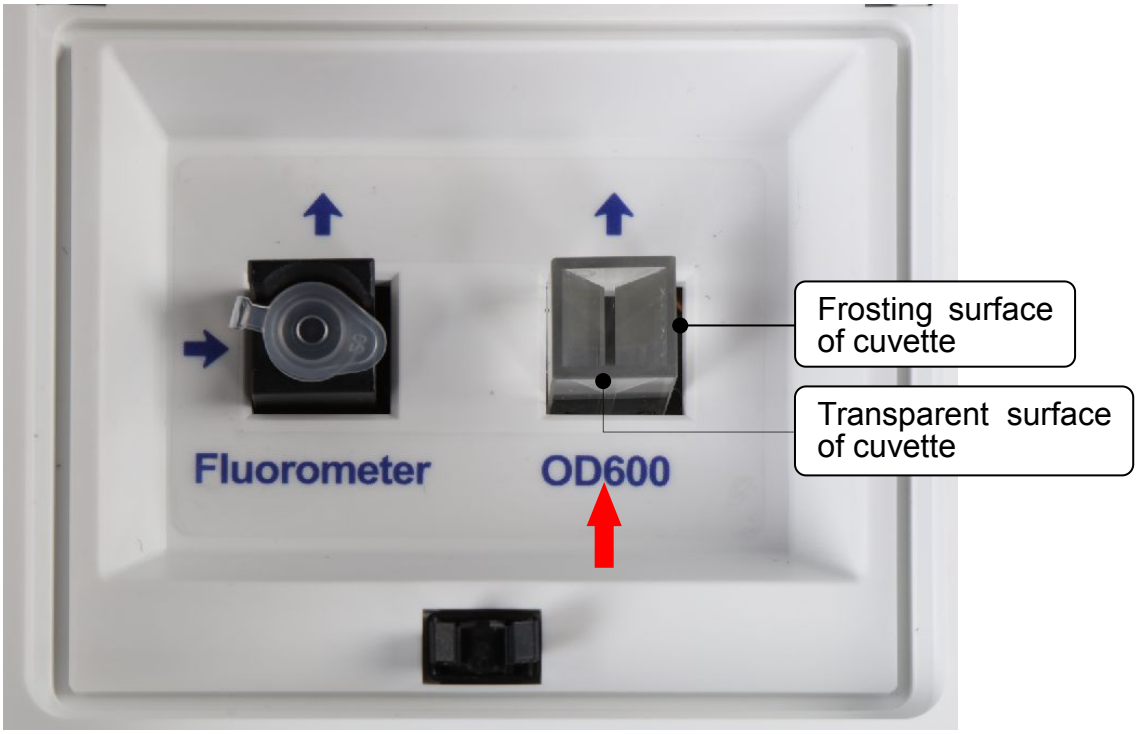


Fig 3.5 OD600 and Fluorometer

Notes:The Light path direction is showed as the arrow as above picture, please pay attention to the cuvette position when loading.

5. Fluorometer

Nano-500 has the fluorescence detection function, the default equipment is 460nm emission wavelength which excitation wavelength is 525nm. See the fluorescence detection part in chapter 4 for detailed operation.

Chapter 4 Operation

1. Instrument self-testing

Instrument will start self-test once powered on.

Fig 4.1 POST

2. Main interface

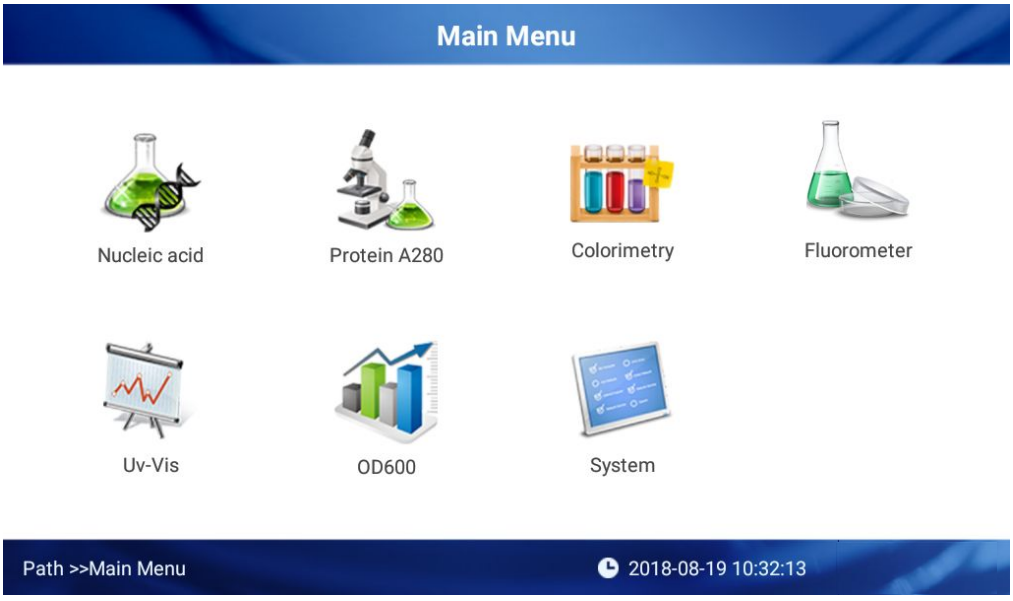


Fig 4.2 Main interface

3. Nucleic acids measurement

3.1. Introduction

Users can measure the concentration of nucleic acid by using the instrument. If want to measure nucleic acids, select Nucleic Acid mode in the “main menu”

The following “Beer — Lambert” equation is used to calculate the nucleic acids concentration:

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

C=DNA concentration, unit: ng/μL

A=AU absorbance

ε=extinction coefficient, unit :ng-cm/μL

b=Path Length, unit: cm

Normally DNA extinction coefficient:

dsDNA:50ng-cm/μL

ssDNA:33ng-cm/μL

RNA:40ng-cm/μL

When selecting pedestal mode, the Micro-spectrophotometer can measure high

concentration nucleic acid sample without dilution from 1.0mm to 0.05mm short path length.

The absorbance value of nucleic acid measurement is consistency of

the reading value under 1cm path length.

Nano-500 can accurately measure double-stranded Nucleic Acid samples up to 12000ng/μL without dilution, it can choose path length automatically.

3.2. Nucleic Acids measurement

Click “Nucleic acid” to enter into the interface as below :

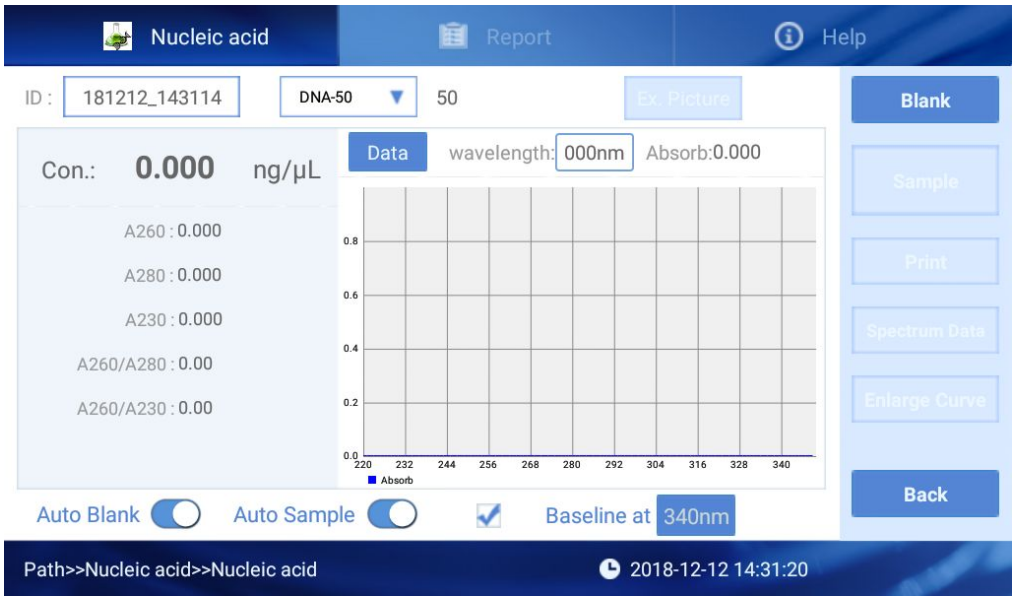


Fig 4.3 Initial interface of Nucleic Acids detection

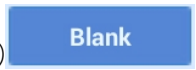
Fig 4.3, there are three options of Nucleic Acids, Report, Help for different functions.

1) Interface Fig 4.3, only the light blue area is clickable.

① ID : 180717_125723 : The sample batch No., default value is the current time, users can also edit ID by self. One ID can include as many as 1000 detection results.

② DNA-50 50 : Click to choose Nucleic Acids type, DNA-50 for dsDNA,

RNA-40 for RNA, ssDNA-33 for ssDNA, when you choose “others” and type in the Nucleic Acids factor the instrument will calculate as you set.

③ 

: Blank the buffer, this step is essential before measurement. Blank absorbance value is during 0.004-0.03 Abs. The validity of blank control is 30 min and after 30 min, the system will automatically remind you to make blank detection，If the blank calibration failed, there is a icon  showed on the top right corner, click it to view the detailed warning information.

④ 

: You can choose or cancel the baseline calibration, the default baseline calibration wavelength is 340nm. User can also input wavelength according to requirement. Any experiment, the baseline is automatically set as the absorbance value of the chose wavelength, all results should minus this value.

Notes: If you don’t calibrate the baseline, the light spectrum will deviate, and lead to unprecise result.

⑤ 

: Click the right icon to select the automatic blank detection, when it is turned on, it will do the blank detection automatically the fist time close the rotating arm. When it is turned off the icon will be 

Note: The automatic blank only takes effect when there is no blank data of the current detection. If you want to do reblank then

need to click the right button "Blank".

⑥ Auto Sample : Click the right icon to select automatic detection, when it is turned on, it will do the detection automatically once the rotating arm is closed. When it is turned off the icon will be Auto Sample

Note: The automatic detection only takes effect when there is blank data of the current detection. If no blank data, need to do blank first.

⑦ Data : Click it to switch to check the history data list as Fig 4.5, and then click Graph to switch to check the curve.

2) Operation steps

① Set the batch NO. and Nucleic Acids type;

② Clean the upper and lower pedestals with dust proof paper, input the 2μL buffer solution to make blank;

③ Clean the buffer solution on the ower pedestals with dust proof paper;

④ Measure sample with volume of 2μL. Click "Measure" and then enter the interface as Fig 4.4;

Note: The sample must be the new adding before your measurement.

⑤ After measurement, pedestals must be cleaned before next measurement.

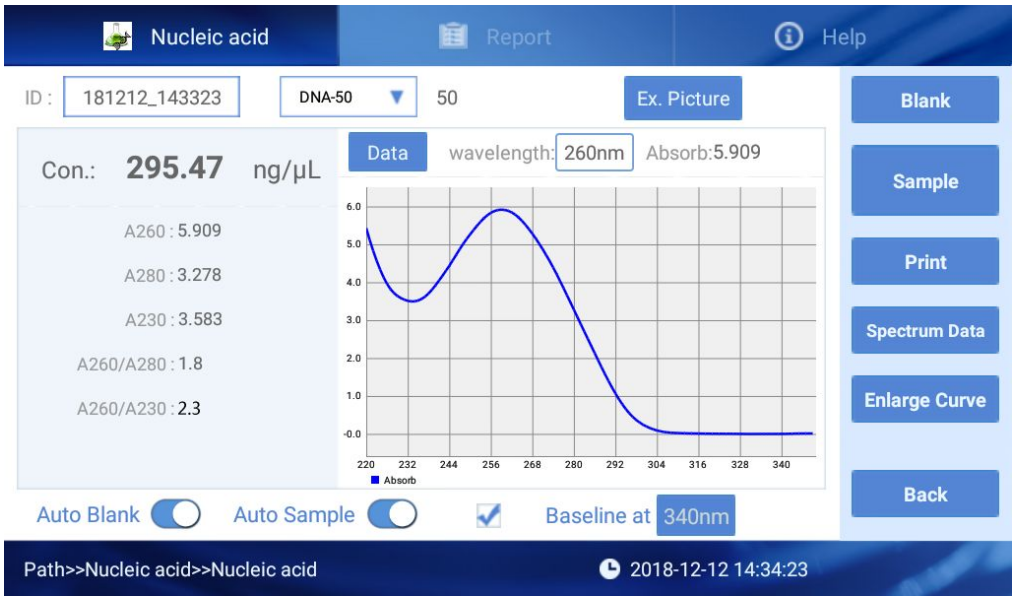


Fig 4.4 Result of Nucleic Acids measurement

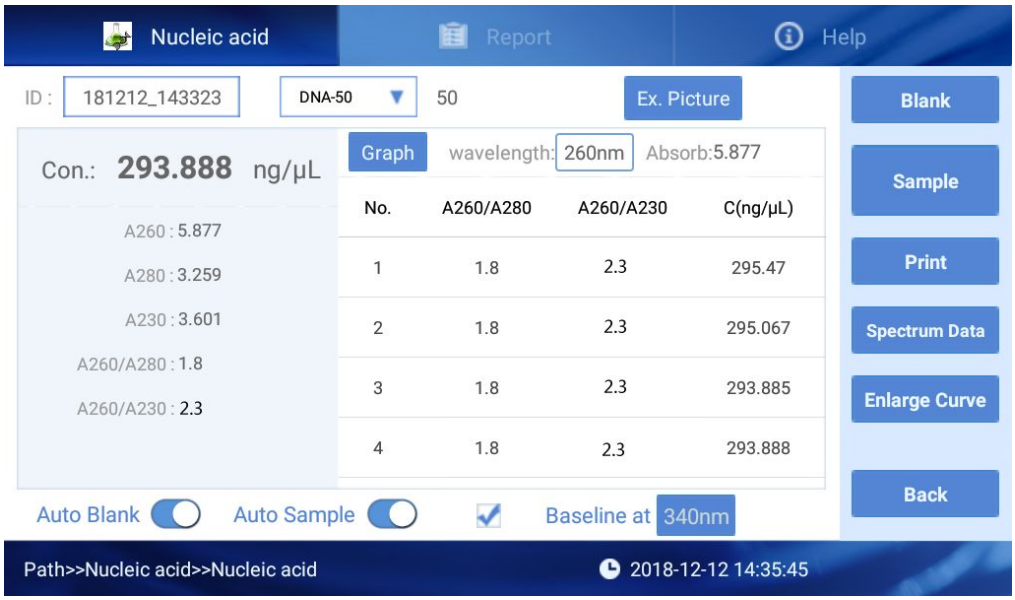


Fig 4.5 Data list

3) **The detection result data will display as Fig 4.4.**

Concentration:Nucleic acid concentration.

A260: The absorbance of 10mm wavelength under 260nm.

A280: The absorbance of 10mm wavelength under 280nm.

A230: The absorbance of 10mm wavelength under 230nm.

A260/A280: The ratio of absorbance 260nm,280nm can be used to judge the purity of DNA or RNA. Pure DNA ratio can reach around 1.8, Pure RNA ratio can reach about 2.0. If the ratio value is lower, it means the sample contains some protein, phenol or other contaminants.

A260/A230: The ratio of absorbance 260nm,230nm, usually is in the range of 1.8-2.2, If the ratio value is lower, it means the sample contains some contaminants.

4) Click it to input the wavelength and then the absorbance accordingly will be displayed as Fig 4.6.

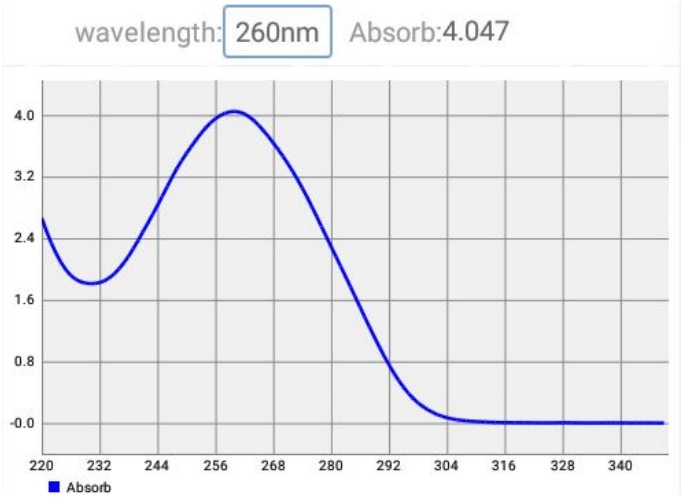


Fig 4.6 Nucleic Acids detection curve

5) The function of buttons:

① Ex. Picture: Export the current interface to the mobile hard disk.

② Sample: Click it to measure the sample.

③ Print: Click it to print the data as Fig 4.5 with the equipped printer.

④ Spectrum Data: Click it to save the full wavelength detection data, if not, only the data of Fig 4.5 will be saved.

⑤ Enlarge Curve: Click it to amplify the Fig 4.6 interface, you can move the red coordinate line to change the wavelength and view the absorbance accordingly.

⑥ Back: Click it back to the main interface.

3.3. Nucleic acids detection report

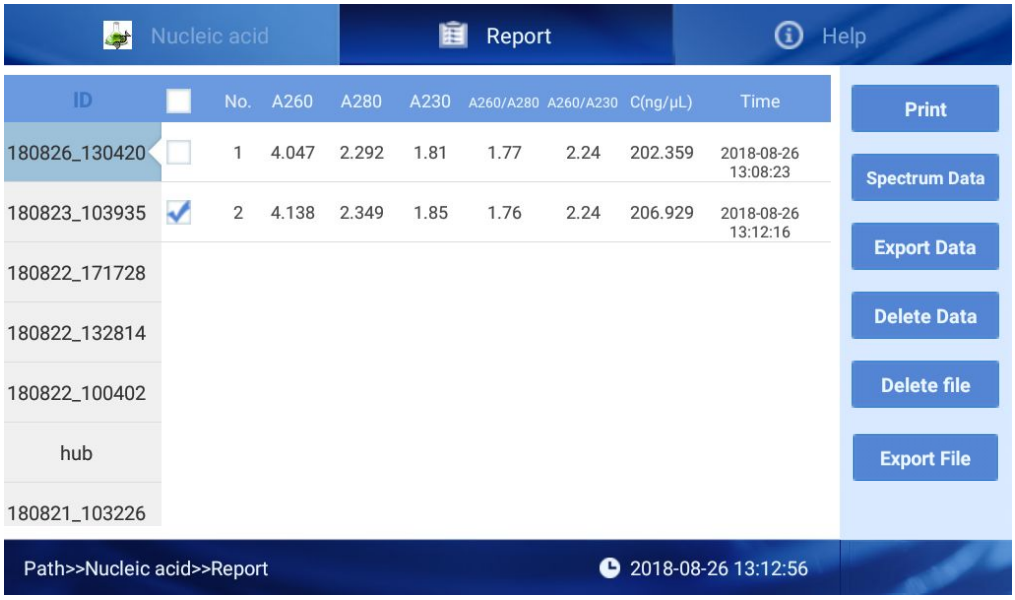


Fig 4.7 Report interface

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

As Fig 4.7, select results by clicking the file name, or can select one or all of the results as showed on Fig 4.7, users also can operate by buttons on the right:

① Print: Click it to print the data as Fig 4.5 with the equipped

printer.

② Spectrum Data: Click it to enter the interface Fig 4.8

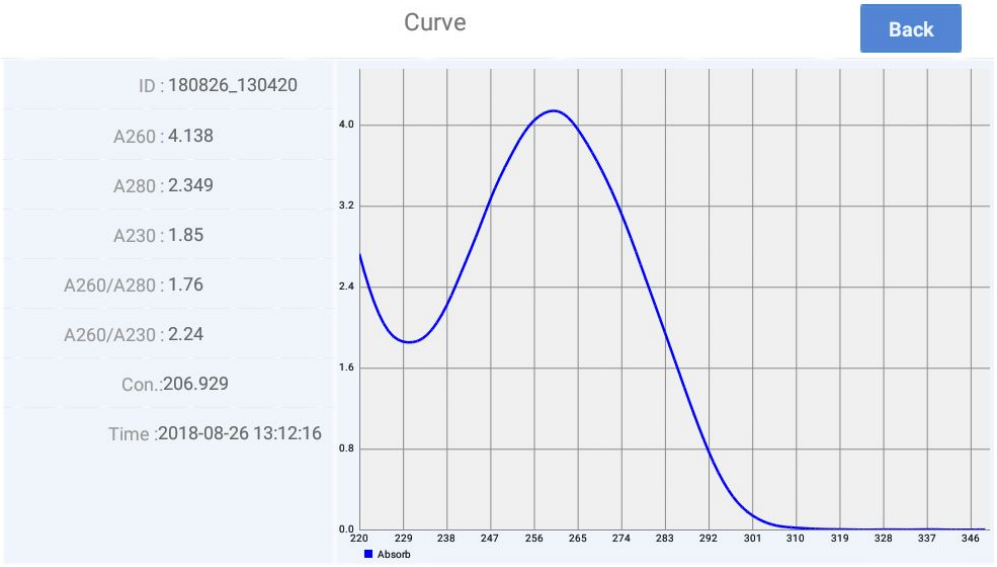


Fig 4.8 Nucleic acid full wavelength detection data.

③ Export Data: Export the result to U disk (Insert the U disk into the USB port at back of instrument).

④ Delete Data: Delete the selected results.

⑤ Delete file: Delete all the files by click “File Name” and click “Delete file”.

⑥ Export File: Click it to export files to the U disk.

3.4. Nucleic acids Help Center

We are sorry to inform you the “Help” has not been finished yet.

4. Protein A280

4.1. Introduction

Proteins, unlike nucleic acids, can exhibit considerable diversity. Protein A280 method is applicable to purified proteins (includes Trp, Tyr residues or Cys-Cys disulfide) exhibiting absorbance at 280nm. It does not require generation of a standard curve. The software calculates the protein concentration directly after measure the absorbance value.

The Protein A280 displays UV spectrum, measures the protein's absorbance at 280nm and calculate the concentration (mg/ml). Like the Nucleic Acids mode, it displays and records 10mm equivalent data.

The Spectrophotometer will accurately measure protein samples up to 90mg/ml BSA) without dilution. When the optical intensity (after measurement sample extinction) is lower than 200(under 10mm path length), software will inform the customer to choose shorter path length to make sure the precision of the measurement. Unique screen is shown as below.

The hydrophobic between the water molecules is the main factor of surface tension. In general, the presence solute of liquids ((including protein, DNA, RNA, salt ion, detergent molecule) can significantly reduce surface tension. Although, for most samples, a 1μL sample size is enough, a 2μL sample size is recommended for protein measurements that the

liquid column be formed.

4.2. Protein A280 measurement

Click “Protein A280” enter the interface Fig 4.9.

Fig 4.9 Protein detection interface

As Fig 4.9, there are three options at the top of the screen, Protein A280, Report, Help.

1) Interface Fig 4.9, only the light blue area is clickable.

① ID : 180826_131326 : The sample batch No., default value is the current time, users can also edit ID by themselves. One ID can include as many as 1000 detection results.

② A280 10.0 : Click to choose Nucleic Acids type, when you choose “others” and type in the Nucleic Acids factor the instrument will calculate as you set.

③ Blank : Blank the buffer, this step is essential before

measurement. Blank absorbance value is during 0.004-0.03 Abs. The validity of blank control is 30 min and after 30 min, the system will automatically remind you to make blank detection，If the blank calibration failed, there is a icon  showed on the top right corner, click it to view the detailed warning information.

④ 

: You can choose or cancel the baseline calibration, the default baseline calibration wavelength is 340nm. User can also input wavelength according to requirement. Any experiment, the baseline is automatically set as the absorbance value of the chose wavelength, all results should minus this value.

Notes: If you don't calibrate the baseline, the light spectrum will deviate, and lead to unprecise result.

⑤ 

: Click the right icon to select the automatic blank detection, when it is turned on, it will do the blank detection automatically the fist time close the rotating arm. When it is turned off the icon will be 

Note: The automatic blank only takes effect when there is no blank data of the current detection. If you want to do reblank then need to click the right button "Blank".

⑥ 

: Click the right icon to select automatic detection, when it is turned on, it will do the detection automatically once the rotating

arm is closed. When it is turned off the icon will be 

Note: The automatic detection only takes effect when there is blank data of the current detection. If no blank data, need to do blank first.

⑦ 

: Click it to switch to check the history data list and then click 

to switch to check the curve.

2) Operation steps

① Set the batch NO. and Nucleic Acids type;

② Clean the upper and lower pedestals with dust proof paper, input the 2μL buffer solution to make blank;

③ Clean the buffer solution on the ower pedestals with dust proof paper;

④ Measure sample with volume of 2μL. Click “Measure” and then enter the interface as Fig 4.10;

Note: The sample must be the new adding before your measurement.

Fig 4.10 Result of Protein measurement

⑤ After measurement, pedestals must be cleaned before next measurement.

3) The detection result data can be displayed as Fig 4.11.

Fig 4.11 Protein measurement data

Notes: The mass extinction coefficient can be any value if user choose other types, instrument will calculate the concentration according to the mass extinction coefficient.

Con.: Protein concentration;

A260: The absorbance of 10mm wavelength under 260nm；

A280: The absorbance of 10mm wavelength under 280nm；

A260/A280: Ratio absorbance of 260nm and 280nm.

4) Click it to input the wavelength and then the absorbance of it will be displayed as Fig 4.12.

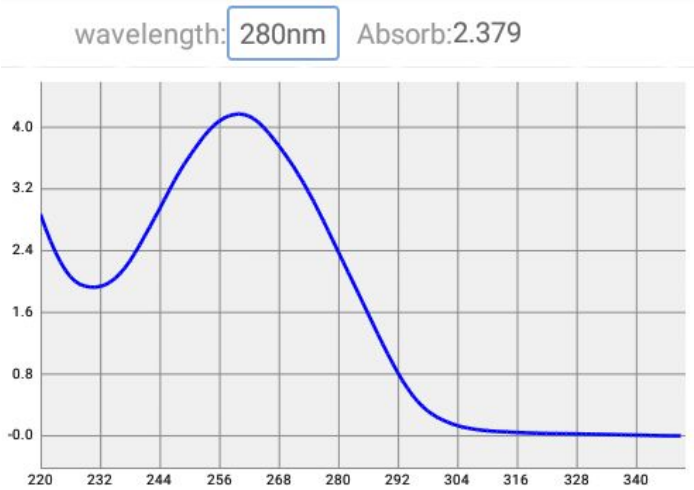


Fig 4.12 Protein detection curve

4.3. Protein A280 detection report

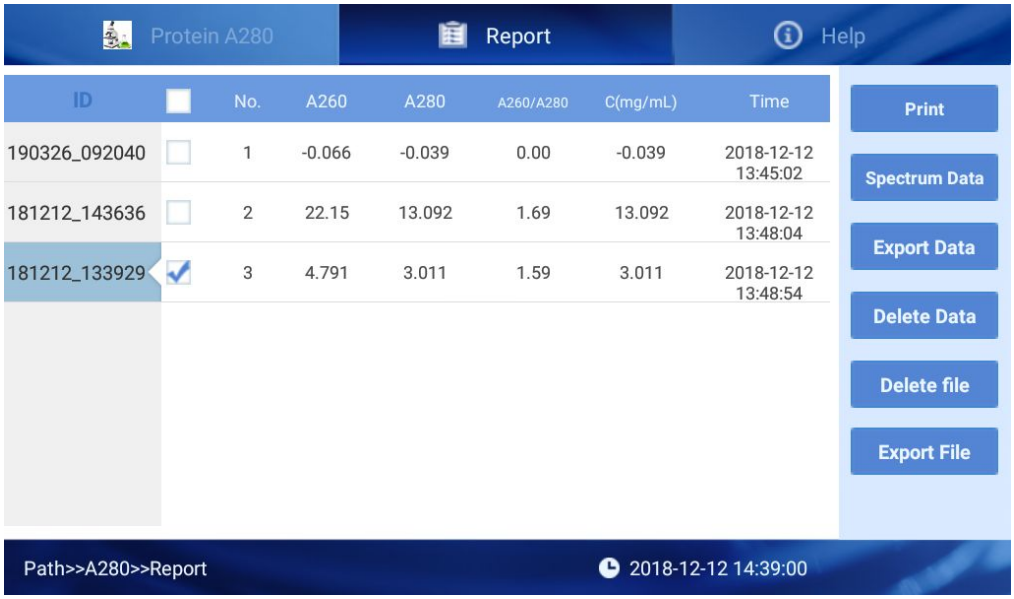


Fig 4.13 Protein detection report interface

Notes: The interface is the same as Nucleic Acids detection report, please refer to 3.3. Nucleic Acids detection report.

Click Spectrum Data to enter the interface Fig 4.14 and move the red coordinate line to change the wavelength and view the absorbance of it.

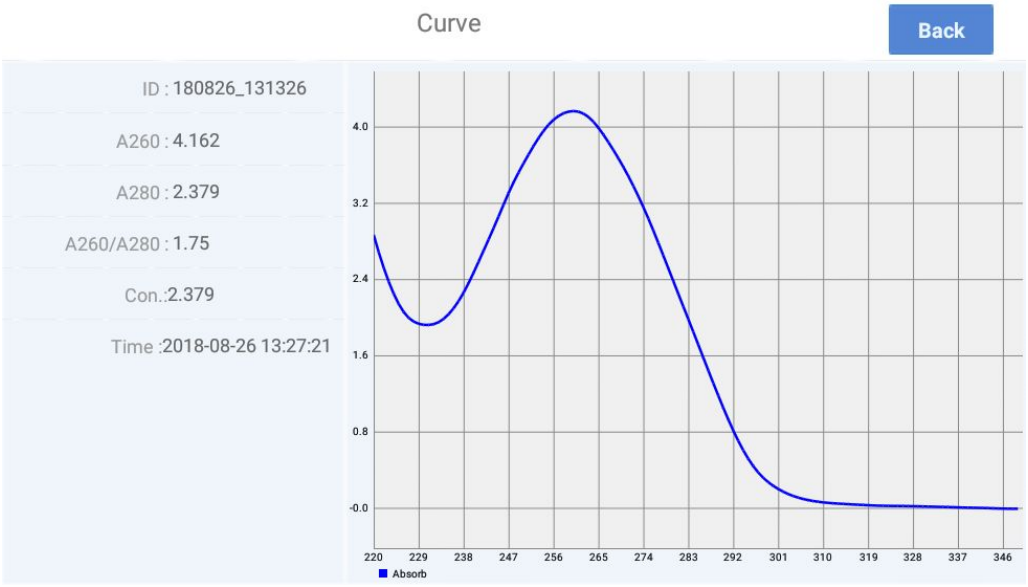


Fig 4.14 Protein full wavelength detection data

4.4. Help

We are sorry to inform you the “Help” has not been finished yet.

5. Colorimetry

5.1. Introduction

BCA, Lowry, Bradford are measured by colorimetry, which requires standard curve.

The BCA Protein Assay is an alternative method for determining protein concentration. It is often used for more dilute protein solutions

and/or in the presence of components that also have significant UV absorbance. Unlike the Protein A280 method, the BCA Assay requires a standard curve to be generated each time it is run, before unknown proteins can be measured. BCA Assay is testing CU^{+1} ion, under alkaline environment, Cu^{+2} ion will be reconditioned to CU^{+1} by protein. Two Biquinoline 2-dicarboxylic acids BCA molecular and one CU^{+1} ion will form purple chelate in the presence of protein. Cu-BCA chelate is measured at its wavelength maximum of 562nm and normalized at 750nm.

Commercial BCA kit procedures for two different protein measurement range:

A regular assay — using a 20:1 reagent/sample volume ratio. This kit measurement range is from 0.20mg/mL to 8.0mg/mL (BSA). When pedestal measuring, we suggest using sample volume of 4μL and 80μL BCA reagent.

A mini assay — using a 1:1 reagent/sample volume ratio. To prepare enough sample volume for pedestal measurement, range from 0.01mg/mL to 0.20mg/mL. We suggest using 10μL samples and 10μL BCA reagent in PCR tubes.

In addition to the kit reagents, protein standards (BSA) for generating a standard curve are provided for the Bradford method by the

manufacturer. Make sure that all measurements use the same incubation times and temperature.

Note: If the Ambient Temperature is higher than 60℃, please double the sample size to avoid the volatilization.

The Lowry Protein Assay is an alternative method for determining protein concentration based on the widely used and cited Lowry procedure for protein quantitation. Like other Assays, the Lowry Assay requires standard curve generation each time it is run. The Lowry procedure involves reaction of protein with cupric sulfate in alkaline solution, resulting in formation of tetradentate copper protein complexes. The Folin－Ciocalteu Reagent is effectively reduced in proportion to the chelated copper-complexes resulting in a water-soluble blue product that is measured at 650nm and normalized at 405nm. The reagents utilizing in the assay, are available in kit form from numerous manufacturers.

To accurately prepare standards, a sample volume of 20μL and 100μL of Lowry reagent is recommended. On the Spectrophotometer, the Lowry assay can run from 0.20mg/mL to 4.0mg/mL. Follow the manufacturer's protocol for the assay. Make sure that all measurements use the same incubation time and temperature. In addition to the kit reagents, protein standards (BSA) for generating a standard curve are provided for the Lowry Protein method by the manufacturer. Since the

Micro-Spectrophotometer can measure higher protein concentrations, you may need to supply your own protein standards at higher concentrations than provided by the manufacturer. A 2μL sample size is recommended for protein measurements.

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. The bradford uses the protein-induced absorbance shift of Coomassie Blue dye to 595 nm as a measurement of protein concentration. The bound protein-dye complex is measured at 595 nm and normalized at 750 nm. Correspondent kits are available from numerous manufacturers Commercial Bradford Protein kit manufacturers typically outline procedures for two different concentration ranges:

a) A regular assay — using a 50:1 reagent/sample volume ratio. This kit measurement range is from 0.10mg/mL to 8.0mg/mL(BSA). The best linearity is in the 0.01-1mg/mL. When pedestal measuring, we suggest using sample volume of 4μL and 200μL Bradford reagent.

b) A mini assay — using a 1:1 reagent/sample volume ratio. To prepare enough sample volume for pedestal measurement, range from 15μg/mL to 125μg/mL. We suggest using 10μL samples and 10μL BCA

reagent in PCR tubes.

In addition to the kit reagents, protein standards (BSA) for generating a standard curve are provided for the Bradford method by the manufacturer. Make sure that all measurements use the same incubation times and temperature.

Note: If the Ambient Temperature is higher than 60℃, please double the sample size to avoid the volatilization.

Since the Micro-Spectrophotometer can measure higher protein concentrations, you may need to supply your own protein standards at higher concentrations than provided by the manufacturer.

5.2. Colorimetry

A standard curve is required every time before measurement.

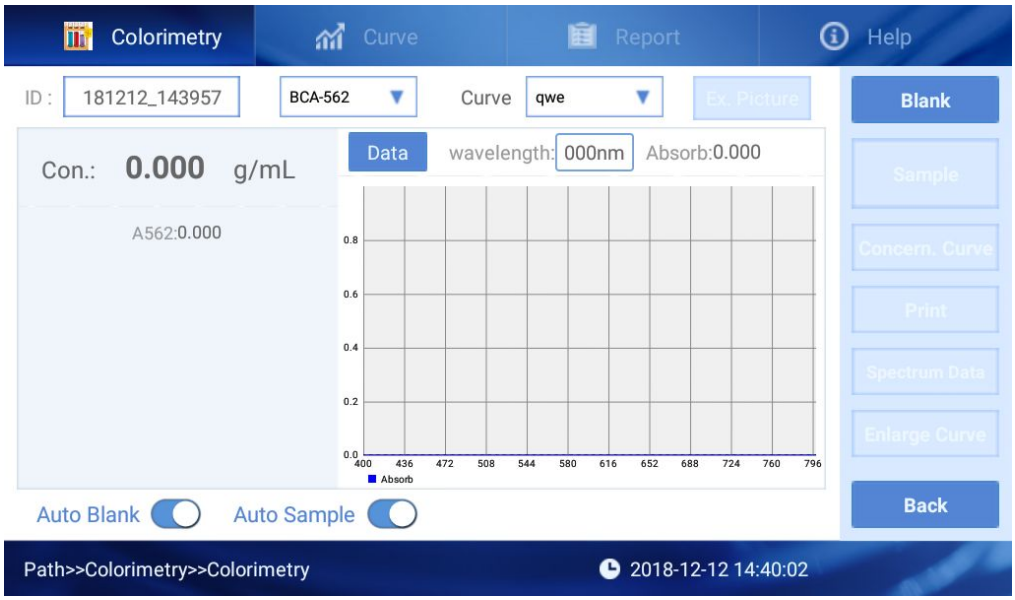


Fig 4.15 Colorimetry detection interface

: Click to select the colorimetry type.

: Curve of the colorimetry type.

Measurement steps:

① Choose colorimetry type, and curve type.

② Use buffer to make blank.

③ Clean the pedestals by dust-free paper, and input the sample name .

④ Measure sample with volume of 2μL.

5.3. Curve

A standard curve is required by colorimetry, and 5 standard samples concentration are needed, the concentration range of standard points should cover all standby sample concentration.

Introduction for Colorimetry interface:

Click “Curve” on the top to build a standard curve before colorimetry assay.

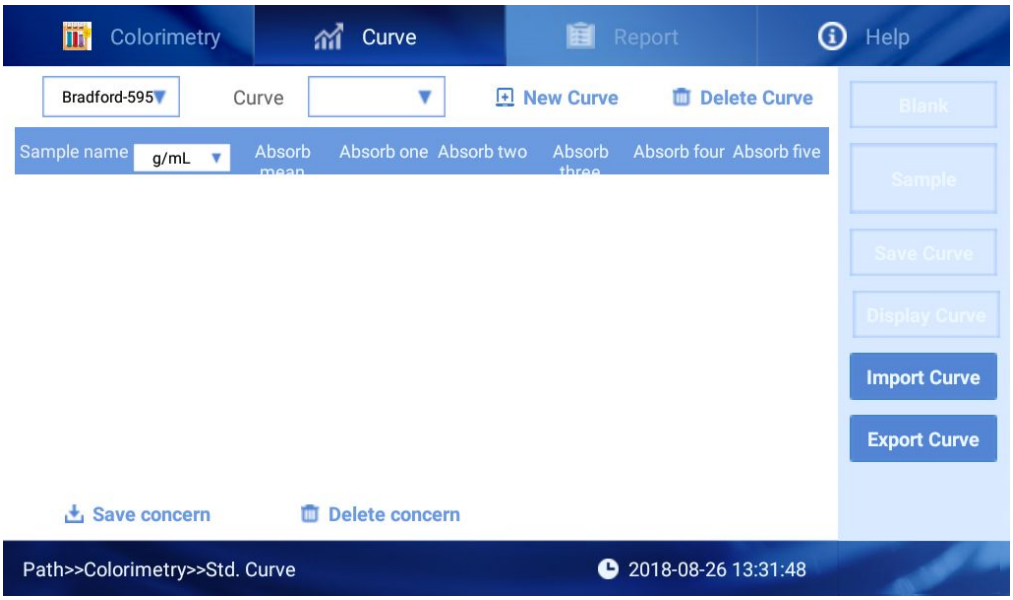


Fig 4.16 Colorimetry detection curve interface

Steps to build up curve:

① Click New Curve , Input curve name, and click “Sure”, then you will come to standard sample table for curve , see Fig 4.17:

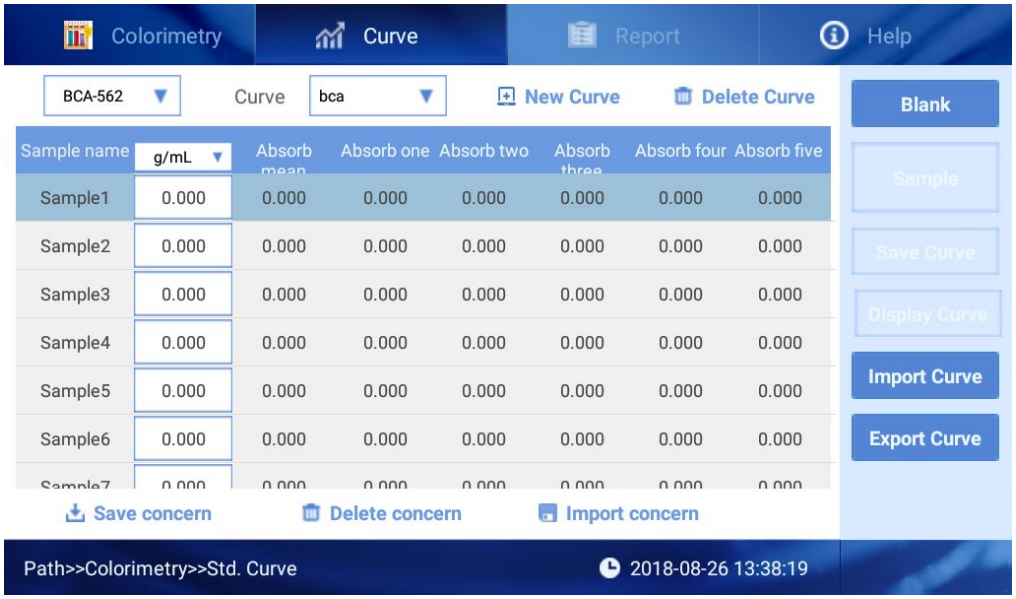


Fig 4.17 Curve interface to input concentration value

② Click g/ml to choose unit for sample, click concentration area, it shows Sample1 0.000 , input the concentration. Sequence of the

standard samples can be random, the added sample should keep consistent with the selected concentration value.

③ Then select a standard sample as Fig 4.17 and then click “Blank” and “Sample” in turn to measure the absorbance of standard sample.

Each standard sample can be measured by 5 times, and the average value can be used to build the standard curve. You can delete the standard sample values (long press sample2, the option window appears), you also can delete some single value among the 5 measurements(long press the one you want to delete, the option window appears).

④ After measuring all samples, click Save Curve to save curve.

Notes: If user plans to leave the interface before building curve complete, the system will appear a dialog window to ask you save curve. You only can find the standard curve at the measurement interface after you save it.

Function for buttons:

① Display Curve: Click it to view the standard curve as below:

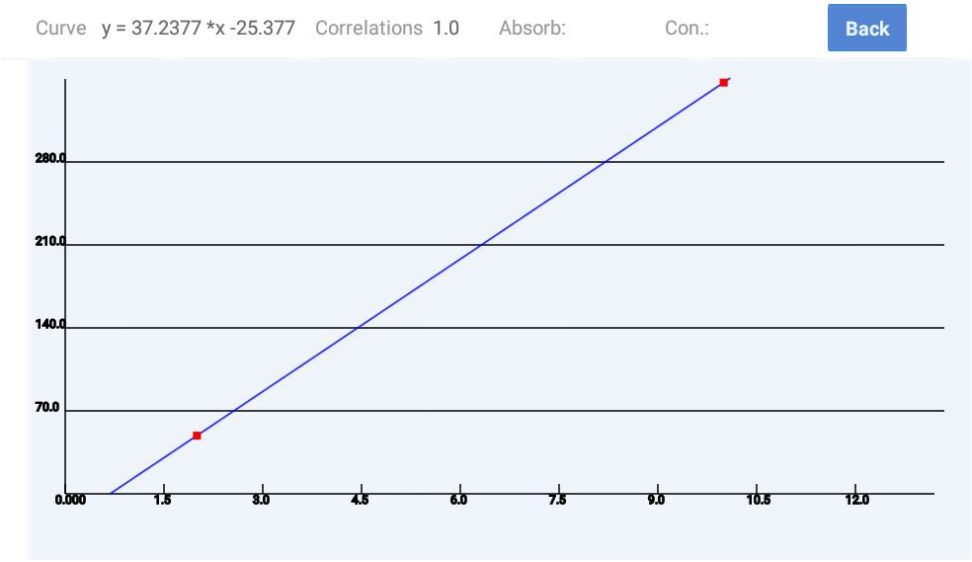


Fig 4.18 New curve

② Import Curve: Click it to import curve.

③ Export Curve: Click it to export curve to the U disk.

④ Save concern: Click it to save the current interface standard sample concentration value.

⑤ Delete concern: Click it to delete the current concentration value.

⑥ Import concern :Click it to import concern

5.4. Colorimetry report

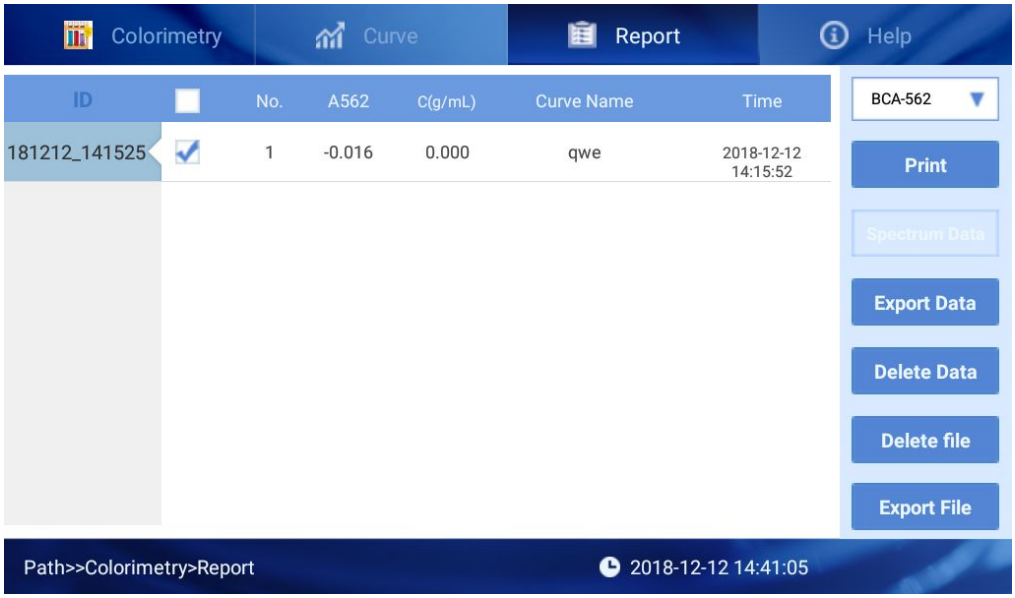


Fig 4.19 Colorimetry detection report interface

It is similar as the Nucleic Acids detection interface, so here only introduce the differences.

: Click it to choose the colorimetry type and the detection data will be displayed.

5.5. Colorimetry help

We are sorry to inform you the “Help” has not been finished yet.

6. Fluorometer

6.1. Introduction

Click “Fluorometer” button in the main interface and enter the Fluorometer interface as Fig 4.20 below. Click the “Fluorescence” button to test the sample fluorescence directly, there is no curve creation and sample concentration analyses in this test. Click “dsDNA”, “Protein” or “Oligo” button to create standard curve, calibrate curve or test samples etc. Click “Kinetics” button to start the kinetic measurement and create the kinetics curve.

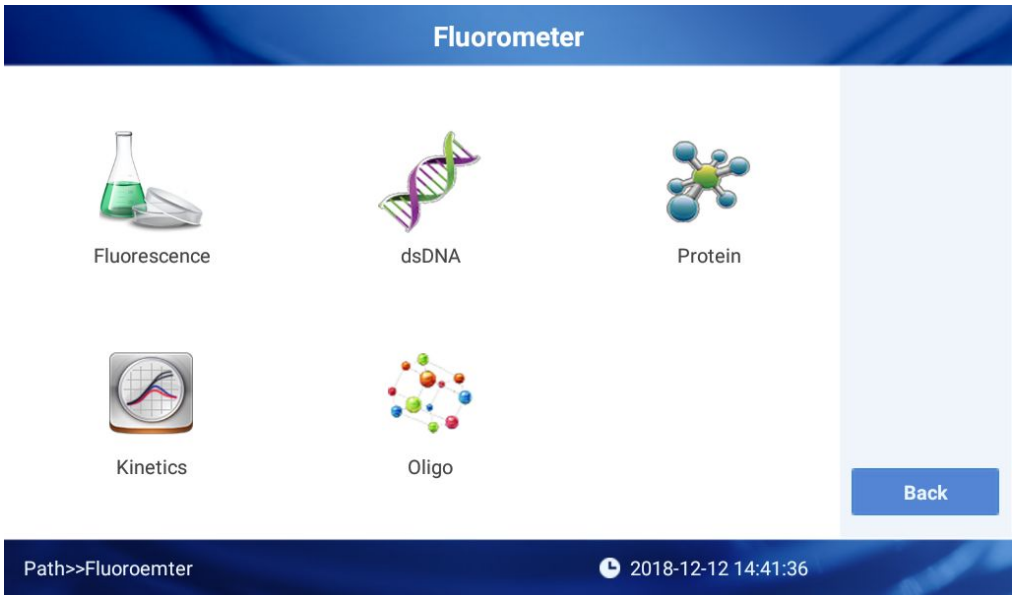


Fig 4.20 Fluorometer interface

6.2. Fluorescence

Click “Fluorescence” button in the Fluorometer interface and enter the interface as Fig 4.21 below.

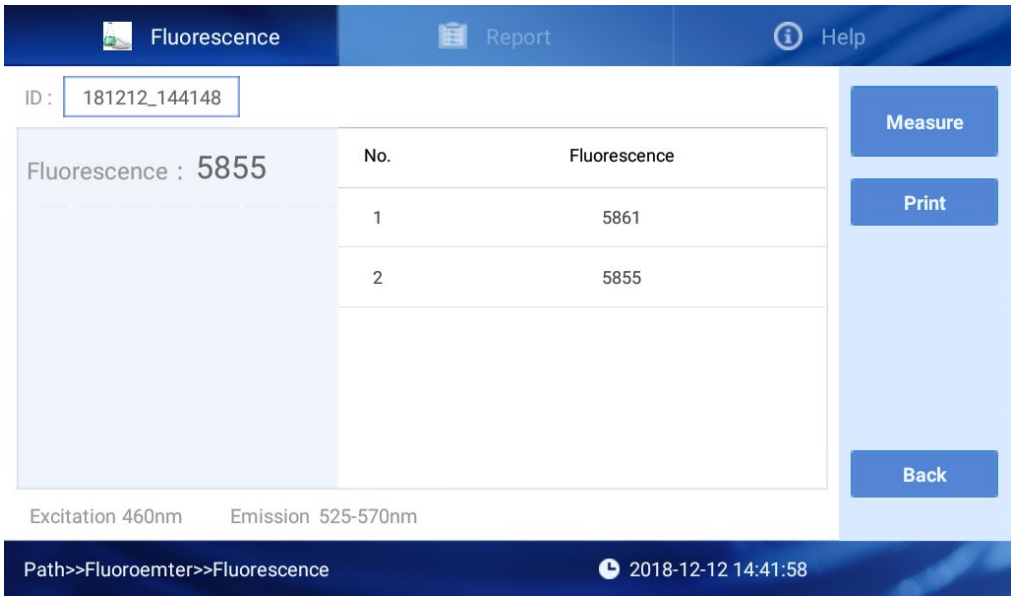


Fig 4.21 Fluorescence test interface

6.2.1. Fluorescence measurement

（1）Button introduction:

①Measure: Click it to measure sample.

②Print: Print current measure result.

③ Excitation 525-570nm Emission 460nm : Current measure wavelength.

（2）Operation steps:

①Set the sample ID.

②Put the cuvette holder into the fluorescence test groove.

③Add 200ul sample into the PCR tube, put the tube into cuvette holder.

④Click “Measure” button to measure the sample and the result will be showed in the left of interface.

6.2.2. Fluorescence Report

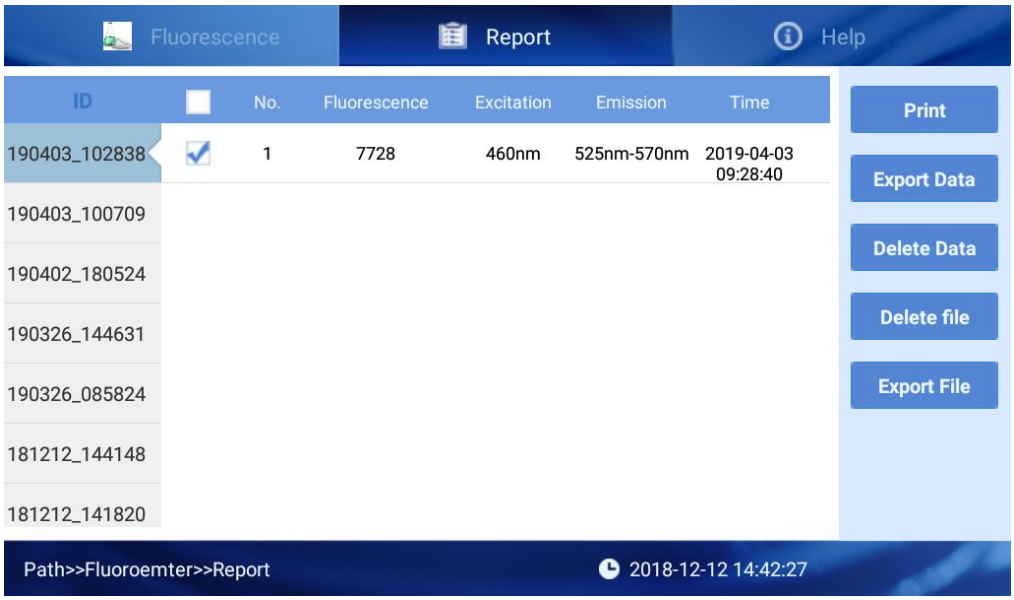


Fig 4.22 Report

The same as the Nucleic acid report.

6.2.3. Colorimetry help

We are sorry to inform you the “Help” has not been finished yet.

6.3 dsDNA、RNA、Protein

Note: As the software function of dsDNA, RAN and Protein are the same, this manual only introduces the software function of dsDNA.

Click “dsDNA” button in the Fluorometer interface to enter the interface as Fig 4.23 below.

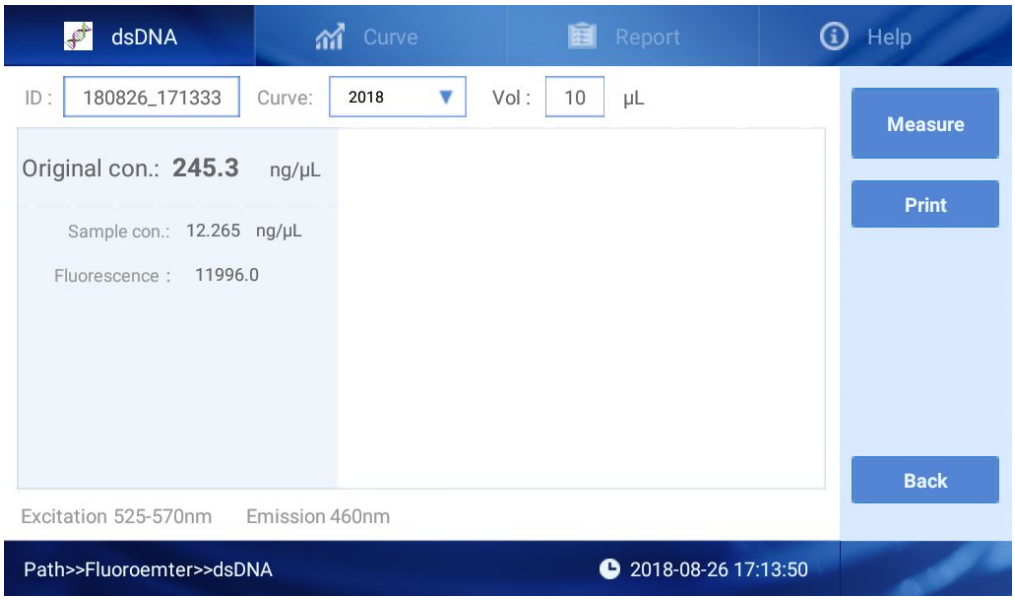


Fig 4.23 dsDNA measure interface

6.3.1. dsDNA

（1）Interface introduction

① ID : 180826_171333 : Set the test ID, the default is current time.

② Curve: 2018 : Click to choose the standard curve, or the sample can not be measured.

③ Vol : 10 μL : Click to input the original volume of sample.

④ Measure : Click it to measure sample and the result will be showed in the right of interface.

Note: The sample can not be measured without standard curve.

⑤ Print : Print current measure result.

⑥Measure result showed as Fig 4.24 below.

Fig 4.24 Result of dsDNA test

Original con.: The original sample concentration.

Sample con.: The PCR tube sample concentration.

Fluorescence: The Fluorescence value of the measurement.

（2）Operation steps

①Add the sample into the PCR tube and dilute the total volume to 200μl, put the tube into the cuvette holder.

②Set the test ID, standard curve and sample original volume.

③Click Measure button to test and the result will be showed in the left of interface.

Note: The default sample test volume is 200μl, make sure the correct volume before the measurement.

6.3.2. Curve

You need to create the standard curve before the measurement, a simple standard curve can be made with two points, in order to make sure the accuracy of the result, a hypodispersion five points standard curve is

necessary.

Click “Curve” enter the standard curve interface as Fig 4.25 below.

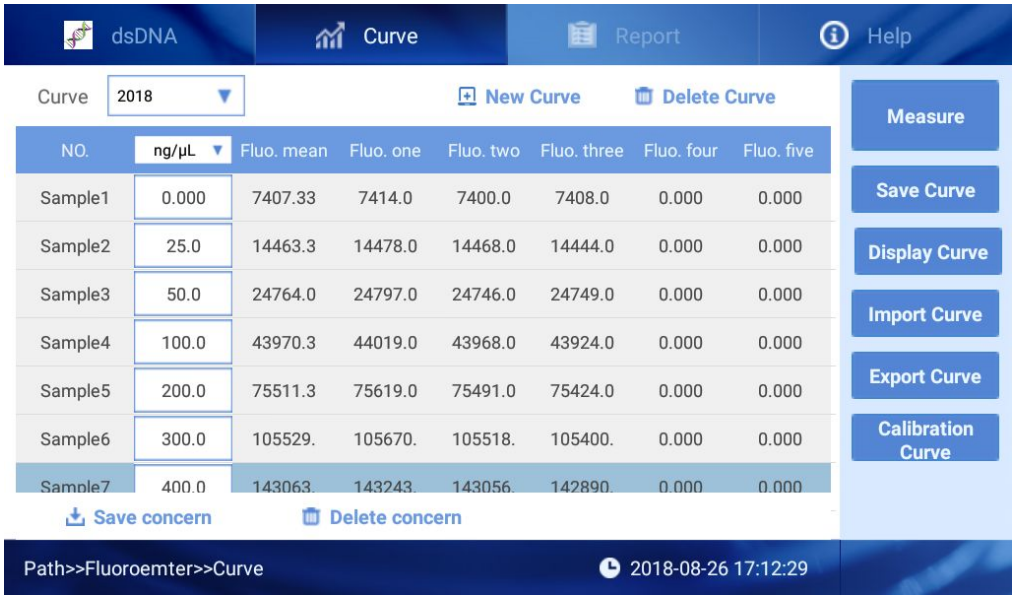


Fig 4.25 Fluorescence standard curve

（1）Interface introduction

The main layout of the interface is the same as the standard curve interface of the colorimetry, Here are several different layouts.

①There is no “Blank” button, click “Measure” to test the sample directly.

②Calibration Curve: Calibrate the created standard curve to eliminate the drift error of the device.

（2）Operation introduction

New Curve:

①Click New Curve to input the ID and choose the type of curve.

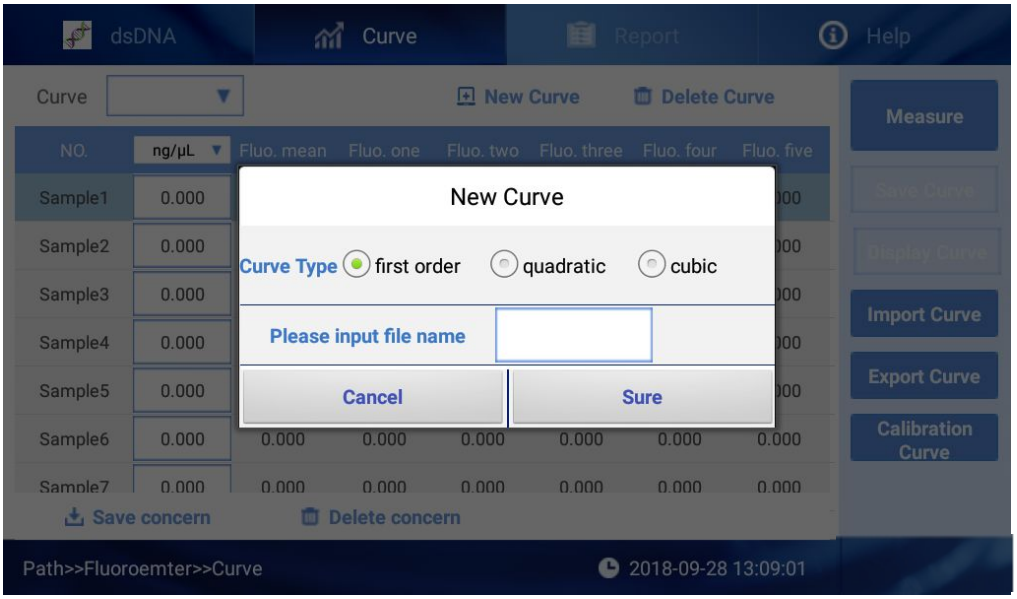


Fig 4.26 choose the type of curve

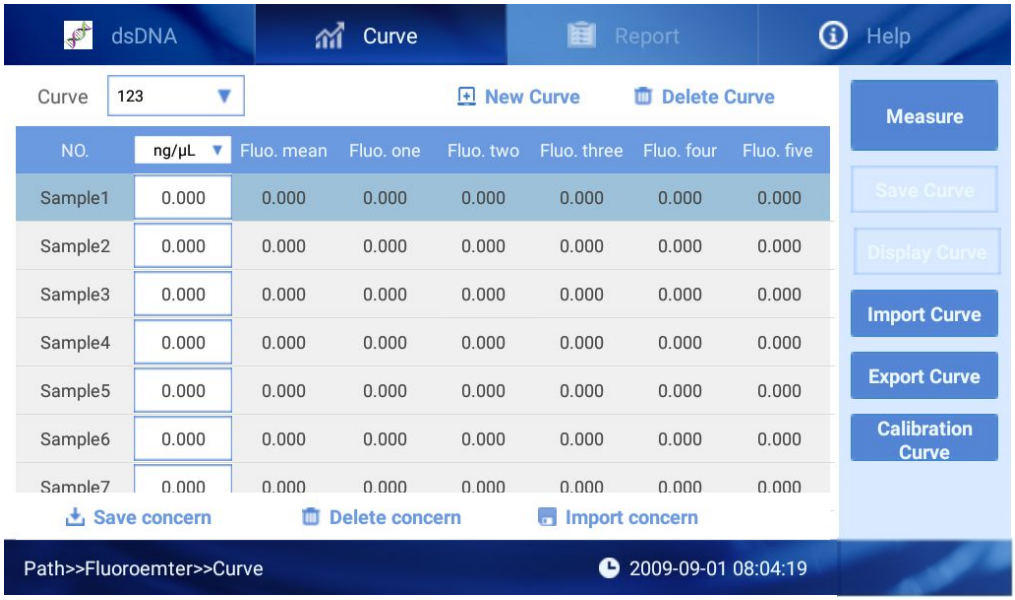


Fig 4.27 New Curve

②Click ng/μL to set the units of standard sample and input the concentration of it in 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.

③In the interface as Fig 4.27, when a standard sample is chosen, the bottom colour will be changed blue, then click “Measure” to test the fluorescence of it. Each standard sample can be tested 5 times and the average value is the standard curve sample point. Hold the area of the name of standard sample to delete the standard sample, click the fluorescence value to delete the tested value.

④Click Save Curve to save the created standard curve.

Calibration curve:

①Click Calibration Curve enter the calibration curve interface as Fig 4.26 below, the calibration point range is 1-3.

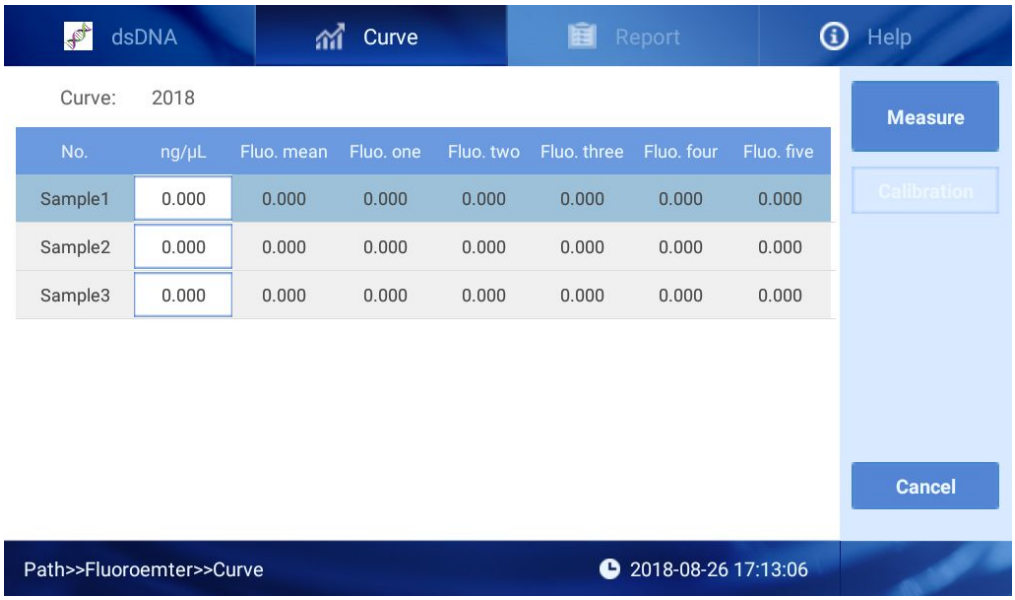


Fig 4.28 Calibration curve interface

②Input the concentration of the calibration sample into the box 

. There is no requirement of the orders when set the concentrations.

③Click “Measure” to test the fluorescence of current standard sample.

④Click “Calibrate” to complete the calibration.

6.3.3. Report

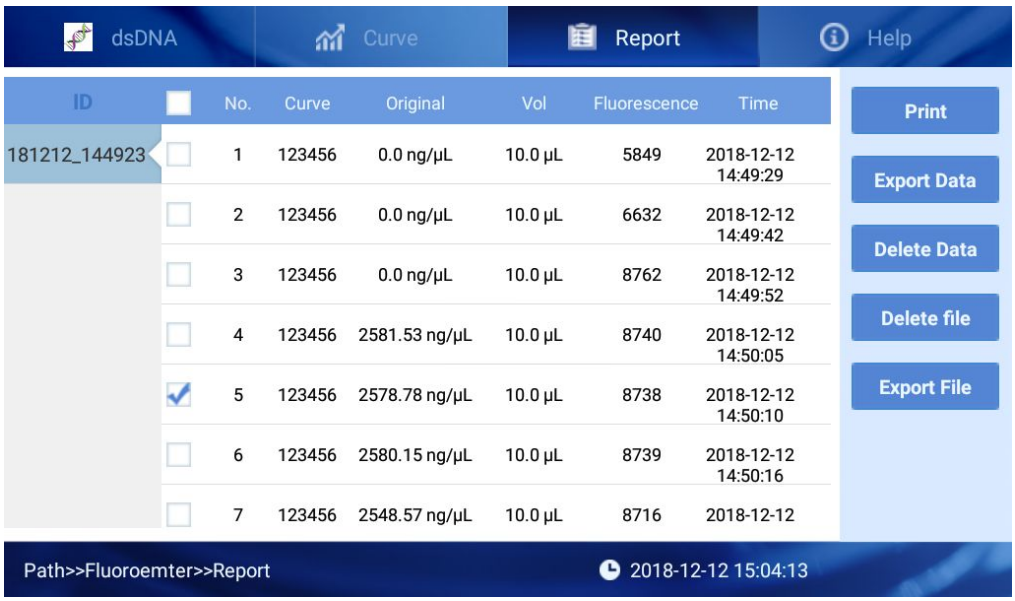


Fig 4.29 Report

The same as the Nucleic acid report.

6.3.4. Colorimetry help

We are sorry to inform you the “Help” has not been finished yet.

6.4. Kinetics

In the Fluorometer interface, click “Kinetics” enter the interface Fig 4.28 below.

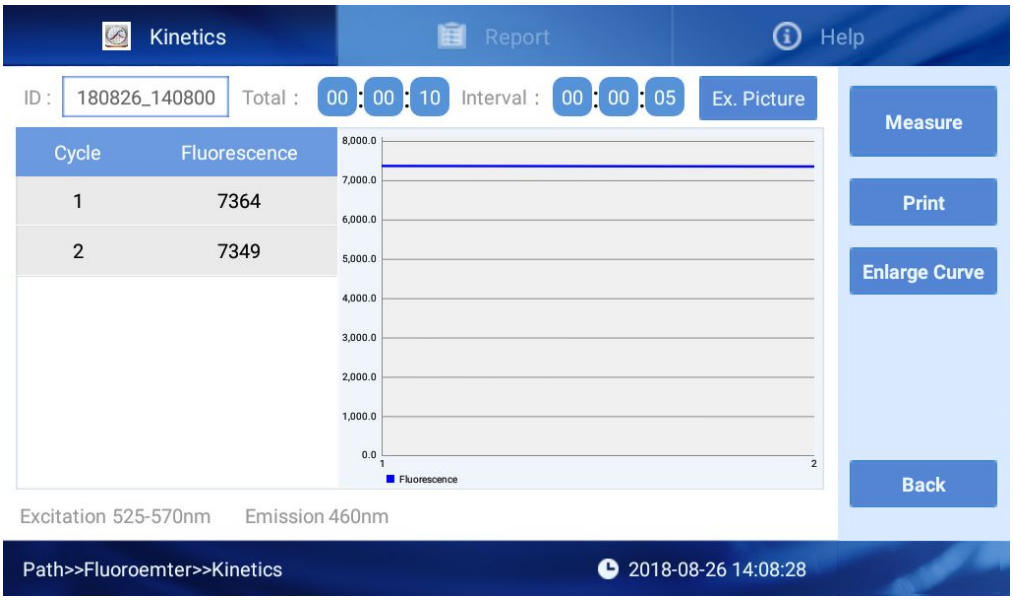


Fig 4.30 Kinetics interface

6.4.1. Kinetics test

（1）Interface introduction

①ID : 180826_140800: Set the test ID, the default is current time.

② Total : 00 : 00 : 10 : Set the total time, the “00:00:00” correspond to “Hour: Minute :Second”.

③ Interval : 00 : 00 : 05: Set the interval between two tests, the “00:00:00” correspond to “Hour: Minute :Second”.

④ Measure: Click it start the measurement and enter the interface as Fig4.29 below, click “Stop” button to stop the current measurement.

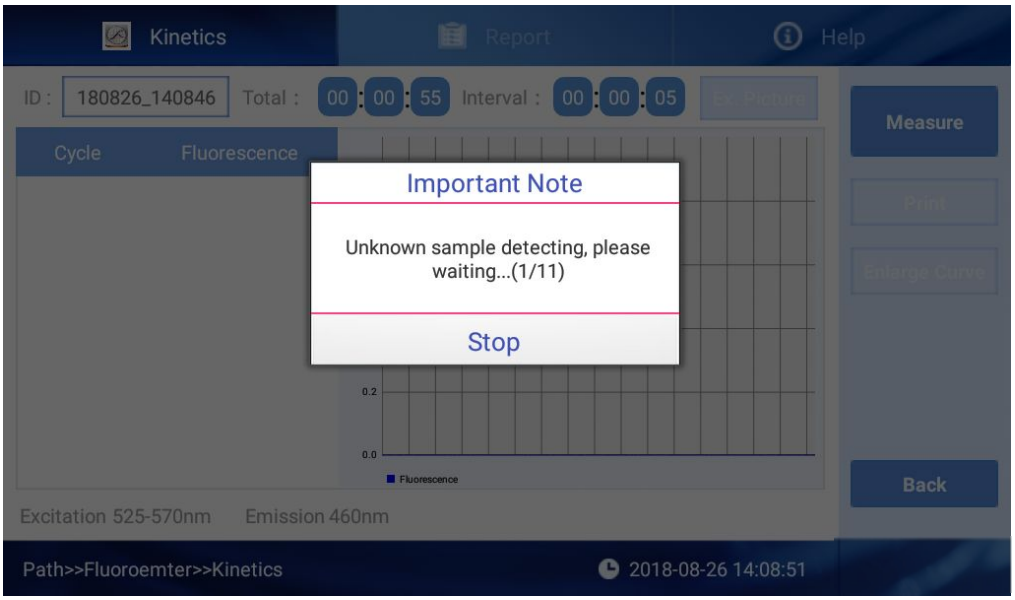


Fig 4.31 Kinetics test interface

⑤ Print: Click to print test result.

⑥ Enlarge Curve : Click it to check the amplified curve after measurement

⑦ Ex. Picture: Click it to export the curve as picture format to the U disk.

（2）Operation steps

①Set the test ID, total time and interval time.

②Put the sample into the cuvette holder and close the lid.

③Click the “Measure” to start the measurement.

④Test times and fluorescence value will be showed in the left and the curve will be made in the middle of the interface.

Note: 1. The maximum test time is 99, if set more than 99

times, the device can only test 99 times.

2. Click “Stop” in the testing, it will stop when the next test complete and it can not continue again.

6.4.2. Kinetics test report

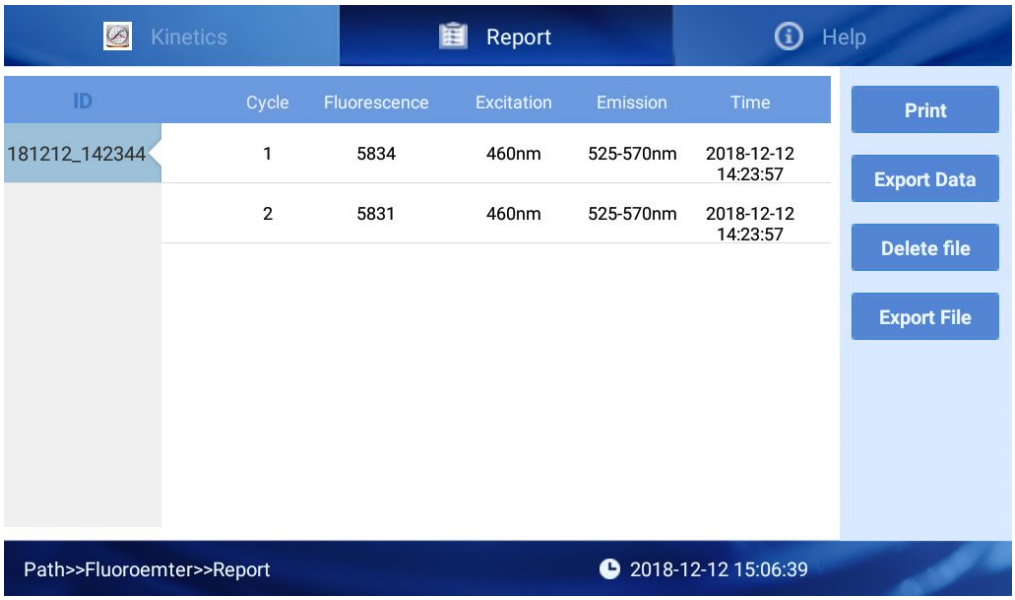


Fig 4.32 Kinetics test report

The same as the Nucleic acid report.

6.4.3. Colorimetry help

We are sorry to inform you the “Help” has not been finished yet.

7. Uv-Vis Full-spectrum Scanning

7.1 Introduction

UV-VIS module allows the Spectrophotometer to function as a conventional spectrophotometer. Sample absorbance is displayed on the screen from 200nm to 800nm.

Samples with high absorbance (up to 240A equivalent at 10mm path) can be measured directly.

7.2 Uv-Vis measurement

Uv-Vis measurement interface as Fig 4.33:

Fig 4.33 Uv-Vis detection interface

It is similar as the Nucleic Acids detection interface, here only introduce the differences.

①Click Blank to make blank and then Blank data is available,

click it to enter the interface Fig 4.34. It shows the 200-800 wavelength light intensity of blank sample.

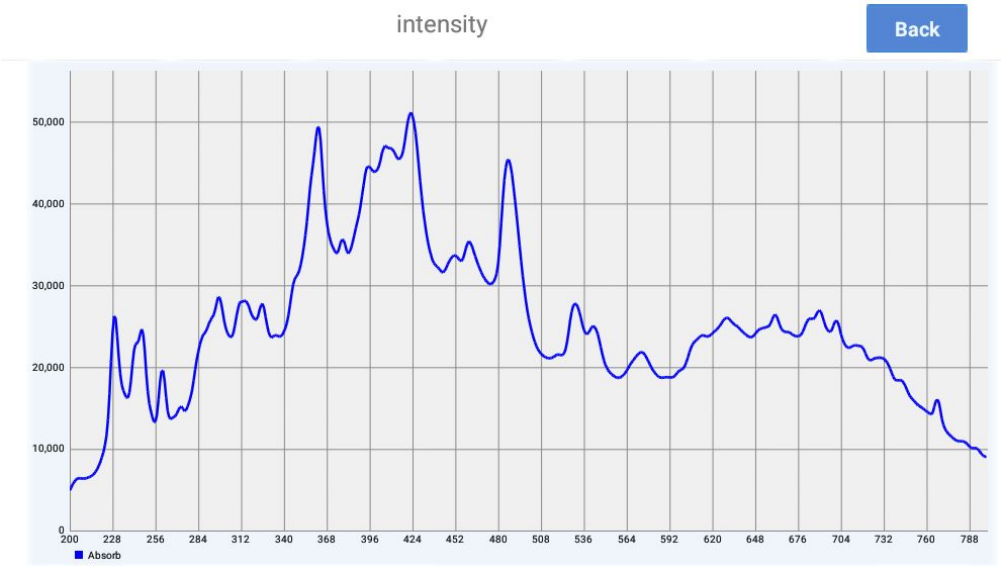


Fig 4.34 Blank light intensity

②You can input the wavelength as Fig 4.35 before the detection and the absorbance will be showed after the detection.

No.	Wave	Absorb
1	230	0.000
2	260	0.000
3	492	0.000
4	630	0.000
5	000	0.000

Fig 4.35 Check the absorbance of wavelength

③ After blank detection, click Sample and then Sample data will be available. Click it enter the interface as Fig 4.36. It shows the light

intensity of 200-800 wavelength.

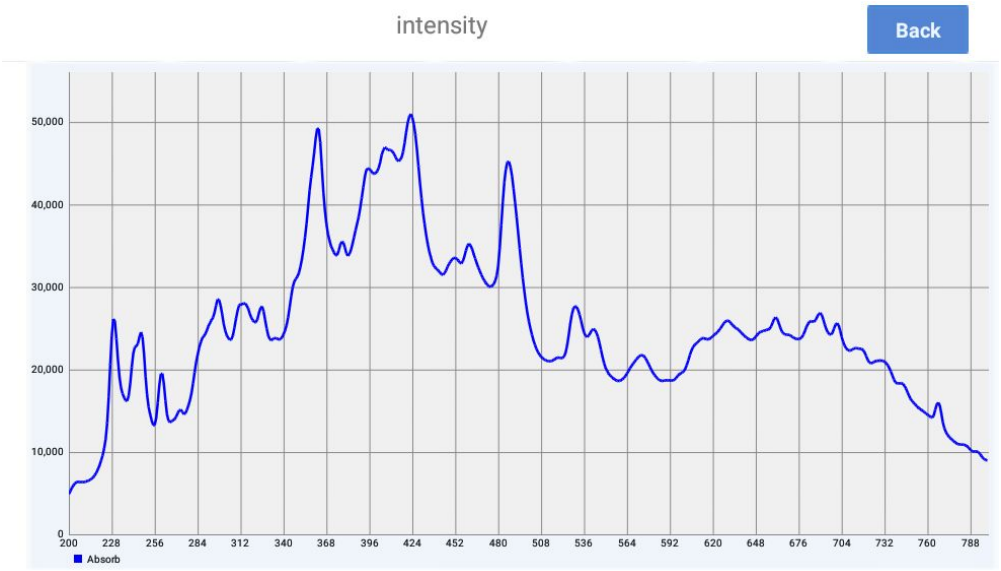


Fig 4.36 The sample light intensity

Operation steps:

① Set the batch NO. and Nucleic Acids type;

② Clean the upper and lower pedestals with dust proof paper, add 2μL buffer solution to make blank;

③ Clean the buffer solution on the pedestals with dust proof paper;

④ Measure sample with volume of 2μL and click “Measure” to detect the sample;

Note: The sample must be the new adding before your measurement.

⑤ After measurement, pedestals must be cleaned before next measurement.

7.3. Uv-Vis Report

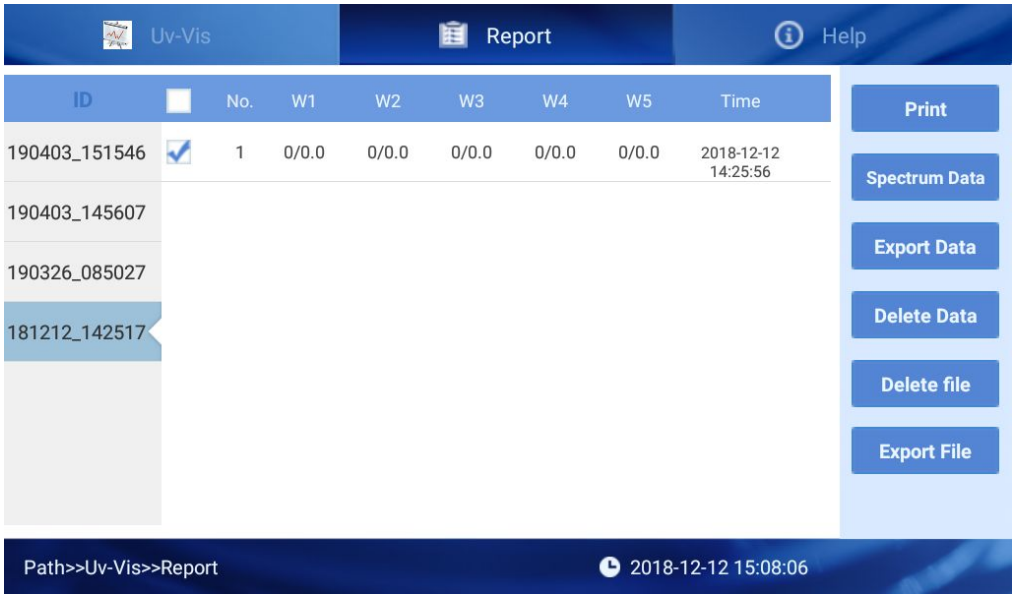


Fig 4.37 Uv-Vis detection report

It is similar as the Nucleic Acids detection, here only introduce the difference.

Spectrum Data: Click it to enter the interface as Fig 4.38

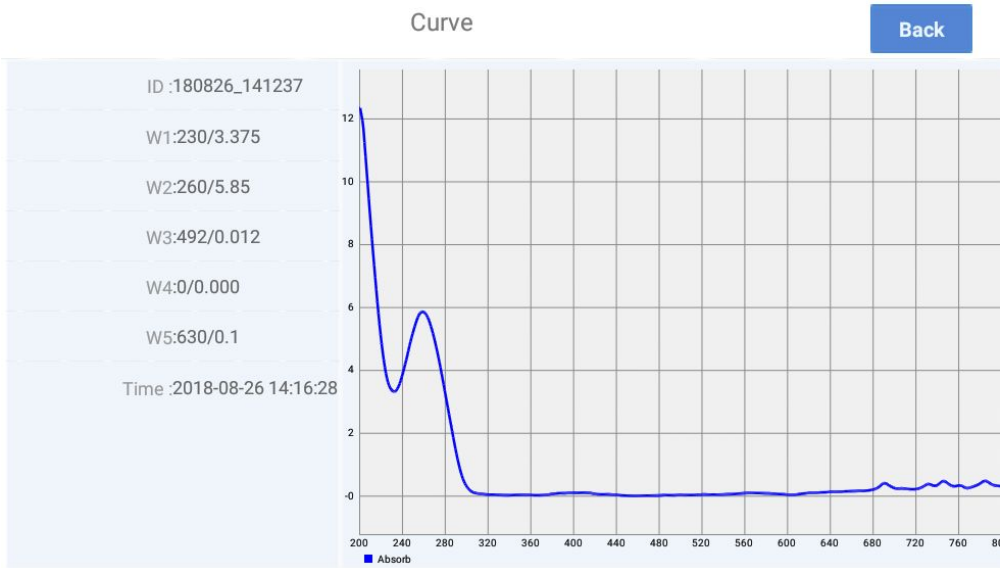


Fig 4.38 Uv-Vis optical wavelength data

7.4. Uv-Vis Help

We are sorry to inform you the “Help” has not been finished yet.

8. OD600

8.1. Introduction

OD600 mean a solution absorbance value at under wavelength of 600nm .

An important application is to measure bacterial density, which tests the culture solution concentration by the bacterial ABS.

8.2. OD600 measurement

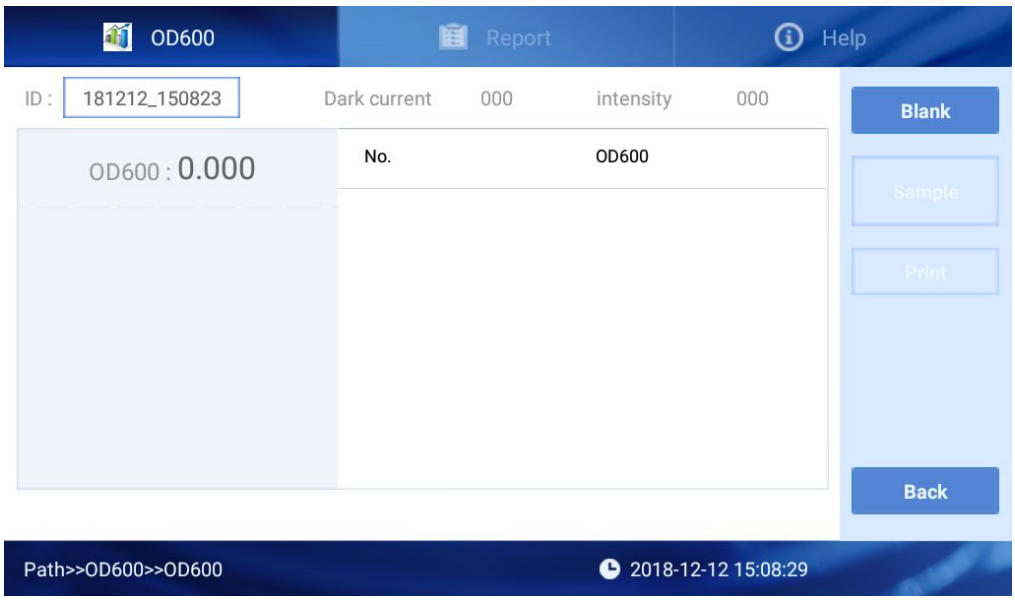


Fig 4.39 OD600 detection interface

Operation steps:

① Set the batch NO. and Nucleic Acids type;

② Blank before each measurement. Users can make blank without

anything, blank with empty cuvette, or buffer in cuvette.

③ Add 2ml~3ml sample into the cuvette after blank.

④ Click Measure, the OD600 value will show at the left.

8.3. OD600 Report

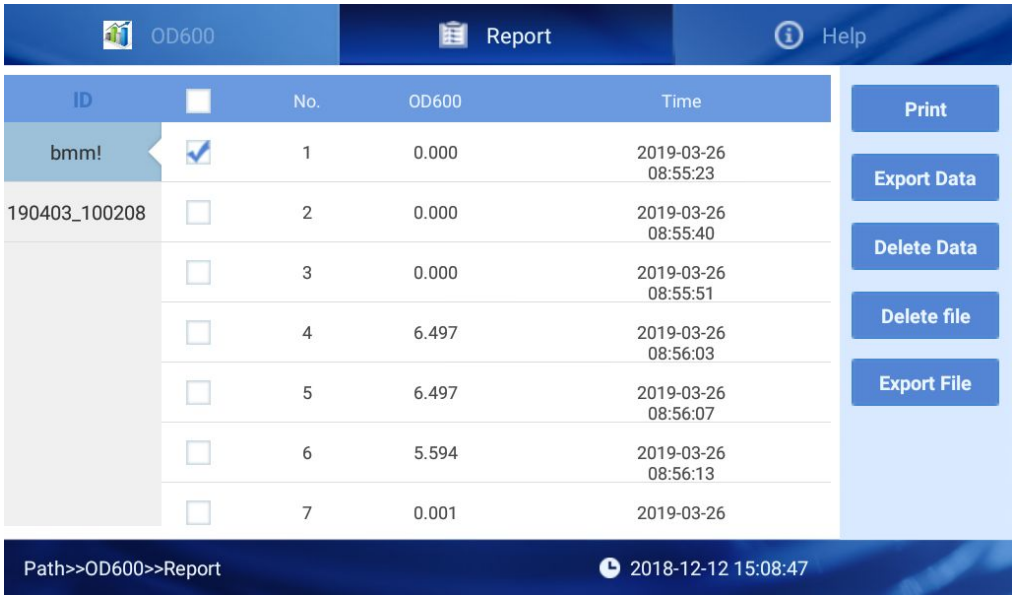


Fig 4.40 OD600 detection report interface

8.4. OD600 Help

We are sorry to inform you the “Help” has not been finished yet.

9. System

Click “System” on the main interface, as Fig 4.41:

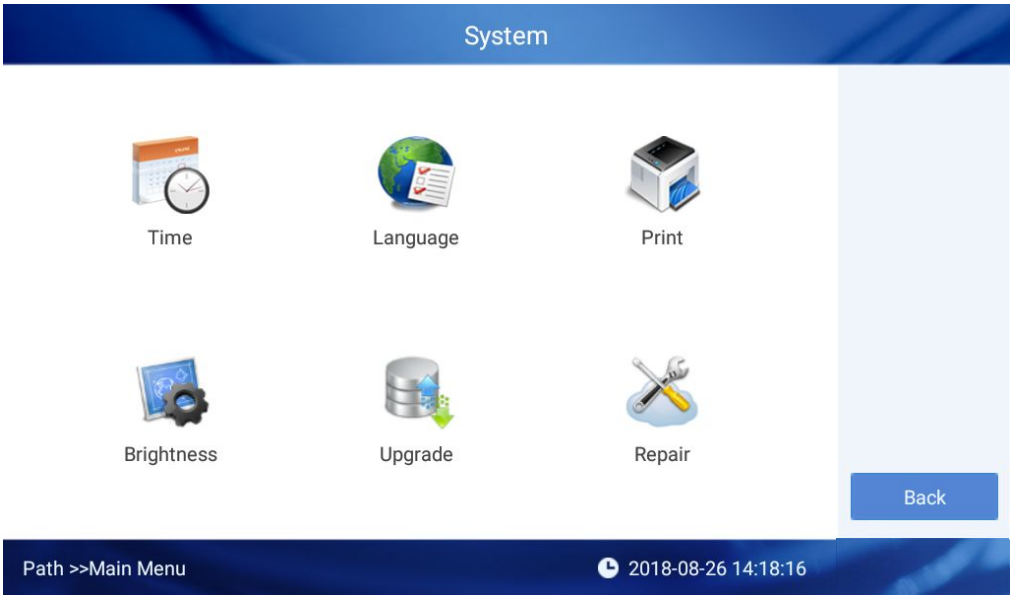


Fig 4.41 System setting

9.1. Time setting

Click “Time” to start setting, as Fig 4.42.

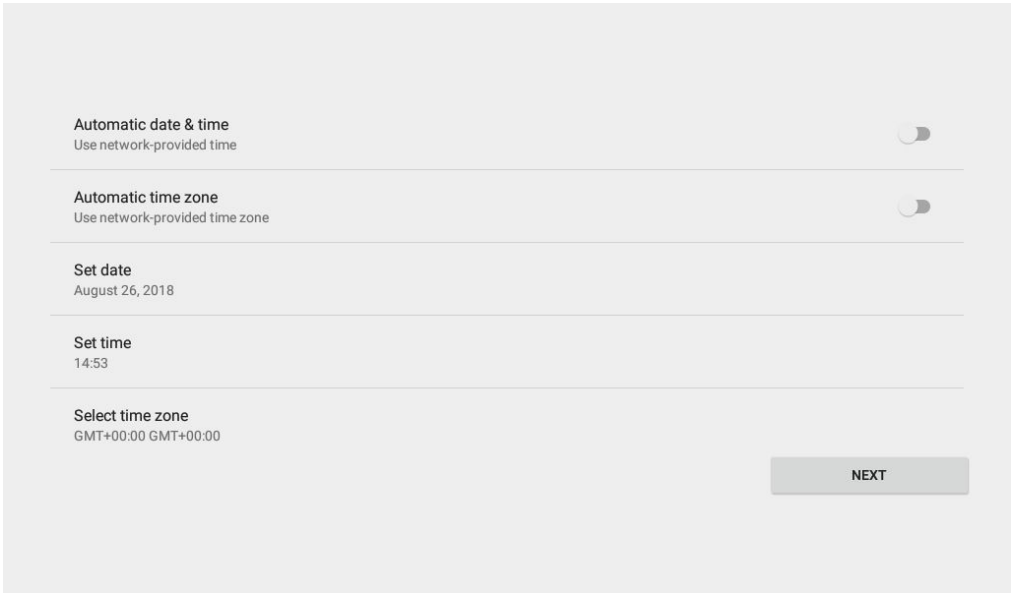


Fig 4.42 Time setting interface

①“Automatic date & time”: It needs to connect the internet to calibrate time automatically, it is unavailable at present.

②“Automatic time zone”: It needs to connect the internet to calibrate time zone automatically, it is unavailable at present.

③“Set date”: Click it enter the date setting interface as Fig 4.43 below.

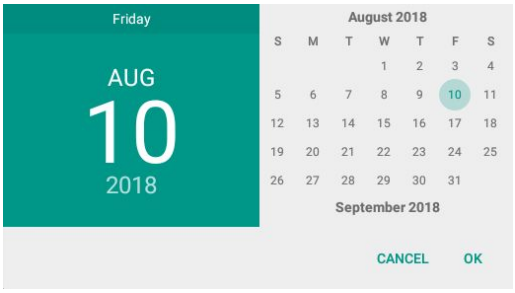


Fig 4.43 Set date

④“Set time”: Click it enter the time setting interface as Fig 4.44 below.

Fig 4.44 Set time

⑤“Select time zone”: Click it enter the time zone setting interface as Fig 4.45 below.

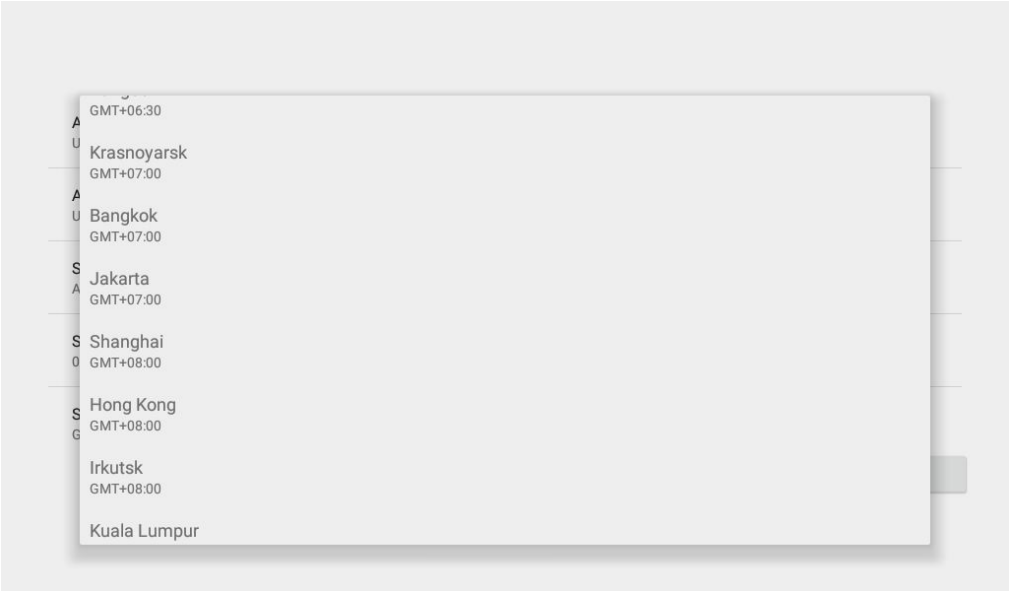


Fig 4.45 Select time zone

⑥“Use 24-hour format”: Set the 24-hour format as Fig 4.46 below.

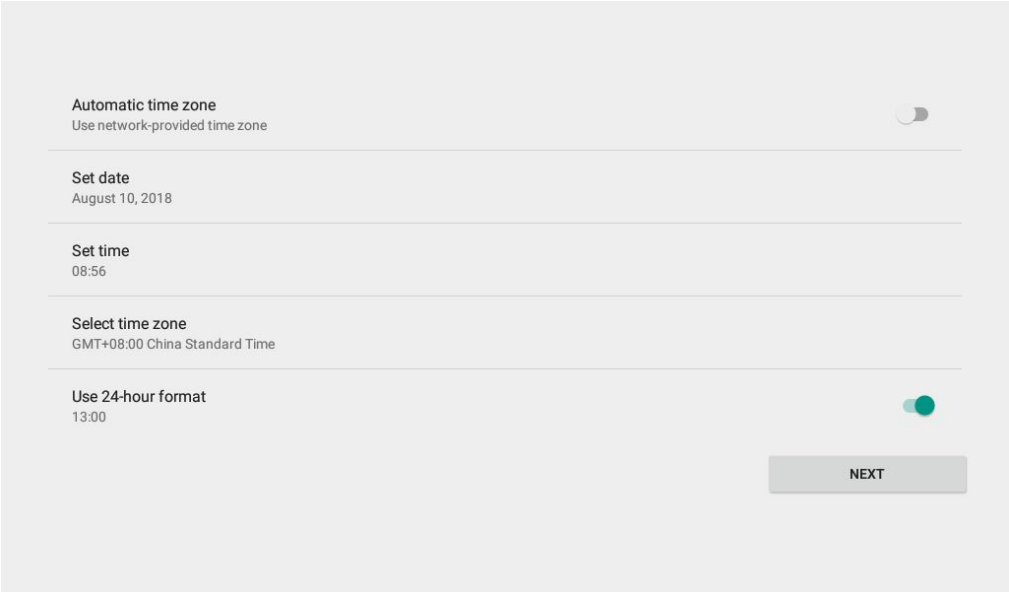


Fig 4.46 Use 24-hour format

9.2. Language setting

Click the “Language” icon, set language at the dialog window. As Fig 4.47.

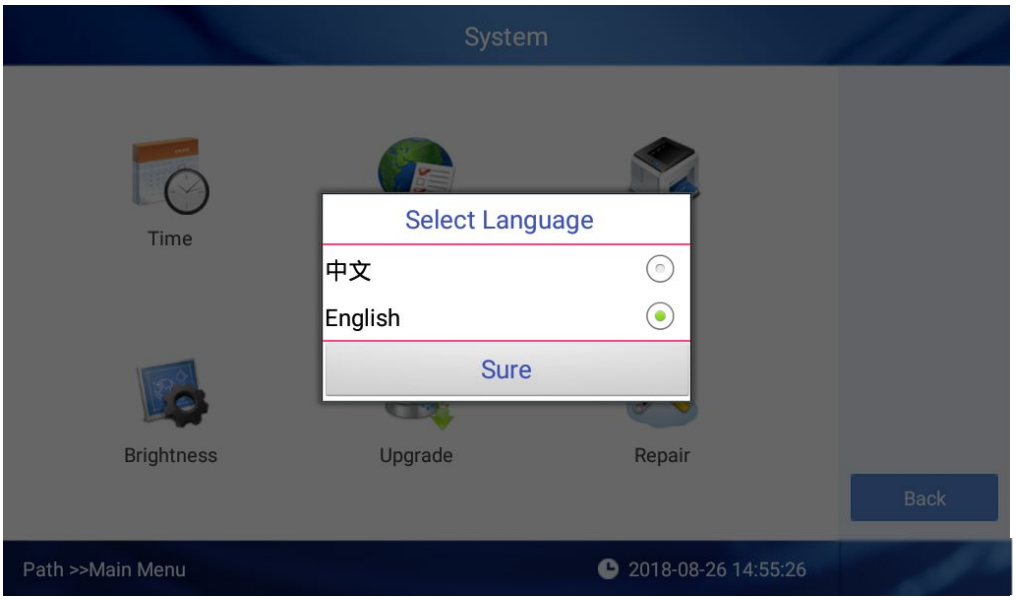


Fig 4.47 Language setting

9.3. Print

Click “Print” icon, set the print mode on the dialog window. As Fig 4.48.

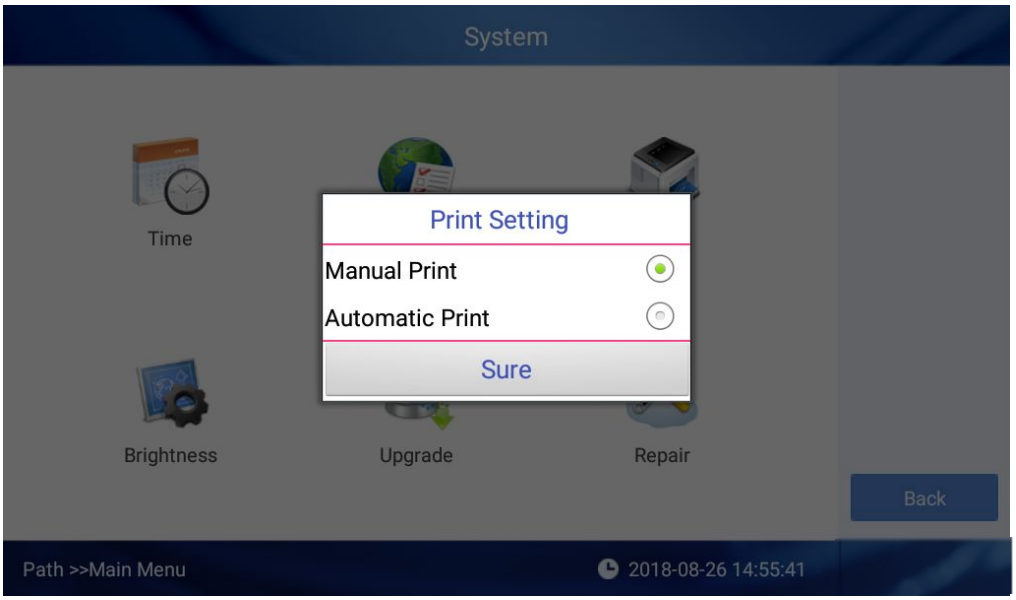


Fig 4.48 Print setting

9.4. Brightness

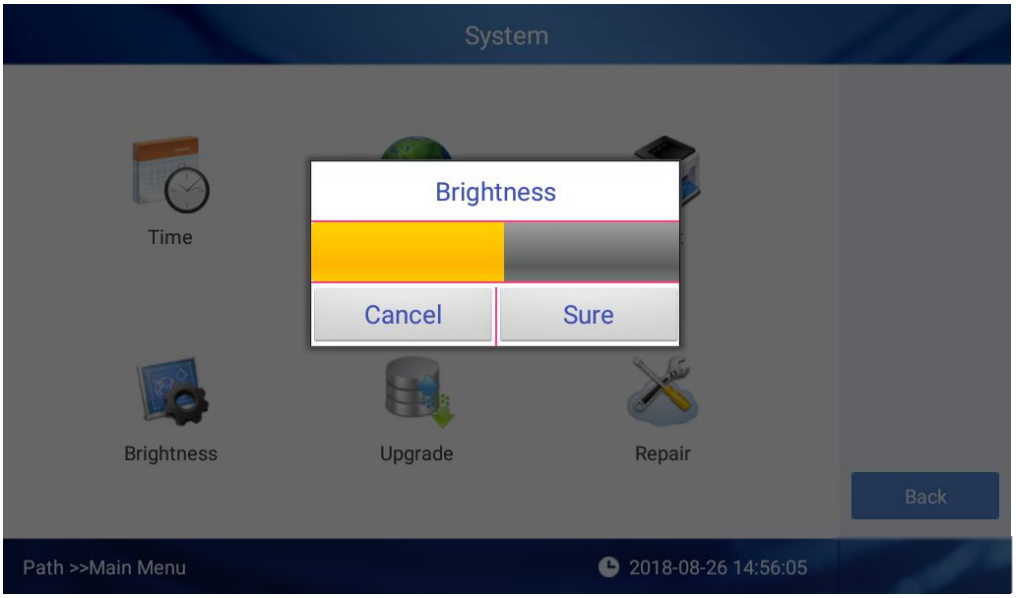


Fig 4.49 Brightness setting

Click “Brightness” icon, slide to set the brightness to a suitable one. As Fig 4.49.

9.5. Upgrading

Put the upgrading software on the root directory of mobile hard disk drive and insert it into the instrument, then click “upgrade” icon to install the software.

9.6. Maintenance

This part is for production and maintenance , which is not allowed to enter into.

Chapter 5 Trouble and shootings

No.	**Fault phenomenon**	**Cause analysis**	**Shootings**
1	Instrument can not turn on.	No power supply, Switch defective, Power adapter defective.	Check the power supply, Replace the switch, Contact the vendor.
2	Measurement result not precise	Liquid column unformed, Pedestal contaminated, others.	Add sample again, make sure the liquid column formed well, Clean the pedestals, Contact supplier or manufacturer.
3	OD600 module failure	Poor connection between cable and board.	Contact supplier or manufacturer.
4	Insufficient light intensity error	Analysis module defective, optical fiber broken.	Contact supplier or manufacturer.
5	Touch screen hops	Power supply without grounding.	Provide effective grounding power supply.
6	Communication timeout	Analysis module communication failure.	Restart instrument, or contact supplier or manufacturer.

Memo