



Micro-Spectrophotometer Manual

Version 2021

AE-NANO600



A & E LAB (UK) CO.,LTD

Foreword

Thanks for purchasing our micro spectrophotometer, This Manual contains function and operation introductions. In order to use the instrument properly, please read this manual carefully before operation.

Please check the instrument and accessories with the packing list at the first time you open the instrument packing case.

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Safety and Warnings

1 Operation Information

Users should know the working principle of the instrument before operation.
Please read this manual carefully.

2 Safety

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 an effect on the instrument.



Indoor used instrument.



Read the Manual carefully before operation. Only trained personnel can operate the instrument.



Turn off the power in case of stop working, unplug the power connector from the socket in case of long term nonuse and cover the instrument with a cloth to avoid the dust in.

Unplug the power connector, contact vendor or maintenance man who was trained in case as follows :



- There is some liquid flowing into the Instrument
- Instrument get wet through rain or water
- Can't work normally, especially with odd sound or smell.
- Instrument falls down or out shell damaged
- The function has obviously changed

3 The Maintenance

Clean the sample pedestal by soft and clean cloth with water, don't with alcohol. Clean the instrument outside with mild cleansing cream.

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Chapter 1 Introduction

AE-NANO600 is a UV and Visible spectrophotometer, utilized to test micro volume purified nucleic acid and protein.

With pre-installed software and touch screen, it can measure sample volume of 0.5~2ul, which is precise and repeatable. Sample is shaped liquid column between the upper and lower pedestals due to surface tension, it allows high concentration sample can be measured without dilution. Benefit from the working principle (200~800nm) NanoOne, can measure high concentration samples.

The device is equipped with cuvette slot to enable measure diluted sample in cuvette.

Chapter 2 Features

1. Working condition

Ambient temperature: 5°C ~ 35°C

The relative humidity: ≤70%

Voltage: DC12V 4A

2. Basic features and parameters

Model	AE-NANO600	
Sample volume	0.5ul~2ul (2ul recommended)	
Path Length	0.05mm, 0.2mm or 1mm	
Light source/Life	Xenon Lamp/flicker times>10 ⁹	
Detector type	2048 CCD array	
Wave Length	200~800nm	
Wave length accuracy	±1 nm	
Spectral resolution	≤3nm (FWHM@Hg 253.7nm)	
Absorbance precision	0.003Abs (1mm wavelength)	
Absorbance accuracy	±1% (7.332Abs at 260nm)	
Absorbance range	0.04~90 (10mm wave length at 260nm)	
Nucleic acid range	2ng/ul dsDNA ~ 15000ng/ul dsDNA	
Detection time	<6S	
OD600	Abs range	OD600
	Abs stability	Abs stability
	Abs repeatability	Abs repeatability
	Abs accuracy	Abs accuracy
Voltage	DC12V 4A	
Power	25W	
Dimension	208×280×186 mm (W×D×H)	
Weight	3.6 kg	

Chapter 3 Basic Operation

1. Structure

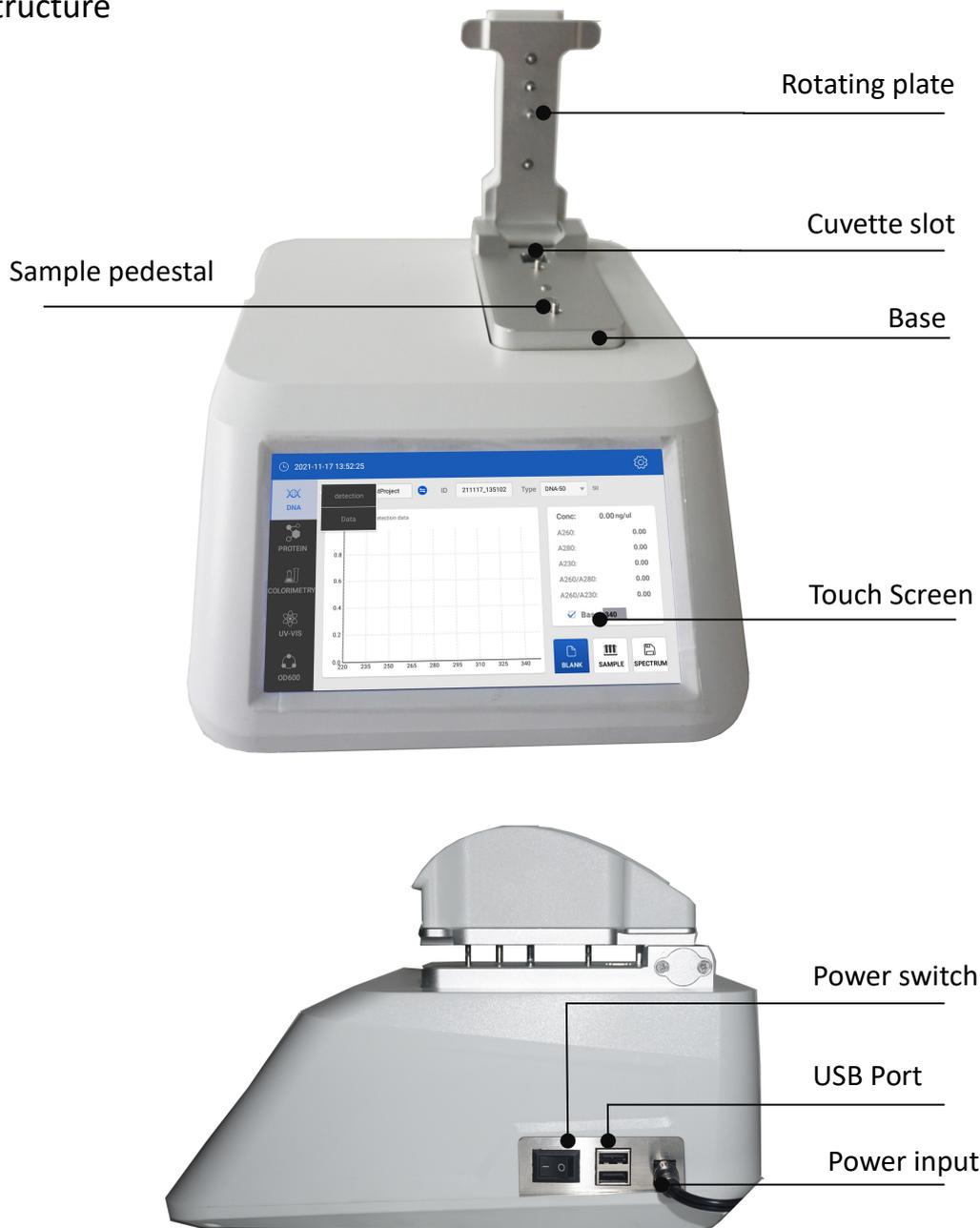


Fig 3.1 Structure

Note: Power supply requires valid grounding wire, or there will be jump-point on the screen.

2. Sample volume

Sample volume is a key factor affecting the measurement result, make sure to form the liquid column between the upper and lower pedestals. Precise pipette (0~2ul) is required for sampling, and volume 2ul is recommended.

3. Pedestal

3.1 Lift the upper pedestal, drop the sample(2ul) on to the lower pedestal.



Fig 3.2 sample drop

3.2 Lay down the upper pedestal to form the liquid column as Fig 3.3, to start measure.

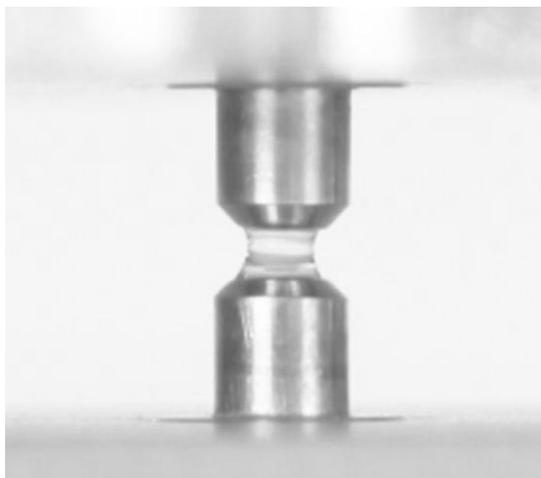


Fig 3.3 liquid column

3.3 Lift the upper pedestal after measurement, clean the two measurement heads with dust-free cloth, make sure there is no residual sample which may affect next measurement.



Fig 3.4 Clean upper and lower pedestal

Note: Clean the detection pedestals three times with pure water after measurement.

4. OD600 detection

AE-NANO600 is able to do OD600 detection. Lift the upper pedestal, enter into OD600 interface. First, make blank measurement, which is various depending on experiments requires, such as air, empty cuvette or cuvette with blank solution. Add 2~3ml sample to cuvette, and insert the cuvette to the slot to start OD600 detection

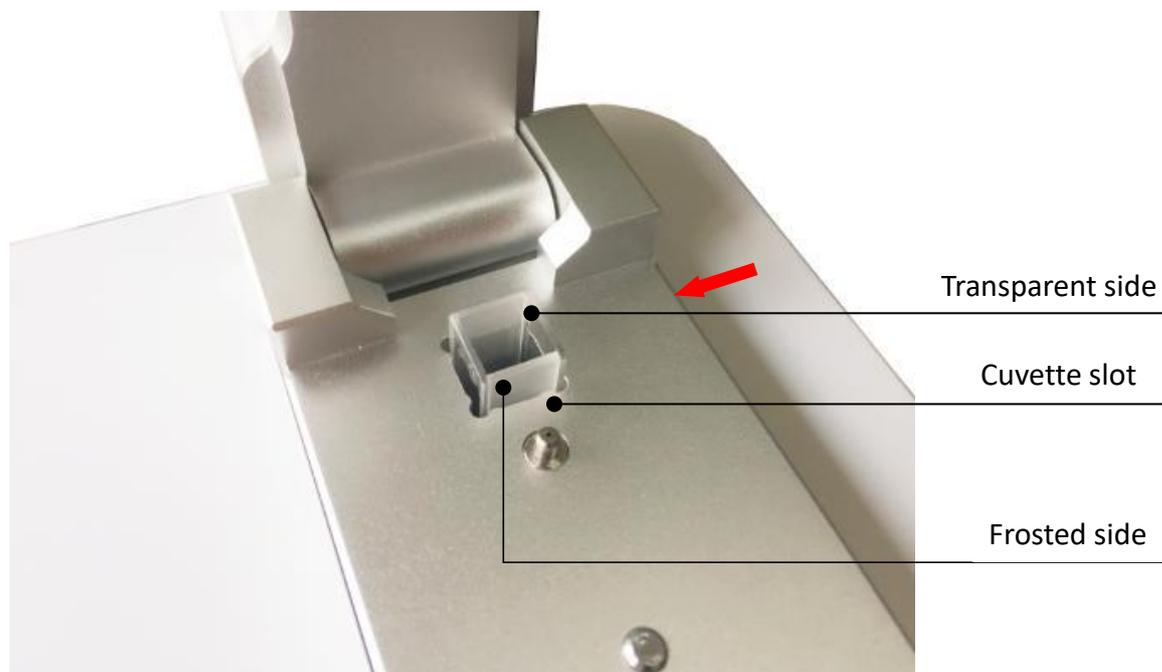


Fig 3.5 Cuvette slot and light path

Note: The arrow direction is the detection (light) direction, the transparent side should be vertical with the arrow.

Chapter 4 Software Operation

This chapter introduces AE-NANO600 software operation.

1. Instrument self-checking

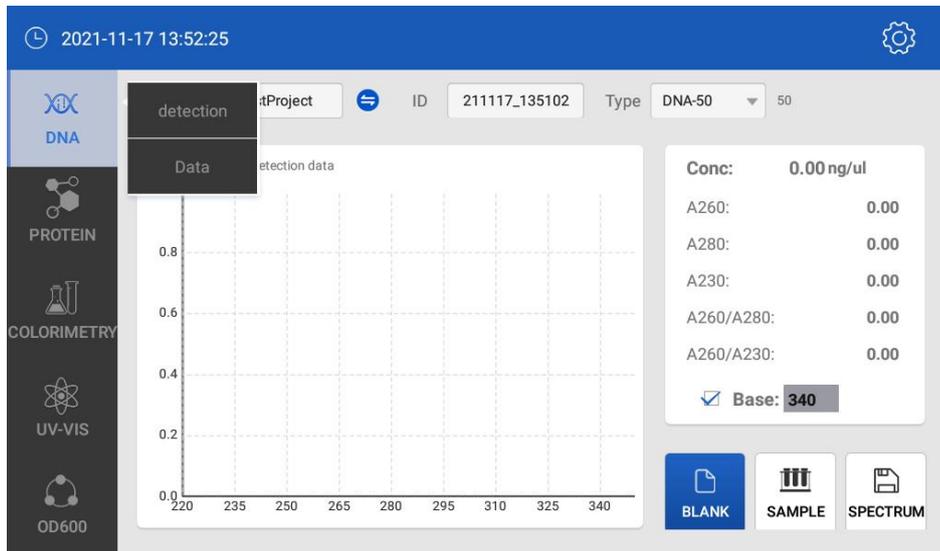
Connect to power supply, lay down the pedestal, instrument starts to self-checking after it is turned on.



Fig 4.1 Self-checking

2. Main interface

Instrument enters into the main Menu after self-checking. Here are some different applications interface. Introductions are as below:



3. Fig 4.2 Main interface

3. Nucleic acid detection

3.1 Summary

AE-NANO600 can easily detect the concentration of nucleic acid , choose “ nucleic acid” on the main interface.

Utilize Beer—Lambert principle to calculate nucleic acid concentration:

$$c = (A * \epsilon) / b$$

C=nucleic acid concentration, unit is ng/ul

A=AU Abs

ε=extinction coefficient, unit is ng-cm/ul

b=path length, unit is cm

Commonly, the nucleic acid extinction coefficient:

Double stranded DNA: 50ng-cm/ul

Single stranded DNA: 33ng-cm/ul

RNA: 40ng-cm/ul

Under pedestal mode, high concentration samples can be detected by wave length of 1.0mm or 0.2mm or 0.05mm without dilution.

The nucleic acid Abs is the value of standard under 1cm wave length.

AE-NANO600 can detect the double stranded DNA sample concentration ≤15000ng/ul, software can choose a suitable wave length for different samples.

3.2 Nucleic acid interface

Click “DNA”:

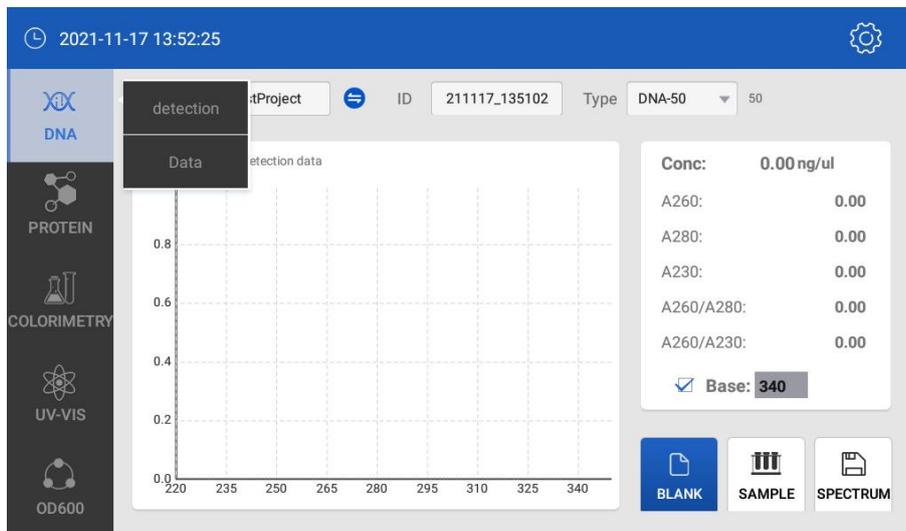
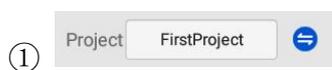


Fig 4.3 Initial interface of Nucleic acid detection

Fig 4.3 shows nucleic acid **detection and data**, enter into anyone by click.

(1) Button function introduce

Fig 4.3 shows, buttons with blue back ground and white characters are workable, with white back ground are unworkable.



① : Users can rename the project according to needs.



② : Sample batch No., default is current time, which also can be reset

according to need. One ID can save more than 1000 detection results.

-  : Choose nucleic acid type, DNA-50 for dsDNA, RNA-40 for RNA
- ③  Detection, ssDNA-33 for ssDNA detection. Choose “other”, input nucleic acid factor, instrument can calculate according to factors
- ④  : Before measurement sample, make blank with buffer solutions, buffers absorbance is usually at 0.004-0.03 Abs . Usually, blank is valid within 30min, if no samples detection exceeding 30 min after blank.
- ⑤  : click this button after blank, to detect samples.
- ⑥  : After sample detection, click this button to save spectrum.
- ⑦  : detect under this project.
- ⑧  : can choose or cancel baseline calibration. Nucleic acid detection

Baseline default is 340nm, users can input a wavelength according to experiment with different wave length. Commonly, users can input other wave length for baseline. Usually the baseline wavelength is not sensitive to the target sample. All the wavelength Abs should minus the baseline wavelength Abs.

Note: Baseline calibration should be done before detection, it will be invalid set after detection. Spectral value would be deviated, concentration detection would be changed in case of without baseline calibration.

(2) Operation steps:

- ① Set the project name and sample No.:
- ② Blank with TE buffer: add 2ul TE buffer on the lower pedestal, lay down the upper pedestal and start to “Blank”.
- ③ Clean the pedestals by a dust free cloth after blank.
- ④ Add 2ul sample onto the lower pedestal, lay down the upper pedestal, and press the “sample” button to measure. Fig 4.4 will show on the display after completing measurement,

Note: make sure the sample measured once dropping on the pedestal.

- ⑤ Clean the sample away from by dust free cloth, before next measurement.

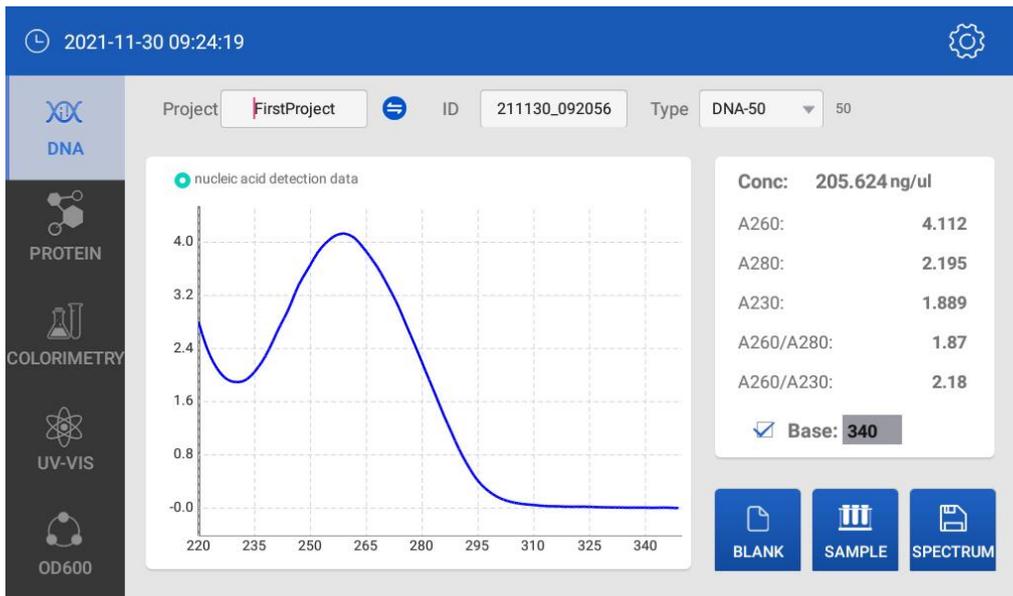


Fig 4.4 Measurement result

(3) from Fig 4.4, we can see the detection result by data as Fig 4.5

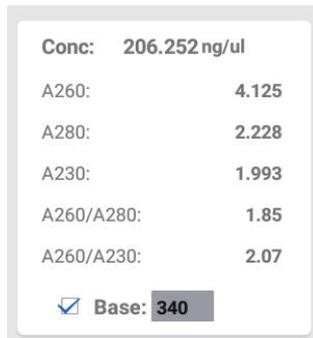


Fig 4.5 detection data

Conc: concentration of the sample

A260: shows Abs of 260nm under 10mm

A280: shows Abs of 280nm under 10mm

A230: shows Abs of 230nm under 10mm

A260/A280: Abs ratio of 260nm and 280nm, this value is for purity of DNA and RNA. Purified DNA should be about 1.8, Purified RNA should be 2.0

There might be contamination of protein, phenol or others in sample.

A260/A230: Abs ratio of 260nm and 230nm, which shows the concentration of nucleic

Acid. This ratio is higher than 260/280, which is between 1.8-2.2, there might be contaminations in nucleic acid if the value is lower than the range.

(4) Fig 4.6 shows as below:

The screen is multipoint touch, you can zoom in or out of the curve to check the Abs at different wave length.

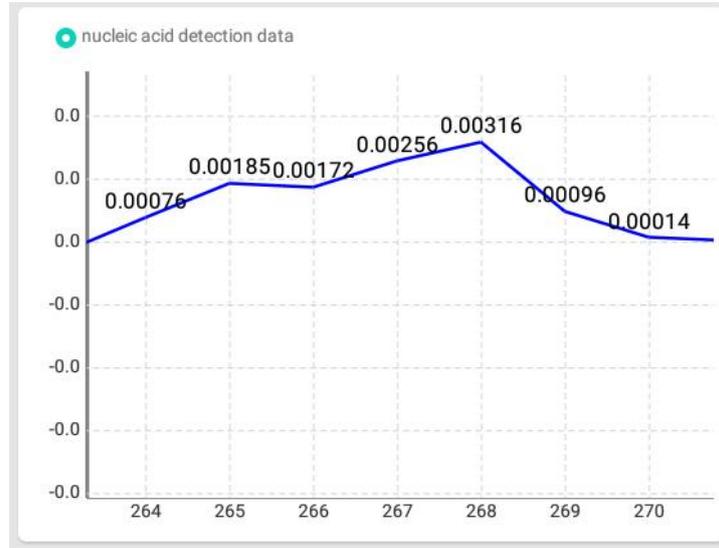


Fig 4.6 Nucleic acid detection curve

3.3 Nucleic acid detection data

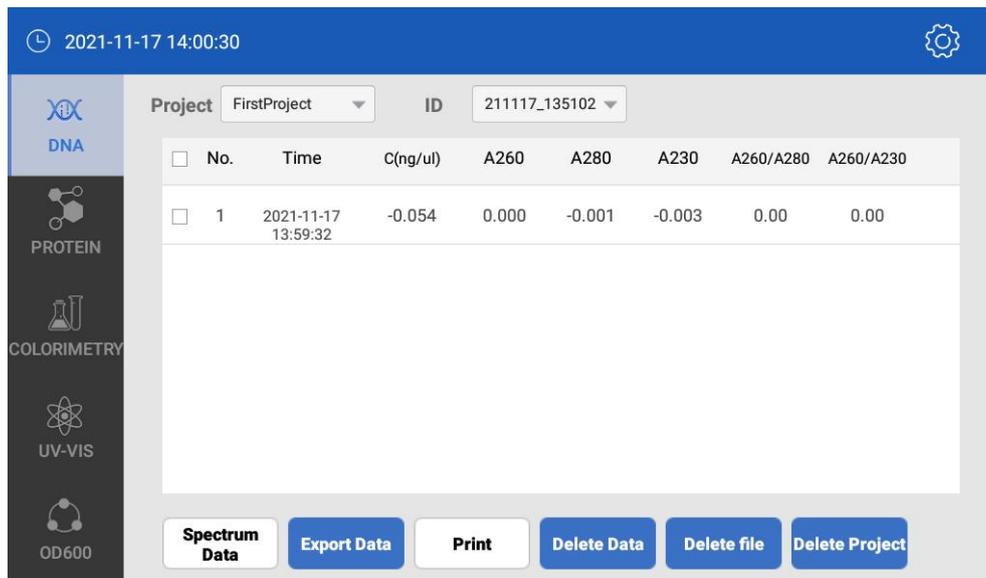
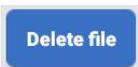


Fig 4.7 Nucleic acid detection data

Press “data” to enter into the details. At left side of the interface, ID shows the sample ID No., choose one ID, you will see the all the data under this ID No.

Button functions:

- ① **Spectrum Data** : click this button, to check all the Abs under 200-800nm of this interface.

- ②  : Data export, click this button to export data to U disc.
- ③  : Delete data.
- ④  : Delete ID, a dialog will pop up, confirm it to delete.
- ⑤  : Delete project, a dialog will pop up, confirm it to delete.

4. Protein A280

4.1 Summary

Protein is different from nucleic acid, which is various. Protein A280 is mainly used to detect the protein containing Trp, Tyr or Cys-Cys, which has a strong absorbance under wavelength of 280nm. This instrument does not require standard curve, it can calculate the result directly after detecting the absorbance.

Protein A280 display UV absorbance spectrum, detect the absorbance of 280nm and Calculate the concentration (mg/ml). Same as nucleic acid, Protein A280 record and display the data under wavelength of 10mm.

AE-NANO600 can detect the BSA concentration 90mg/ml without dilute under pedestal mode.

When the light intensity is less than 200 (10mm wave length) after detection, the system Will reminder user to shift to a shorter wave length to ensure the accuracy. It will show as below Fig 4.9 The liquid surface tension depends on the hydrogen bond of H₂O, usually, the stuffs in Water such as protein, saline ions, detergent which will destroy the hydrogen bond to reduce the surface tension. For most samples, 1 ul sample is enough for detection, 2 ul volume is recommended to form the liquid column due to the surface intension reduce.

4.2 Detection protein A280

On the main interface, click "PROTEIN" to enter into detection.

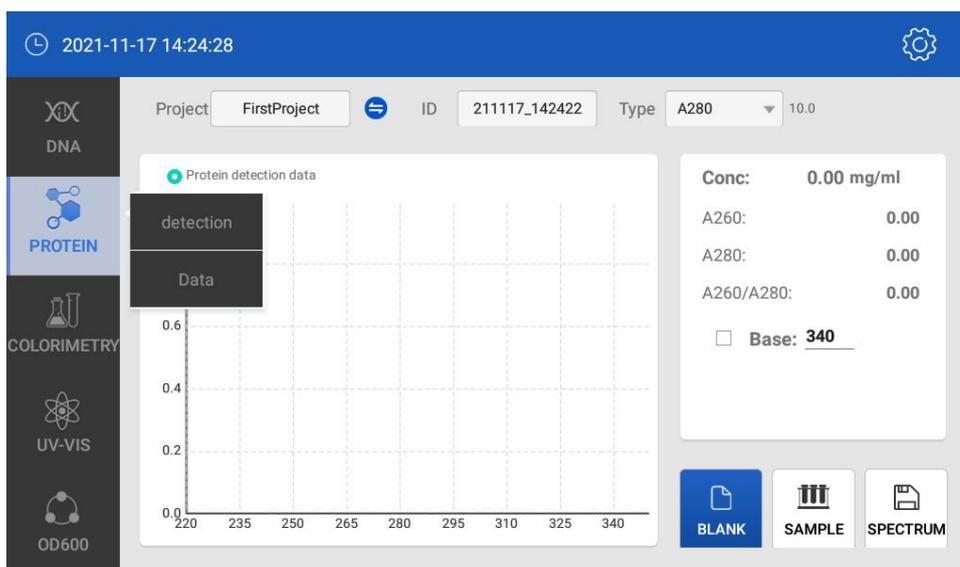
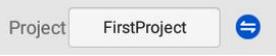


Fig 4.9 Protein interface

As Fig 4.9, at the top , there are two interface of “A280”, “data”, click the button to enter into the corresponding area.

- (1) As showed Fig 4.9, blue-ground-colored buttons are active, white-ground-colored buttons are inactive.

①  : Project name, make a proper name according to users' need.

②  : ID No. , default name is the current time, users also can make a new ID name according to need. Each ID can save 1000 data.

③  : Click to choose protein type, when users choose “other”, users can input the value according to need. Instrument will calculate the result.

④  : Blank before detection by TE buffer, the buffer Abs should be 0.004-0.03 Abs. In case that the user does not detect more than 30 min after blank, instrument requires another blank.

⑤:  : users can choose or cancel baseline calibration. Protein detection Baseline default is 340nm, users can input a wavelength according to experiment with different wave length. Commonly, users can input other wave length for baseline. Usually the baseline wavelength is not sensitive to the target sample. All the wavelength Abs should minus the baseline wavelength Abs.

Note: Baseline calibration should be done before detection, it will be invalid set after detection. Spectral value would be deviated, concentration detection would be changed in case of without baseline calibration.

(2) Operation steps:

- ① Set the project name and sample No.:
- ② Blank with TE buffer: add 2ul TE buffer on the lower pedestal, lay down the upper pedestal and start to “Blank”.
- ③ Clean the pedestals by a dust free cloth after blank.
- ④ Add 2ul sample onto the lower pedestal, lay down the upper pedestal, and press the “sample” button to measure. See Fig 4.10

Note: make sure the sample measured once dropping on the pedestal.

- ⑤ Clean the sample away from by dust free cloth, before next measurement.

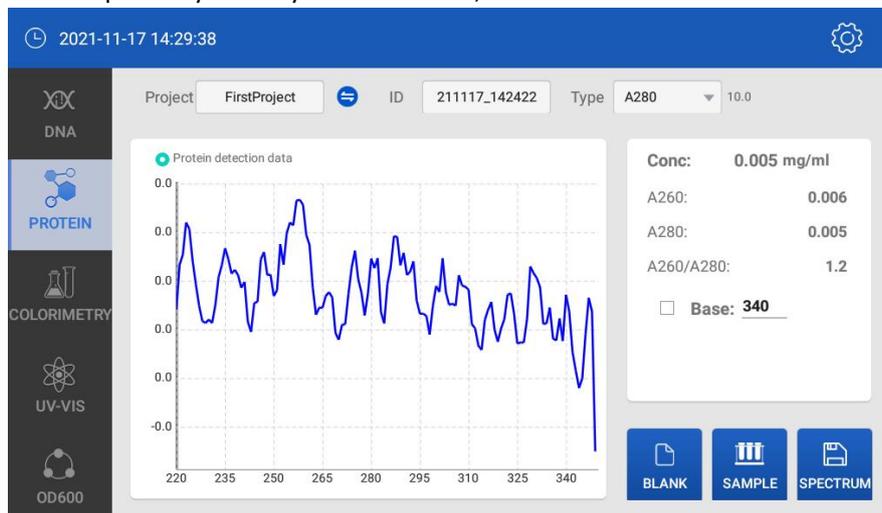


Fig 4.10 Protein detection result

(3) As Fig 4.11 (From Fig 4.10), the data result as below

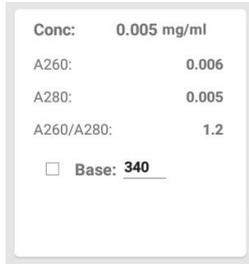


Fig 4.11 Protein result

Conc: Protein concentration

A260: shows Abs of 260nm under 10mm

A280: shows Abs of 280nm under 10mm

A230: shows Abs of 230nm under 10mm

As showed Fig 4.12:

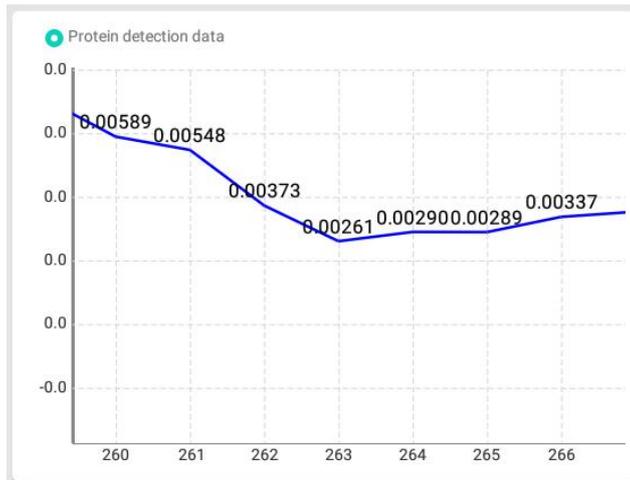


Fig 4.12 Protein detection curve

The screen is multipoint touch, you can zoom in or out of the curve to check the Abs at different wave length.

(4) **Button function:** Refer to the introduce of nucleic acid part.

4.3 Protein A280 data

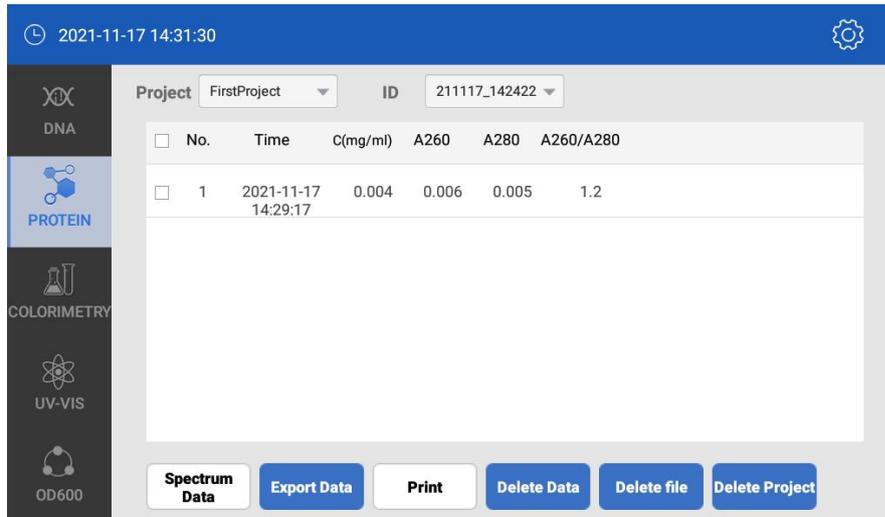


Fig 4.13 Protein detection interface

This interface layout is same as nucleic acid, refer to the nucleic acid part.

5. Colorimetry

5.1 Summary

BCA、Lowry、Bradford are all colorimetry to measure unpurified protein which requires a standard curve when measuring protein, so these three methods are set into colorimetry.

BCA is one of the colorimetry to measure diluted unpurified protein and protein containing impurities which has absorbance under UV light. BCA is a method to detect Cu+1 ion, under alkaline environment Cu+2 ion can be returned to Cu+1 by protein. Two Biquinoline dicarboxylic acid BCA molecules and one Cu+1 ion can form purple chelate.

Under this situation, Cu-BCA chelate has a high absorbance at wave length 562nm, standardized 750nm light coefficient.

Commercialized BCA kits offer two protein measurement range:

Normal detection use reagent/Protein sample volume ratio is 20:1, this kind kit measurement range is 0.20mg/ml to 8.0mg/ml(BSA). When use the pedestals to detect, 4ul sample and 80ul BCA reagent are required.

Micro volume detection use 1: 1 reagent/sample, protein concentration 0.01mg/ml to 0.20mg/m. Abundant sample is need for pedestal detection, 10ul sample and 10ulBCA reagent (Use PCR tube).

Operate and build a standard curve, prepare sample according to reagent vendor's instruction. Ensure the detection is under the same time and temperature.

Note: If temperature required higher than 60℃, please use sample of double volume to avoid volatilization which may affect the result.

Lowry protein quantification is a widely used method. Lowry forms protein and copper sulfate into compound under alkaline environment. Folin—Ciocalteu reagent can return the compound and produce blue outcome which equals protein quantity, and it can be detected under 650nm, calibrate under 405nm. Reagent can be bought from many manufacturers.

Prepare standard sample precisely, 20ul protein sample and 100ul Lowry reagent are recommended.

This instrument can measure concentration 0.20mg/ml to 4mg/ml. Operate and build a standard curve, prepare sample according to reagent vendor’s instruction. Ensure the operation is under the same time and temperature. This instrument can measure wider range of concentration than normal device, so we suggest users to build a wider standard curve, and 2ul sample is recommended.

Bradford is a common protein quantification method which usually use to measure low concentration protein. Bradford detection method is according to protein can make CBB(Coomassie brilliant blue) absorb displacement , which is detect Abs under 595nm. Protein-dyestuff (CBB) can be detected under 595nm, standardized under 750nm. Reagent can be bought from many manufacturers. Commercialized Bradford kits offer two protein measurement range:

Normal detection use reagent/Protein sample volume ratio is 50:1, this kind kit measurement range is 0.10mg/ml to 8.0mg/ml(BSA). Best linear range should be 0.01-1mg/ml. When use the pedestals to detect, 4ul sample and 200ul Bradford reagent are required.

Micro volume detection use 1: 1 reagent/sample, protein concentration c15ug/ml to 125ug/ml. Abundant sample is need for pedestal detection, 10ul sample and 10ulBCA reagent (Use PCR tube).

Operate and build a standard curve, prepare sample according to reagent vendor’s instruction. Ensure the detection is under the same time and temperature.

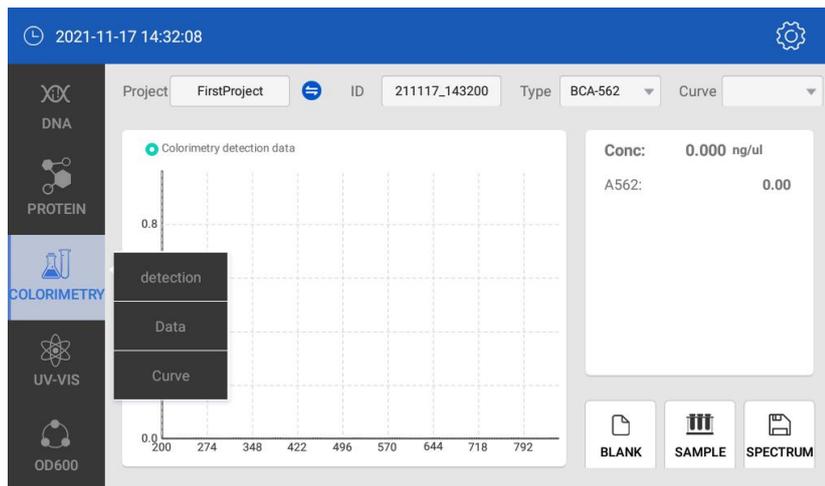
Note: If temperature required higher than 60°C, please use sample of double volume to avoid volatilization which may affect the result.

In Bradford kit, there is standard sample for building up standard curve. This instrument can detect higher concentration sample than cuvette detection, users should use higher concentration sample than reagent vendor’s advice.

5.2 Colorimetry detection

Note: Build up standard curve before measurement.

Click “colorimetry” on the main interface to enter



(1) The layout is same as nucleic acid, here introduce some other layout.

① Type BCA-562 : Click to choose one colorimetry

② Curve qwe : The present displayed curve is relative with the previous set.

This system can offer three types: first order polynomial, quadratic polynomial, cubic polynomial

(1) Operation steps:

- ① Set the project name and sample No., colorimetry type, and curve,
- ② Blank with TE buffer: add 2ul TE buffer on the lower pedestal, lay down the upper pedestal and start to “Blank”.
- ③ Clean the pedestals by a dust free cloth after blank.
- ④ Add 2ul sample onto the lower pedestal, lay down the upper pedestal, and press the “sample” button to measure. See Fig 4.10

Note: make sure the sample measured once dropping on the pedestal.

5.3 Standard curve

Build up a standard curve before measurement, a simple curve is constituted by two points. In order to make sure measurement accuracy, we advice five points to build up curve.

Standard sample concentration should cover the samples concentration, and equispaced. Here introduce colorimetry standard curve interface, functions and operations.

Click “Curve”, as Fig 4.16, there is not standard curve displayed, which need users to build up.

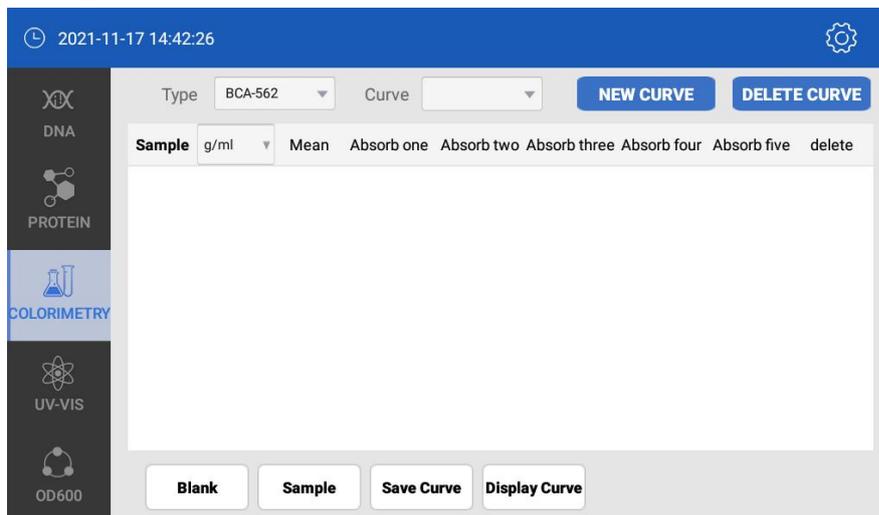


Fig 4.16 Standard curve interface of colorimetry

(1) Build up curve.

- ① Click **NEW CURVE** a dialog box displayed as below, input a name, and confirm.

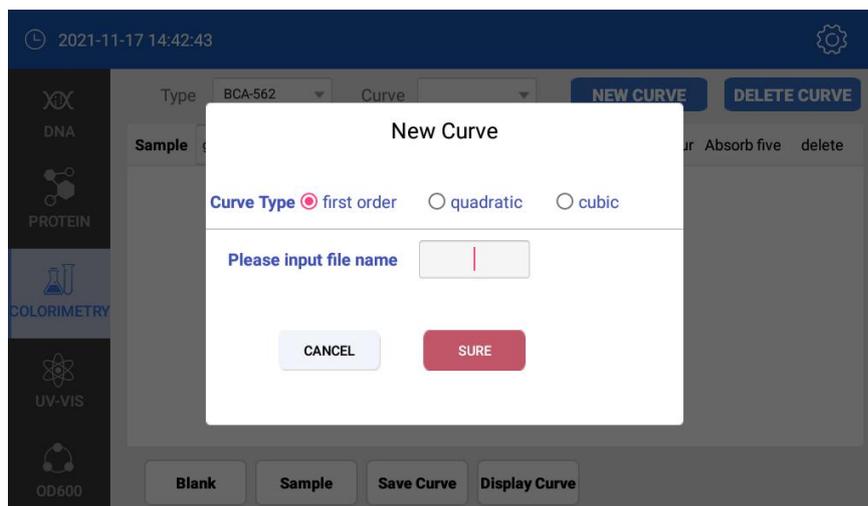




Fig 4.17 input the concentration to build up standard curve.

② Click  , Choose unit for standard sample, input standard sample concentration

③ Click the standard sample name (as Fig 4.17) to choose one standard sample, which will be back-ground-colored blue. According to blank, sample detection order to get the sample Abs. Same method for other samples.

Each standard sample can be detected for five time, and get the average. Users can delete the standard sample by long click the standard sample name or other area of the line.

④ After all standard samples detected, click “ save curve” 

Note: New curve must be saved before you choose from drop-down list.

(2) Other buttons introduce

①  : click this button to display the current curve, as Fig 4.18

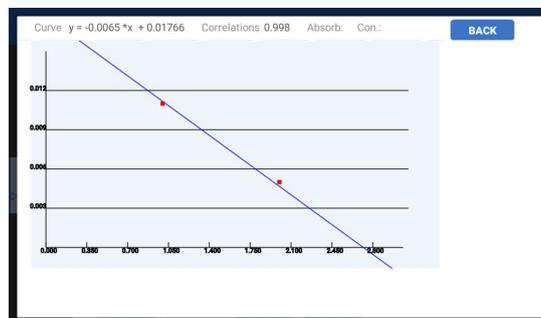


Fig 4.18 New curve

5.4 Colorimetry Data

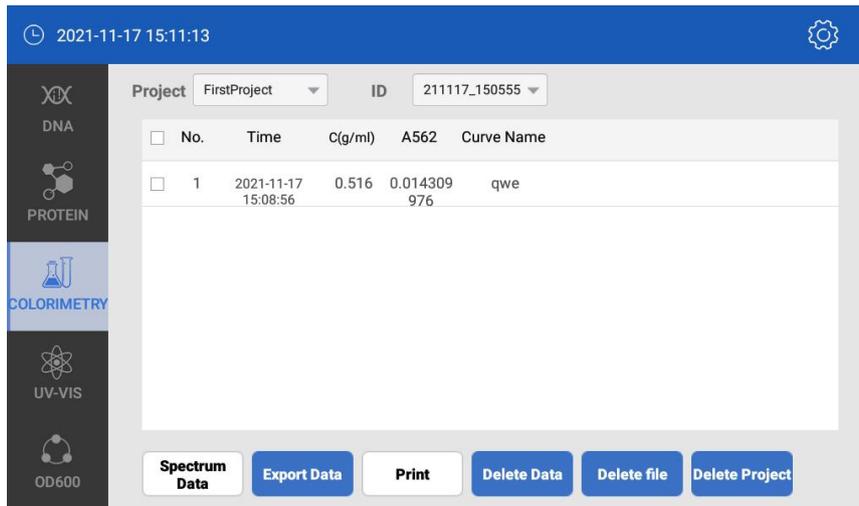


Fig 4.19 Data interface

6. Uv-Vis scan

6.1 Summary

Uv-Vis function can make the instrument detects samples with wavelength of 200-800nm. Instrument can choose wavelength according to Abs, the max measurement can reach 90 Abs equals 10mm.

6.2 Uv-Vis Detection

Click “Uv-Vis” on the main interface.

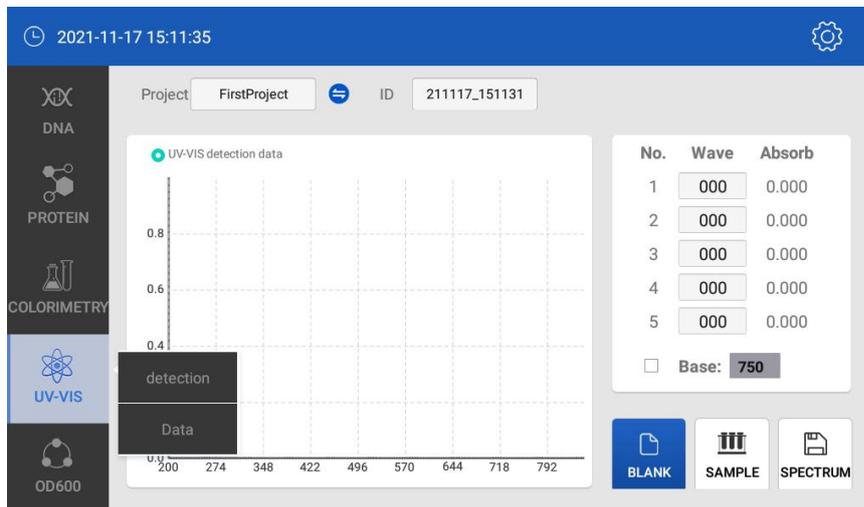


Fig 4.20 Uv-Vis measurement initial interface

(1) The layout is same as nucleic acid, here introduce some other layout.

① Click  , Fig 4.21 will displayed on screen after blank.

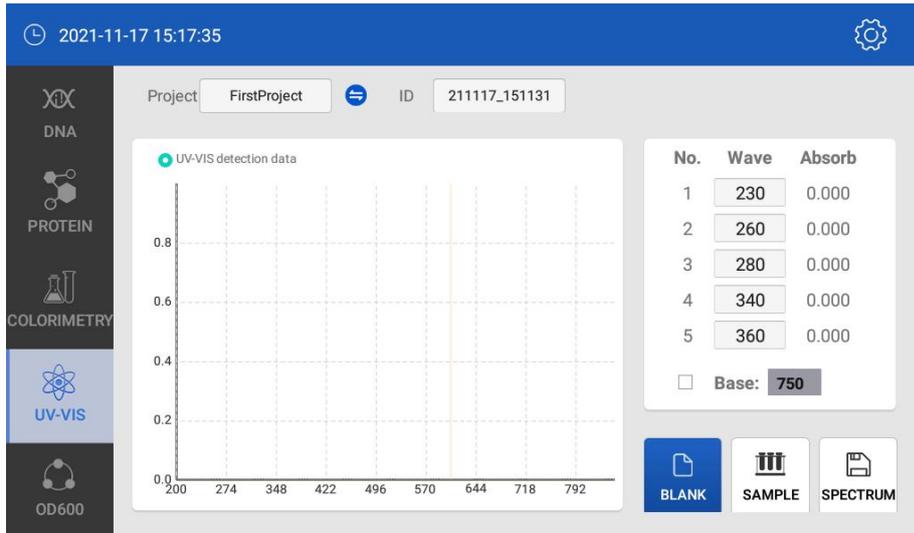


Fig 4.21 check the characteristic absorbance

- ② On the interface Uv-Vis, Fig 4.20, input the characteristic wavelength before measurement, absorbance will display accordingly.



Fig 4.22 check characteristic wavelength

- ③ Click  after blank, Fig 4.23 on screen which shows sample absorbance under wavelength 200-800nm.

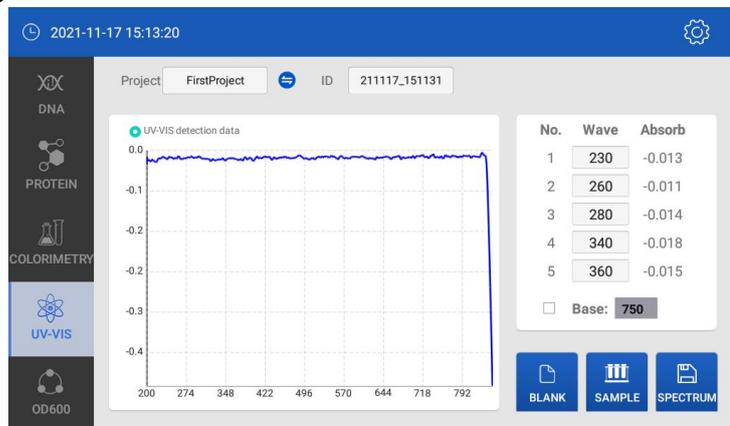


Fig 4.23 sample absorbance

(2) Operation steps:

- ① Set the project name and sample No.:
- ② Blank with TE buffer: add 2ul TE buffer on the lower pedestal, lay down the upper pedestal and start to “Blank”.
- ③ Clean the pedestals by a dust free cloth after blank.
- ④ Add 2ul sample onto the lower pedestal, lay down the upper pedestal, and press the “sample” button to measure. See Fig 4.10

Note: make sure the sample measured once dropping on the pedestal.

- ⑤ Clean the sample away from by dust free cloth, before next measurement.

6.3 Uv-Vis Data

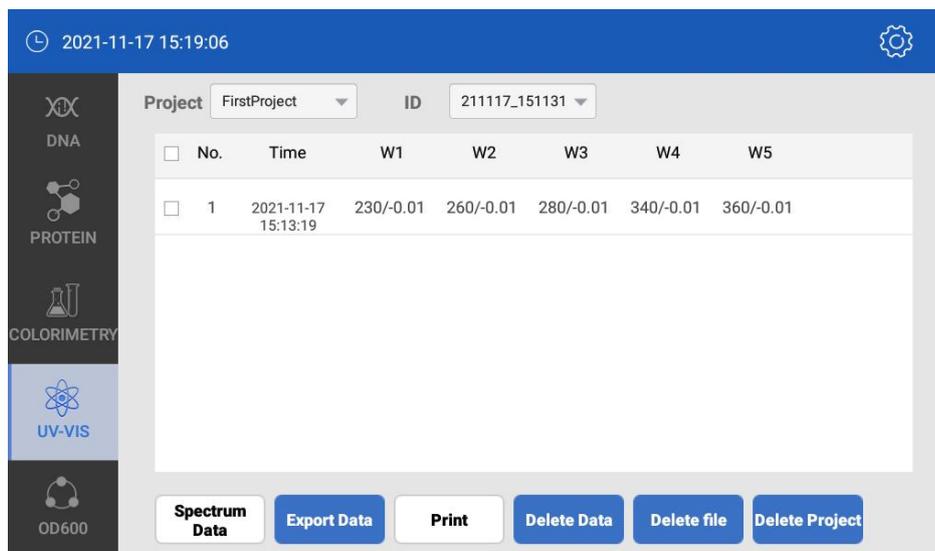


Fig 4.24 Uv-Vis Data

The layout of this part is similar to nucleic acid, please refer to nucleic acid part.

The screen is multipoint touch, you can zoom in or out of the curve to check the Abs at different wave length.

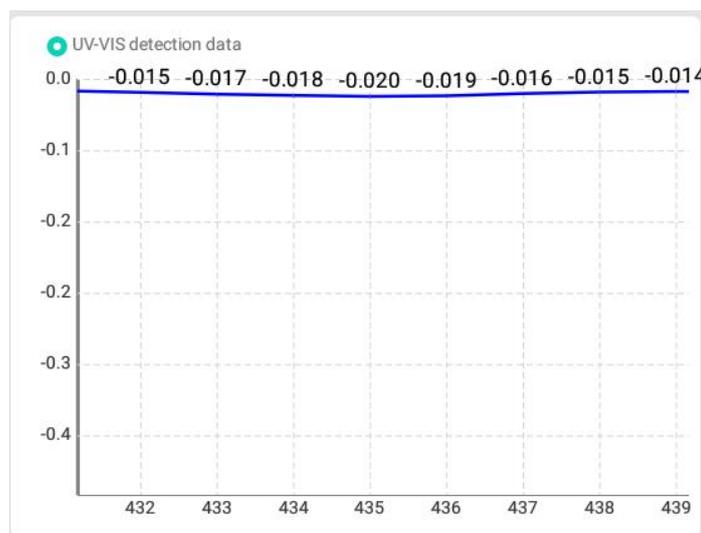


Fig 4.25 Uv-Vis data

7. OD600

7.1 Summary

OD600 means a liquid absorbance under wavelength 600nm.

The application of OD600 : The bacteria absorbance is used to measure the concentration of bacteria culture solution to estimate the bacteria growth.

7.2 OD600 detection

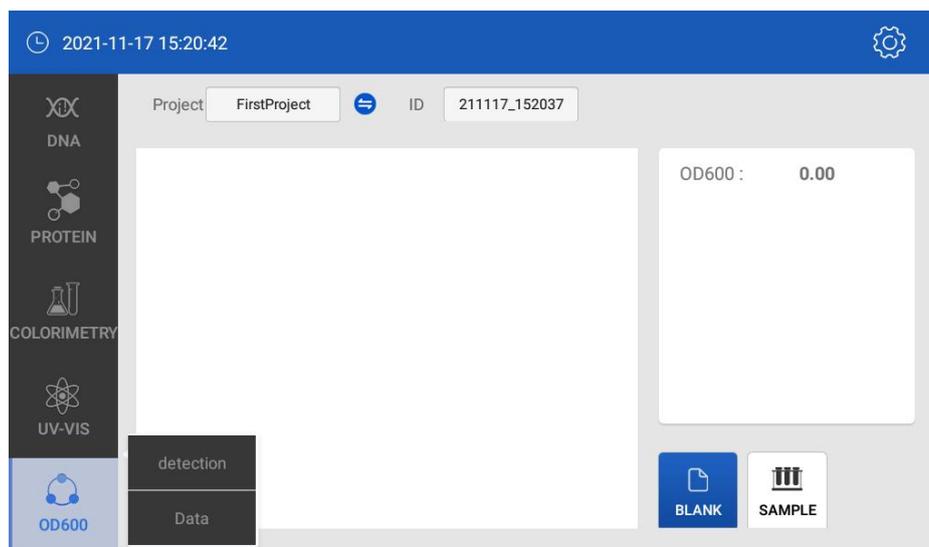
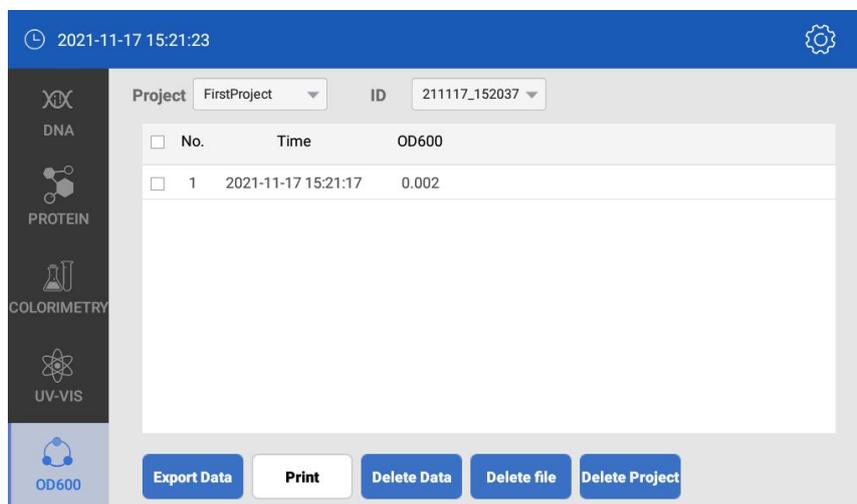


Fig 4.26 OD600 initial interface

Operation steps:

- ① set project name, sample ID (or system will make a default name)
- ② Blank: blank the air, or empty cuvette, or blank solution according to experiment.
- ③ Add 2ml~3ml sample to the cuvette after blank.
- ④ Click “sample” to detect, result show as below.

7.3 OD600 measurement result.



8. Setting

Click “setting” on the main interface to start set.

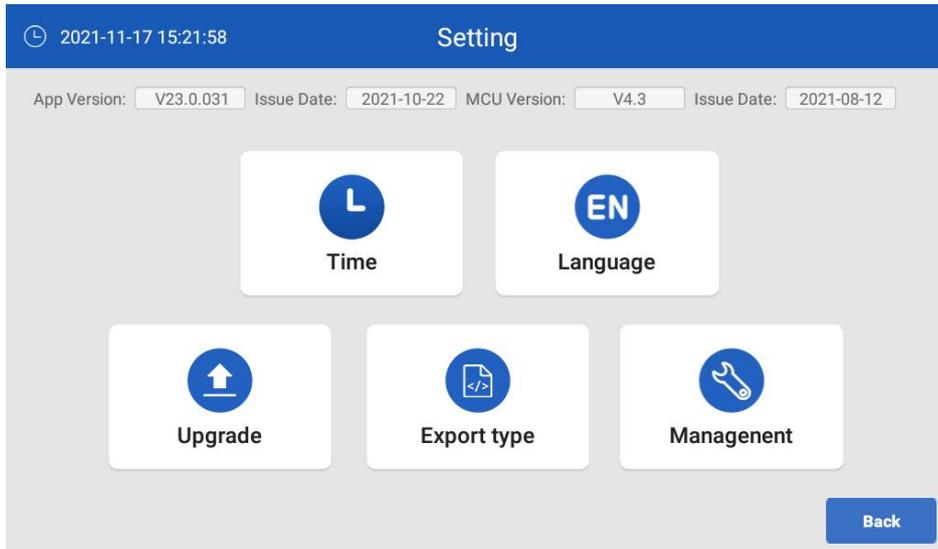
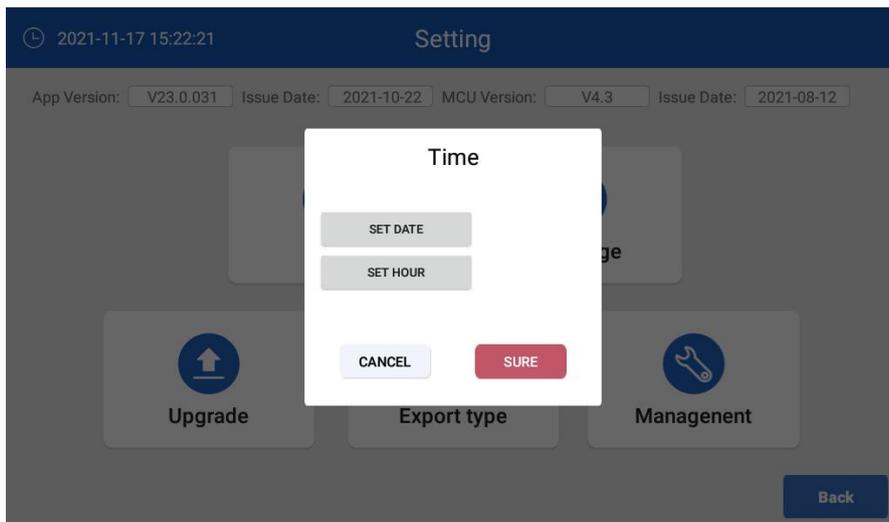


Fig 4.28 system setting

8.1 Time set

Click “time” icon to set system time.



8.2 Language

Click” language” icon to choose one you need, as fig below.

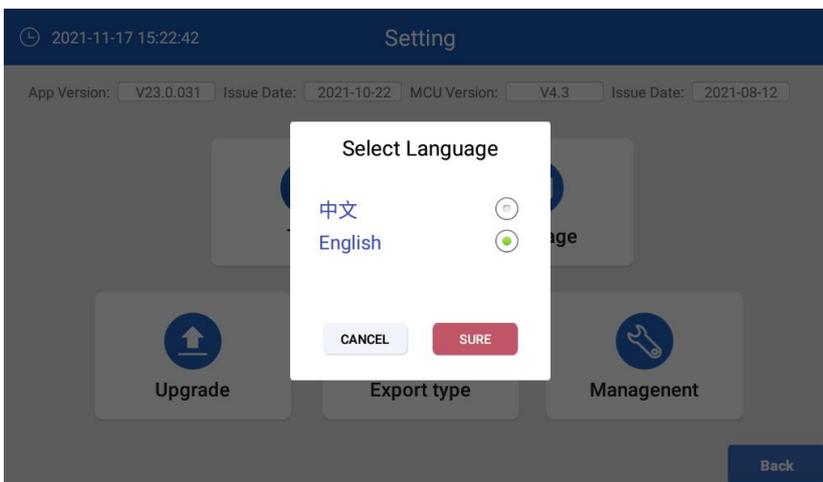


Fig 4.32 Select Language

8.3 Upgrade

Save the upgrade software in U disc root directory, insert the U disc to NanoOne, click“ upgrade”, as fig 4.35 click install if you need upgrade.

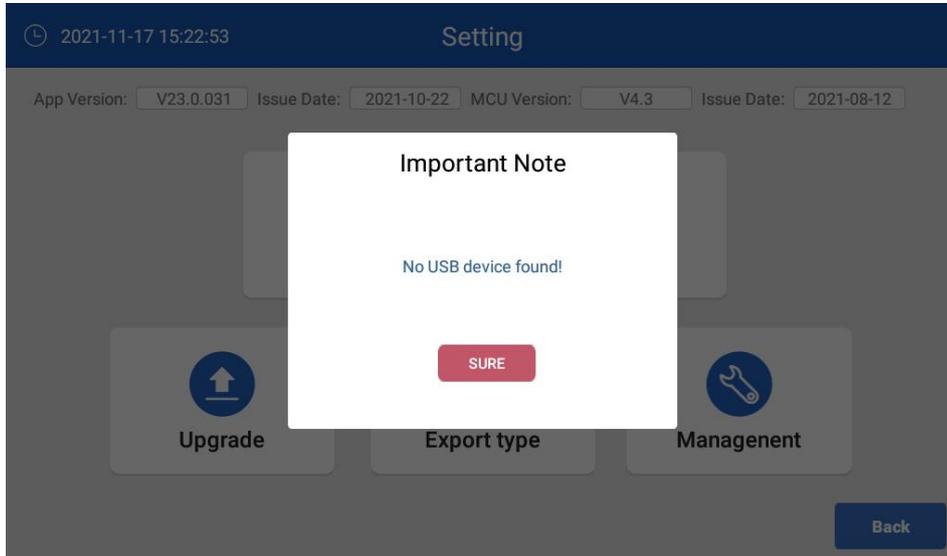


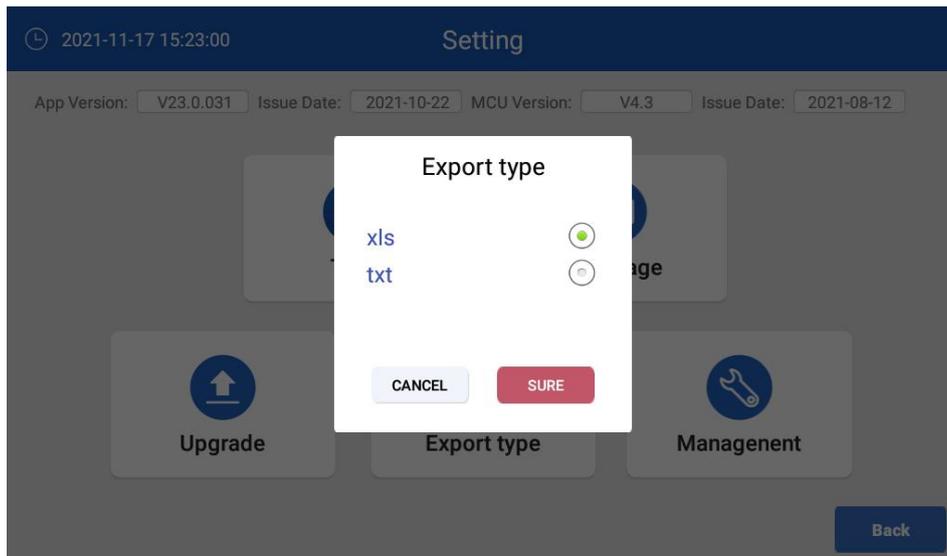
Fig 4.35 upgrade

8.4 Maintenance

Only professional technicians are allowed to enter the maintenance interface with password for instrument debugging and maintenance.

8.5 Format

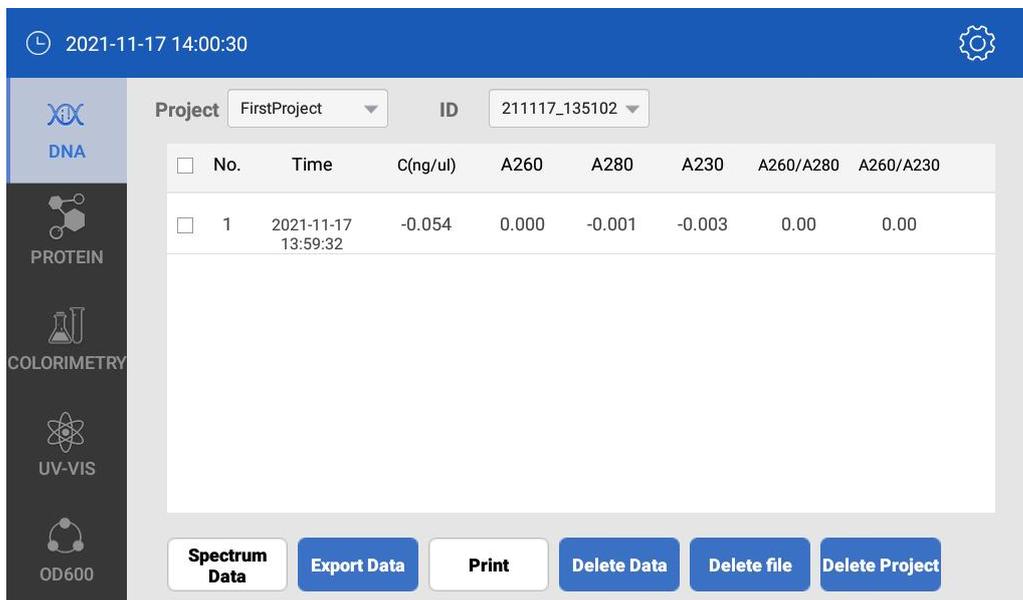
File format are *.xls and *.txt.



9. Optional functions

9.1 Printer

Printer function is available for each sample type, here is DNA as sample.



The screenshot displays the software interface for the AE-NANO600. At the top, the date and time are 2021-11-17 14:00:30. The interface is divided into a sidebar on the left and a main content area. The sidebar contains icons and labels for DNA, PROTEIN, COLORIMETRY, UV-VIS, and OD600. The main content area shows a 'Project' dropdown set to 'FirstProject' and an 'ID' dropdown set to '211117_135102'. Below this is a table with the following data:

<input type="checkbox"/>	No.	Time	C(ng/ul)	A260	A280	A230	A260/A280	A260/A230
<input type="checkbox"/>	1	2021-11-17 13:59:32	-0.054	0.000	-0.001	-0.003	0.00	0.00

At the bottom of the main content area, there are several buttons: 'Spectrum Data', 'Export Data', 'Print', 'Delete Data', 'Delete file', and 'Delete Project'.

Connect printer to the AE-NANO600 by USB before switch on. The button “ printing” is workable, press the button to print the measurement result.

9.2 Battery

Users can choose AE-NANO600 with option of Built-in Battery, which make it work on condition of power supply unavailable.

Chapter 5 Troubles and Shootings

No.	Troubles	Causes	Shootings
1	Can't turn on	No power; Broken switch; Broken power; Others	Check the connection of power Change the switch Change the power Contact the seller
2	The results not right	The sample not enough; Pedestal pollution; Others	Add the sample; Clean the pedestal times with pure water; Contact to the seller
3	OD600 not work	Poor contact between cable and main board	Contact the seller
c4	Insufficient light	CCD array broken Optical filter broken	Contact the seller
5	Touch screen jump-point	The power not grounded	Provide effective grounded power
6	Over-time communication	No response from the CCD array	Restart instrument Contact the seller

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