

# NP3000 Micro-Spectrophotometer Manual



LAB  
WAVE



# NP-3000 USER MANUAL

LABWAVE®

## I. Introduction

The NP3000 is an ultraviolet-visible spectrophotometer specifically designed for micro-volume analysis of purified nucleic acids and various proteins. The NP3000 comes with pre-installed software and a touchscreen display. This ultra-micro spectrophotometer can detect samples ranging from 0.5 to 2  $\mu\text{L}$ , offering high accuracy and reproducibility. The sample retention system utilizes surface tension to hold the sample between two detection fibers, allowing the instrument to measure higher concentration samples without the need for dilution. Using this technology, the NP3000 ultra-micro spectrophotometer, with a full wavelength range (180-910nm), can detect sample concentrations that are hundreds of times higher than those detected using standard cuvettes. The instrument is equipped with a cuvette holder for analyzing diluted samples using standard UV-visible cuvettes.

## II. Features

### 1. Normal Operating Conditions

Operating Ambient Temperature: 5°C to 35°C

Relative Humidity:  $\leq 70\%$

Power Supply: DC 12V 4A

### 2. Basic Performance and Parameters

<b>Model</b>	NP3000	
<b>Sample Volume</b>	0.5 $\mu\text{L}$ ~ 2 $\mu\text{L}$ , recommended 2 $\mu\text{L}$	
<b>Optical Path Length</b>	0.05 mm, 0.2 mm, 1 mm	
<b>Light Source/Lifetime</b>	Xenon flash lamp / Flash count > $10^9$	
<b>Detector Type</b>	2048-pixel linear silicon CCD array	
<b>Wavelength Range</b>	180 ~ 910 nm	
<b>Wavelength Accuracy</b>	$\pm 1$ nm	
<b>Wavelength Resolution</b>	$\leq 1.5$ nm (FWHM @ Hg 254 nm)	
<b>Absorbance Precision</b>	0.003 Abs (1 mm optical path)	
<b>Absorbance Accuracy</b>	$\pm 1\%$ (at 260 nm, 7.332 Abs)	
<b>Absorbance Range</b>	0.02 ~ 300 (at 260 nm, equivalent to 10 mm path)	
<b>Detection Concentration Range</b>	2 ng/ $\mu\text{L}$ dsDNA ~ 15000 ng/ $\mu\text{L}$ dsDNA	
<b>Detection Time</b>	< 6 seconds	
<b>OD600</b>	<b>Absorbance Range</b>	0 ~ 4.000 Abs
	<b>Absorbance Stability</b>	[0, 3] $\leq 0.3\%$ , [3, 4] $\leq 2\%$
	<b>Absorbance Reproducibility</b>	[0, 3] $\leq 0.2\%$ , [3, 4] $\leq 2\%$
	<b>Absorbance Accuracy</b>	[0, 2] $\leq 0.005A$ , [2, 3] $\leq 1\%$ , [3, 4] $\leq 2\%$
<b>Input Voltage</b>	DC 12V 4A	
<b>Power</b>	48W	
<b>Dimensions</b>	270 × 210 × 196 mm (W × D × H)	
<b>Weight</b>	3.5 kg	

### III. Basic Operating Instructions

#### 1. Instrument Configuration



**Figure 3.1 Instrument Configuration**

Note: The instrument requires proper grounding for power supply; otherwise, there may be skipping points during touchscreen operation.

#### 2. Sample Volume for Detection

For detection, the volume of the liquid sample is not the key factor for accuracy. However, it is crucial to ensure that a complete liquid column is formed between the upper and lower bases, as this ensures the accuracy of the detection. It is recommended to use a precision pipette and tips with a range of 0–2  $\mu\text{l}$  for sampling to ensure accuracy. If there is uncertainty regarding the sample characteristics or the pipette's precision, it is better to use a sample volume of 2  $\mu\text{l}$  for the detection.

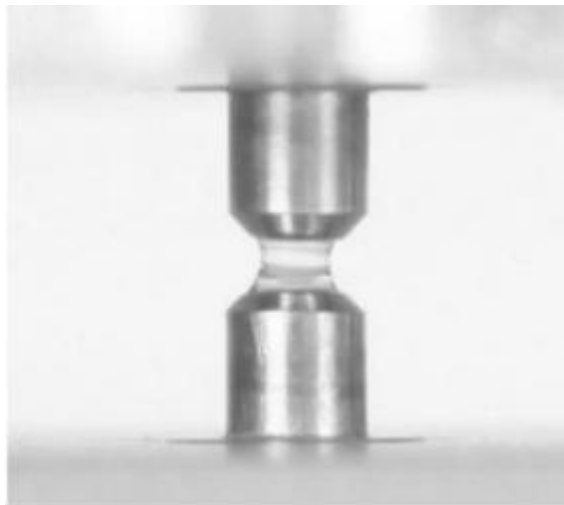
#### 3. Use of the Detection Base

3.1 Lift the upper base and use a precision pipette to add a small sample (2 $\mu$ l) onto the lower base.



**Figure 3.2 Dropping the Sample**

3.2 Lower the upper base, allowing a liquid column to naturally form between the upper and lower bases, and then begin the detection.



**Figure 3.3 Liquid Column Formation Effect**

3.3 After the detection is complete, lift the upper base and use a clean, dust-free cloth to wipe the samples from both the upper and lower bases to prevent sample residue from affecting the next detection.

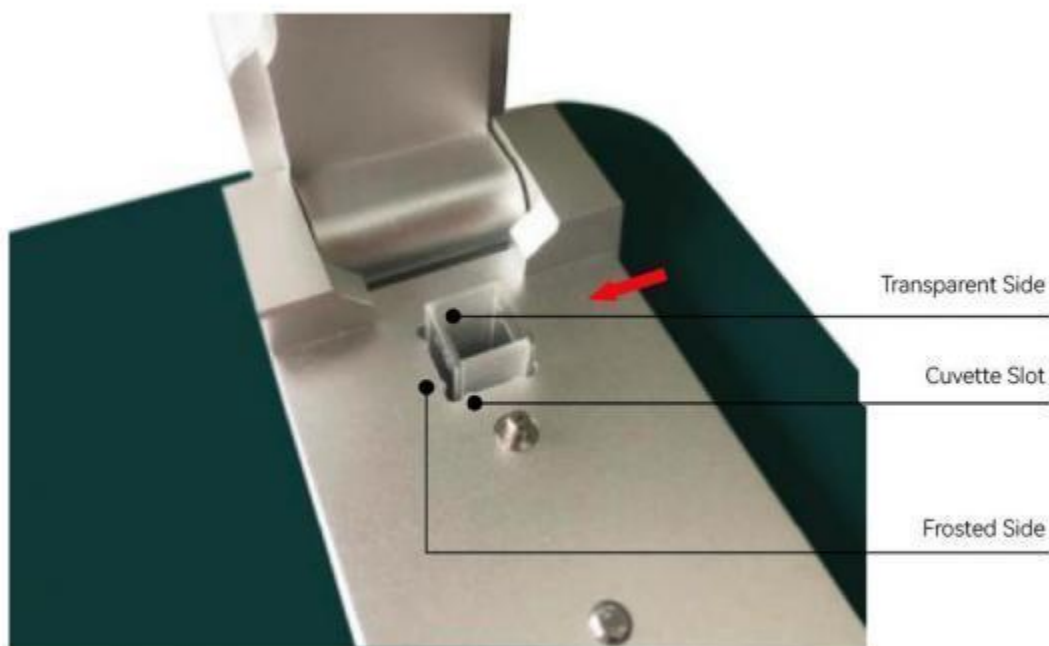


**Figure 3.4 Cleaning Residual Samples from the Upper and Lower Bases**

Note: After testing, please rinse the detection head 3 times with purified water.

### 3.4 OD600 Detection

The NP3000 has an OD600 detection function. To use this function, lift the upper base, enter the OD600 interface, and first perform a blank calibration. Depending on the experiment, the blank can be air, an empty cuvette, or a cuvette containing blank solution. After completing the blank calibration, add 2-3ml of the solution to be tested into the cuvette, insert the cuvette into the cuvette slot, and click on sample detection to complete the OD600 measurement.



**Figure 3.5 Cuvette Slot Position and Light Path**

Note: The arrow direction in the figure indicates the detection (light) direction. When inserting the cuvette into the slot, the transparent side should be perpendicular to the arrow direction.

## IV. Software Operation

This chapter primarily introduces the software operation of the NP3000 micro-volume spectrophotometer.

### 1. Instrument Self-Check

Connect the power supply, lower the upper base, and press the power switch at the back of the instrument. The device will start and enter the self-check interface:



Figure 4.1 Instrument Self-Check at Startup

### 2. Main Interface

After the self-check is complete, the system enters the main interface, which displays various application interfaces. The following sections detail the functionality and use of each application interface.

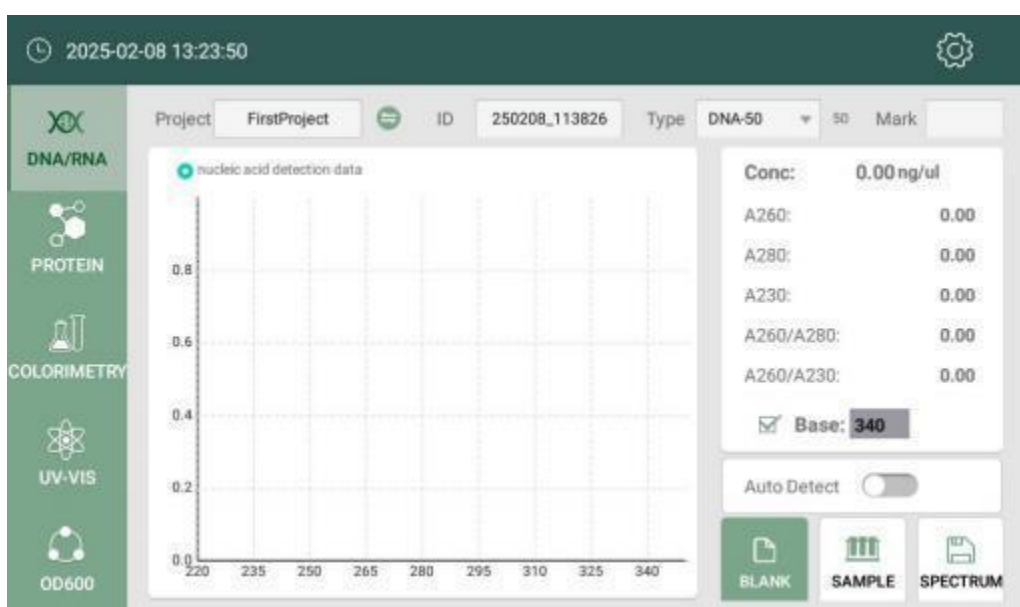


Figure 4.2 Main Interface

### 3. Nucleic Acid Detection

#### 3.1 Overview

The NP3000 enables convenient detection of nucleic acid concentrations. To perform detection, select "Nucleic Acid Detection" on the main interface.

The concentration of nucleic acid is calculated using the Beer-Lambert law:

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

C = nucleic acid concentration (unit: ng/μl)

A = absorbance in AU

ε = extinction coefficient (unit: ng-cm/μl)

b = path length (unit: cm)

The typical extinction coefficients for nucleic acids are as follows:

Double-stranded DNA: 50 ng-cm/ μl

Single-stranded DNA: 33 ng-cm/ μl

RNA: 40 ng-cm/ μl

When the base mode is selected, the NP3000 uses a path length of 1.0 mm, 0.2 mm, or 0.05 mm for detection. This allows the detection of high-concentration samples without dilution.

The absorbance values for nucleic acid detection are standardized to a path length of 1 cm.

The NP3000 can accurately measure concentrations up to ≤ 15,000 ng/ μl for double-stranded DNA without dilution. For each sample, the software automatically selects the optimal path length for detection.

#### 3.2 Nucleic Acid Detection Interface

On the main interface, click the "Nucleic Acid Detection" icon to enter the following interface:

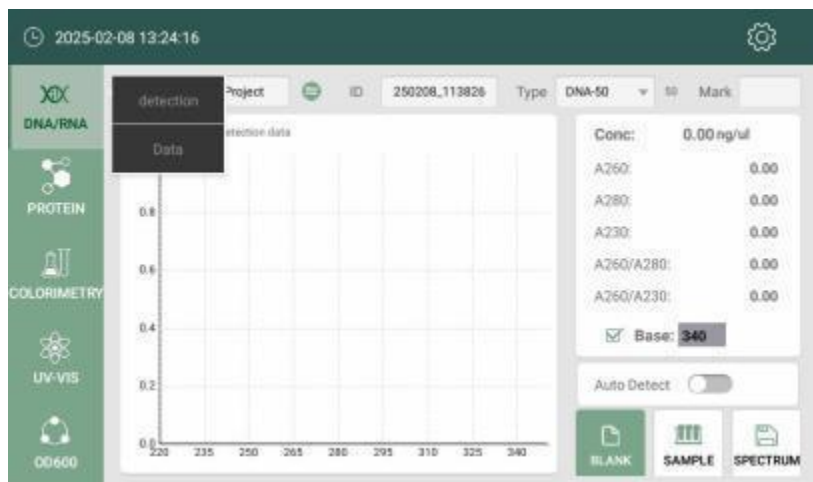
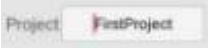




Figure 4.3 Initial Nucleic Acid Detection Interface


In the interface shown in Figure 4.3, the top left side provides two options: "Nucleic Acid Detection" and "Data". You can click on the corresponding areas to enter their respective functional zones.


## (1) Interface Button Functions


In the interface shown in Figure 4.3, the buttons with a blue background are active, while the ones displayed in white are inactive.


1  : Project Name, you can choose an appropriate and easy-to-remember ID , such as the sample name, customer name, etc.

2  : Sample Batch Number, the default is the current time, but it can be reset as needed. An ID can save up to 1,000 test results.


3  : Nucleic Acid Type, click to select the nucleic acid type. Choose DNA-50 for double-stranded DNA (dsDNA) testing, RNA-40 for RNA testing, or ssDNA-33 for single-stranded DNA (ssDNA) testing. If "Other" is selected, nucleic acid factors can be manually entered.

4  : Blank Test, before testing the sample, a blank test must first be performed using the buffer solution. The absorbance of the buffer solution is generally between 0.004-0.03 Abs. It is recommended to re-do the blank test after 30 minutes.


5  : Test Sample, after blank calibration, click the button to test the sample. The instrument will calculate based on the selected nucleic acid factor.


6  : Save Data, after the sample test is completed, click this button to save the spectral data.

7  Base:  : Baseline Calibration, you can choose to enable or disable baseline calibration. The default baseline calibration wavelength for nucleic acid detection is 340nm, but the user can enter a different calibration wavelength based on the test requirements. Generally, the baseline wavelength should be selected at a wavelength where the analyte is insensitive. Under any circumstances, the absorbance readings at the selected baseline wavelength will be subtracted from all wavelength absorbance readings.

8  : Baseline Calibration, you can choose to enable or disable baseline calibration. The default baseline calibration wavelength for nucleic acid detection is 340nm, but the user can enter a different calibration wavelength based on the test requirements. Generally, the baseline wavelength should be selected at a wavelength where the analyte is insensitive. Under any circumstances, the absorbance readings at the selected baseline wavelength will be subtracted from all wavelength absorbance readings.

**Note: Baseline calibration must be set before testing the samples. Setting it after the sample test is invalid. If baseline calibration is not selected, the spectral values will be shifted, which will also alter the calculated concentration.**

9  : You can enter characters to differentiate between different samples.

10  : Once activated, the detection arm can be lowered automatically during the sample detection phase to begin the test.

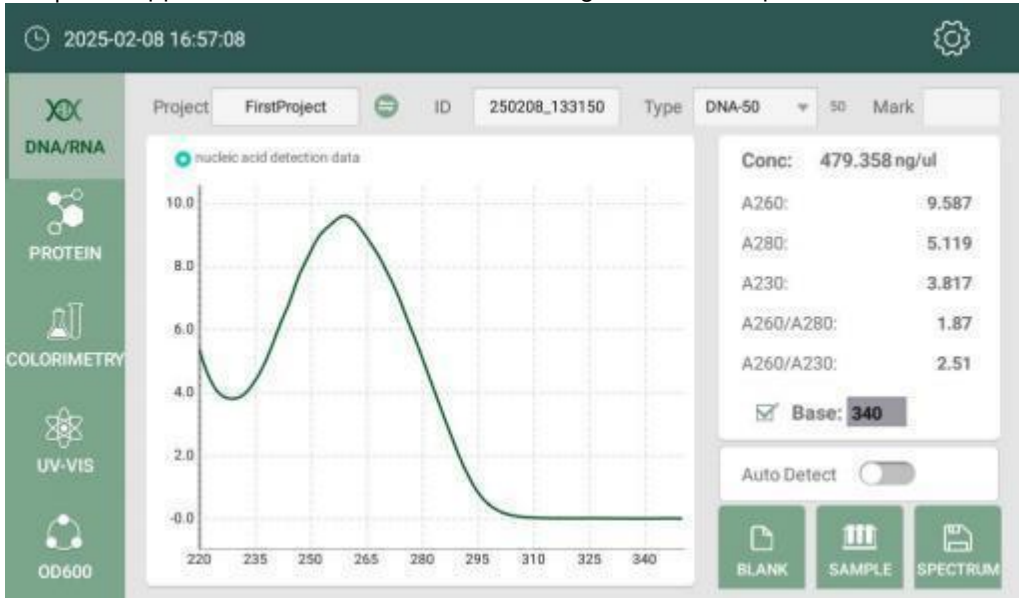
## (2) Operating Steps

- 1 Set Project Name and Sample ID

- 2 Use Buffer Solution to Establish Blank Control: Take 2  $\mu$ l of the blank solution and add it to the lower base. Lower the upper base and click on "Blank."
- 3 Use a clean, lint-free cloth to wipe off the blank solution from the base.
- ④ Take 2  $\mu$ l of the sample and place it on the lower base. Lower the upper base, then click on "Sample Detection" to begin the test. After the test is complete, the interface will look like Figure 4.4.

**Note: Each sample to be tested must be freshly added.**

- 5 After the test is completed, use a clean, lint-free cloth to wipe off the sample from both the upper and lower bases before testing the next sample.



**Figure 4.4 Nucleic Acid Detection Results**

- (3) As shown in Figure 4.5, the detection results are presented in the following data format :



**Figure 4.5 Nucleic acid test data**

**Concentration:** The concentration value of the nucleic acid sample.

**A260:** Absorbance at 260nm with a 10mm pathlength.

**A280:** Absorbance at 280nm with a 10mm pathlength.

**A230:** Absorbance at 230nm with a 10mm pathlength.

**A260/A280:** The ratio of absorbance at 260nm and 280nm, used to determine the purity of DNA and RNA. A pure DNA sample usually has a ratio around 1.8, while pure RNA has a ratio around 2.0. A lower ratio indicates the presence of protein, phenol, or other contaminants.

**A260/A230:** The ratio of absorbance at 260nm and 230nm. This is a secondary indicator of nucleic acid concentration. The ratio for pure nucleic acid is typically higher than the 260/280 ratio, usually ranging from 1.8 to 2.2. A lower ratio suggests contamination in the nucleic acid.

(4) In the interface shown in Figure 4.6:

Since the LCD screen supports multi-touch, you can zoom in or out on the curve. The absorbance at each wavelength will be displayed at the corresponding position on the graph.

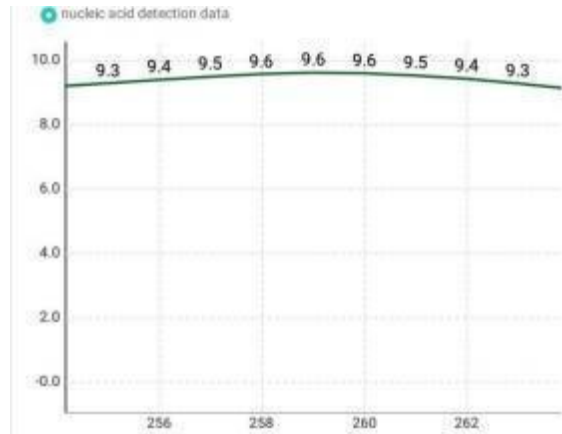


Figure 4.6 Nucleic Acid Detection Curve

### 3.3 Nucleic Acid Detection Data

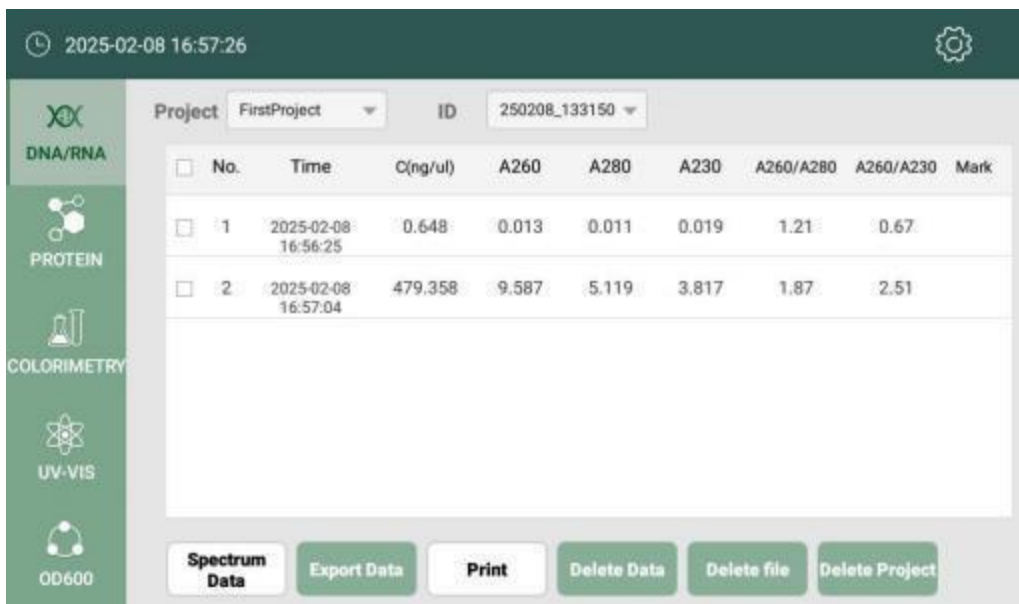





Figure 4.7 Nucleic Acid Data Interface

Click the "History Data" button to enter the nucleic acid data interface. This interface displays all detection data. Select a sample ID, and the middle area will show all test results under that ID.

Interface Bottom Button Functions:

1 **Spectrum Data** : Check the corresponding data and click the button to view the absorbance at each wavelength from 200 to 800nm in this interface.

2 **Export Data** : Export the selected inspection data. In general, the export defaults to a USB flash drive.

- 3  : Deletes the selected data.
- ④  : Click this button to bring up the Select File to Delete dialog box, click OK to delete the selected ID file.
- ⑤  : Click the button to bring up the Select Delete File dialog box, click OK to delete the selected project file.

#### 4. Protein A280

##### 4.1 Overview

Proteins, unlike nucleic acids, exhibit significant diversity. The Protein A280 function is used to detect pure proteins that contain Trp (tryptophan), Tyr (tyrosine) residues, or Cys-Cys disulfide bonds. These proteins show a distinct absorbance at 280nm. This method does not require constructing a standard curve. Instead, the protein concentration is directly calculated based on the absorbance.

Protein A280 displays the UV absorption spectrum and calculates the protein concentration (mg/ml) based on absorbance at 280nm. Similar to nucleic acid detection, the recorded data reflects a 10 mm path length.

Using the base mode, the NP3000 can measure up to 600 mg/ml of BSA without dilution. If the detected light intensity after absorbance measurement is less than 200 (at a 10mm path length), the software will prompt the user to select a smaller measurement path length to ensure accuracy. The interface is shown below.

The primary factor determining the surface tension of a liquid is the hydrogen bonding between water molecules. Substances in the water—such as proteins, salts, and detergents—reduce surface tension by disrupting these hydrogen bonds. While 1µl is sufficient for most samples, due to reduced surface tension, 2µl is recommended to ensure a stable liquid column forms.

##### 4.2 Protein A280 Detection

On the main interface, click the "Protein A280" icon to access the detection interface:

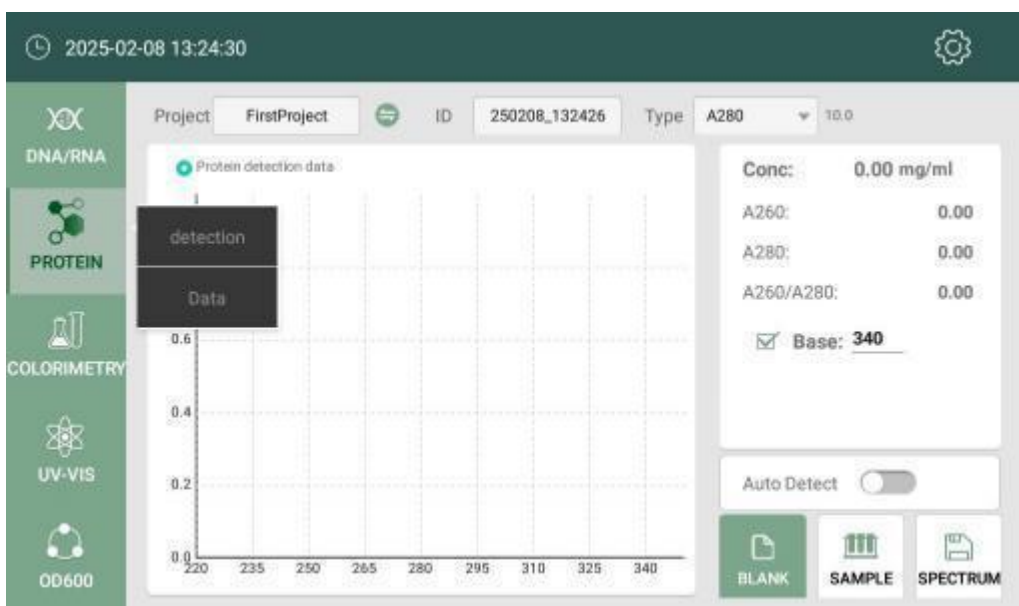
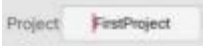




Figure 4.8 Initial Protein Detection Interface


In the interface shown in Figure 4.8, the top-left area provides two options: Protein A280 Interface and Data Interface, and you can click on the respective areas to access their functional zones.

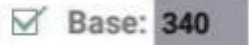
(1) In the interface shown in Figure 4.8, the buttons with a purple background are active and available, while those displayed in white are inactive.

1  :Project Name, select a suitable and memorable name based on your needs, such as the sample name or customer name.

2  :Sample Batch Number, defaults to the current time but can be reset as needed. Each ID can store up to 1,000 detection results.

3  :Selecting Protein Type, when selecting "Other" for the protein type, numerical values can be entered as needed. The instrument will perform calculations based on the set values.

4  :Before detecting samples, a blank calibration must be performed using a buffer solution. The absorbance of the buffer solution is generally between 0.004–0.03 Abs. It is recommended to redo the blank calibration if more than 30 minutes have passed.

5  :Baseline calibration can be selected or canceled. The default baseline calibration wavelength for the protein assay is 340 nm, and the user can enter a different calibration wavelength according to the needs of the test. In any case, the baseline is automatically set to the absorbance at the selected wavelength, and absorbance readings at all wavelengths are the result of subtracting this value.

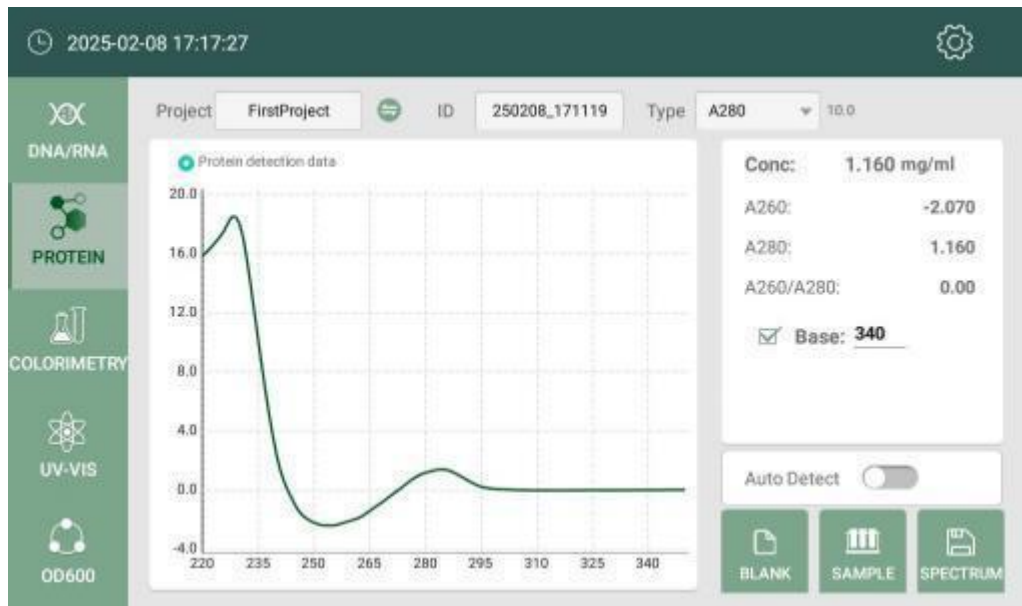
**Note: Baseline calibration must be set before detecting the samples. Setting it after detection will not take effect. If baseline calibration is not selected, the spectrum values may shift, altering the calculated concentration.**

## (2) Steps for Protein Detection

- 1 Set the Project Name, Sample ID, and Protein Type.
- 2 Establish a Blank Control: Add 2  $\mu$ l of blank solution to the lower base. Lower the upper base and click "Blank". Clean the Base.
- 3 Use a clean, lint-free cloth to wipe off the blank solution from the base.
- 4 Add and Detect the Sample: Add 2  $\mu$ l of the sample to the lower base. Lower the upper base and click "Sample" to begin the detection. After completion, the interface will look like Figure 4.9.

**Note: Each sample must be freshly added for detection.**

- 5 After testing, use a clean, lint-free cloth to wipe off the sample from both the upper and lower bases before testing the next sample.



**Figure 4.9 Protein Detection Results**

(3) As in Figure 4.10, the detection results are presented as data:

Conc:	1.160 mg/ml
A260:	-2.070
A280:	1.160
A260/A280:	0.00
<input checked="" type="checkbox"/> Base:	340

**Figure 4.10 Protein Detection Data**

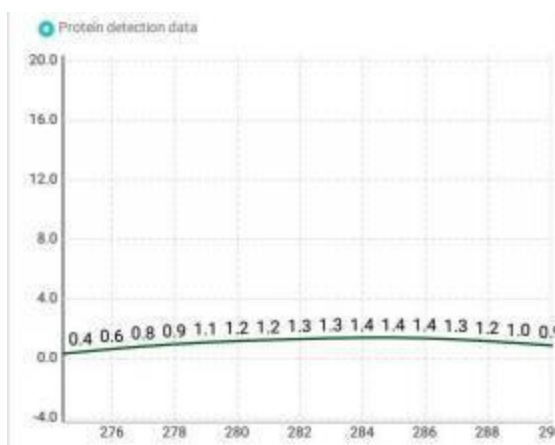
**Concentration:** The concentration value of the protein sample.

**A260:** Absorbance at 260nm with a 10mm pathlength.

**A280:** Absorbance at 280nm with a 10mm pathlength.

**A260/A280:** The ratio of absorbance at 260nm and 280nm.

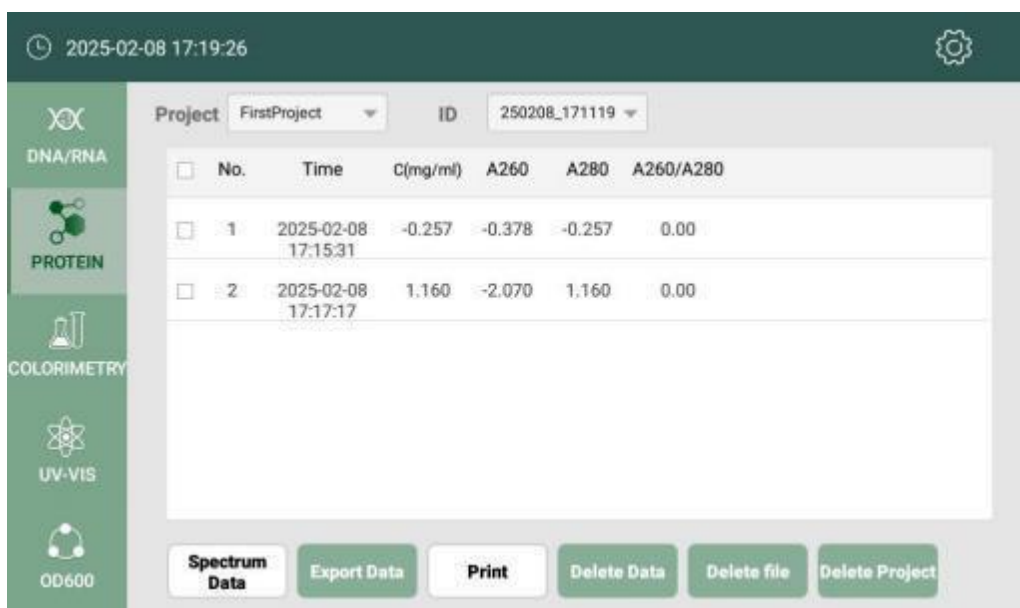
In Figure 4.11, Since the LCD screen supports multi-touch, please zoom in or out on the curve to display the absorbance at the wavelength shown.



**Figure 4.11 Protein Detection Curve**

(4) The other keys are the same as the nucleic acid test with the same name key operation and function, please refer to the nucleic acid test chapter for details.

#### 4.3 Protein A280 Detection Data



**Figure 4.12 Protein Detection Data Interface**

The layout of this interface is identical to the Nucleic Acid Detection Data interface, and buttons with the same names have identical functions. For detailed information, refer to the Nucleic Acid Detection section.

## 5. Colorimetric Methods

### 5.1 Overview

The BCA, Lowry, and Bradford methods are colorimetric techniques used to determine the concentration of impure proteins. These methods require the construction of a standard curve to detect protein concentrations, and all three are grouped under the colorimetric detection function.

The BCA method measures the concentration of impure proteins using colorimetry and is particularly suited for diluted protein samples and proteins with UV-absorbing impurities. It detects  $\text{Cu}^{+1}$  ions formed when  $\text{Cu}^{+2}$  ions are reduced by proteins in an alkaline environment. The  $\text{Cu}^{+1}$  ions form a purple complex with two BCA molecules, with maximum absorbance at 562 nm. Data is standardized at 750 nm.

Commercial BCA kits are available in two protein detection ranges:

The routine assay uses a reagent/protein sample volume ratio of 20:1, and this kit detects from 0.20mg/ to 8.0mg/ml (BSA). When using the base assay, 4ul of sample and 80ul of BCA reagent is recommended.

The micro assay uses a 1:1 reagent/sample and can detect protein concentrations ranging from 0.01mg/ml to 0.20mg/m To prepare enough sample for the baseline assay, 10ul of sample and 10ul of BCA reagent (using a P-tube) is recommended.

Follow the kit manufacturer's instructions to construct the standard curve and prepare samples. Ensure consistent time and temperature across all detections.

**Note: For temperatures above 60°C, double the test volume to prevent evaporation and ensure accurate results.**

The Lowry protein quantification method is a widely used technique for determining protein concentration. In this method, proteins react with copper sulfate in an alkaline environment to form a copper-protein complex. The Folin-Ciocalteu reagent effectively reduces the copper complex, generating a blue product proportional to the protein concentration. The absorbance can be measured at 650nm and calibrated at 405nm. The reagents required for the test can be sourced from multiple manufacturers.

To prepare accurate standards, it is recommended to use 20 $\mu\text{L}$  of protein sample and 100 $\mu\text{L}$  of Lowry reagent for the reaction. On this instrument, the detectable concentration range is 0.20mg/mL to 4mg/mL. Prepare standards and samples following the instructions provided by the reagent kit manufacturer. Ensure consistent handling time and environmental temperature for all samples during the process. Since the base detection concentration range of this instrument is broader than conventional methods, the standard curve should cover a wider range than suggested by the manufacturer. For detection, it is recommended to use 2 $\mu\text{L}$  of sample.

The Bradford method is a commonly used technique for protein quantification, especially for detecting lower concentrations of proteins. This method measures protein concentration based on the absorbance shift caused by proteins binding to Coomassie Brilliant Blue dye, typically detected at 595 nm. The protein-dye complex is measured at 595 nm, with standardization performed at 750 nm. Suitable reagent kits for the Bradford assay are available from multiple manufacturers.

Commercial Bradford reagent kits are available in two protein concentration ranges:

Standard detection: This uses a reagent-to-protein sample volume ratio of 50:1, with a detection range of 0.10 mg/mL to 8.0 mg/mL (BSA). The optimal linear range is 0.01–1 mg/mL. For base detection using this instrument, it is recommended to use 4 $\mu\text{L}$  of the sample and 200 $\mu\text{L}$  of Bradford reagent.

Micro detection: This uses a 1:1 reagent-to-sample ratio and can detect protein concentrations ranging from 15 $\mu\text{g}/\text{mL}$  to 125 $\mu\text{g}/\text{mL}$ . For base detection, it is recommended to use 10 $\mu\text{L}$  of the sample and 10 $\mu\text{L}$  of the Bradford reagent (in a PCR tube). Prepare the standard curve and samples following the reagent kit manufacturer's guidelines, ensuring consistent time and temperature during all steps.

**Note: If the experimental temperature exceeds 60°C, it is advisable to double the reagent and sample volumes to prevent evaporation, which could reduce sample volume and affect test accuracy.**

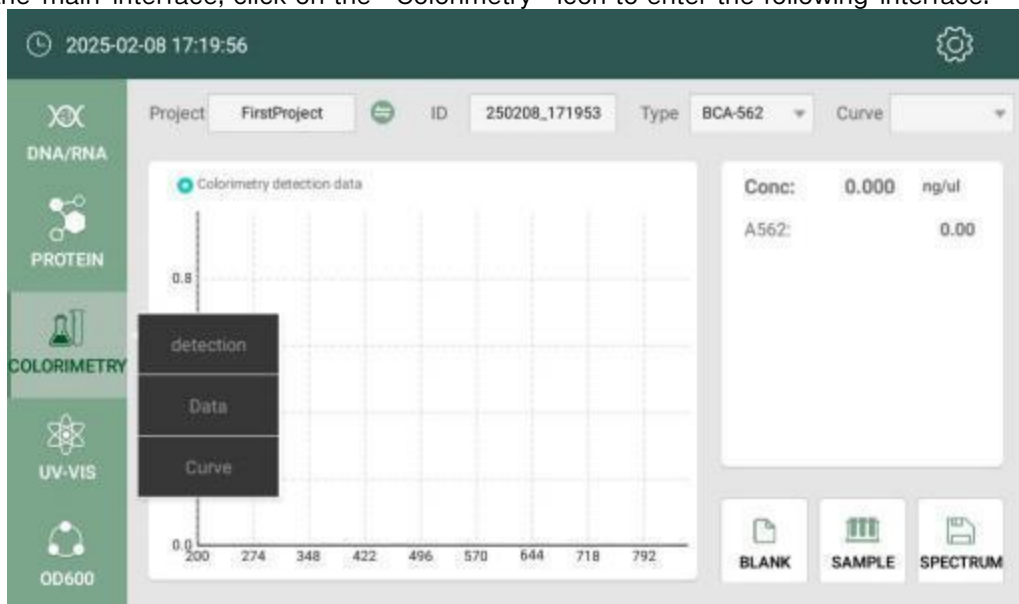
Bradford reagent kits include standard solutions for constructing the standard curve. As this instrument can detect higher concentrations than conventional spectrophotometric

methods, users should use standard solutions with concentrations higher than those recommended by the manufacturer.

## 5.2 Colorimetric Detection


**Note: Before conducting sample detection using the colorimetric method, a standard curve must be established!**

In the main interface, click on the “Colorimetry” icon to enter the following interface:




**Figure 5.1: Colorimetric Detection Initial Interface**

(1) The layout of this interface is the same to the initial nucleic acid detection interface, but with key differences:

1 

:Click to select the colorimetric method type.

2 

:The system displays the curve corresponding to the previously selected colorimetric method. This system provides three types of curves: First-order polynomial, Second-order polynomial and Third-order polynomial

(2) Steps for Operation

1 Set the project name, sample ID, colorimetric method type, and corresponding curve.

2 To set up a blank control with buffer: take 2ul of blank solution and add it to the lower base, lower the upper base and click “Blank” .

3 Wipe the blank solution from the base with a clean, dust-free cloth.

4 Take 2ul of sample and add it to the lower base, put down the upper base, click “Sample” to test, and then display the value of the sample and the spectral curve.

**Note: The sample must be freshly added for each detection.**

## 5.3 Standard Curve

Before performing colorimetric detection, a standard curve must be established. A basic standard curve can consist of two points, but to ensure accuracy, it is recommended to use five or more points. The concentration range of the standards should cover the entire concentration range of the samples and be evenly distributed. This section introduces the functionalities and operations of the standard curve interface for colorimetric methods.

Click "Curve" to access the standard curve interface, as shown in the figure below. If no standard curve exists, a new curve must be created before proceeding with sample detection in the colorimetric detection interface.

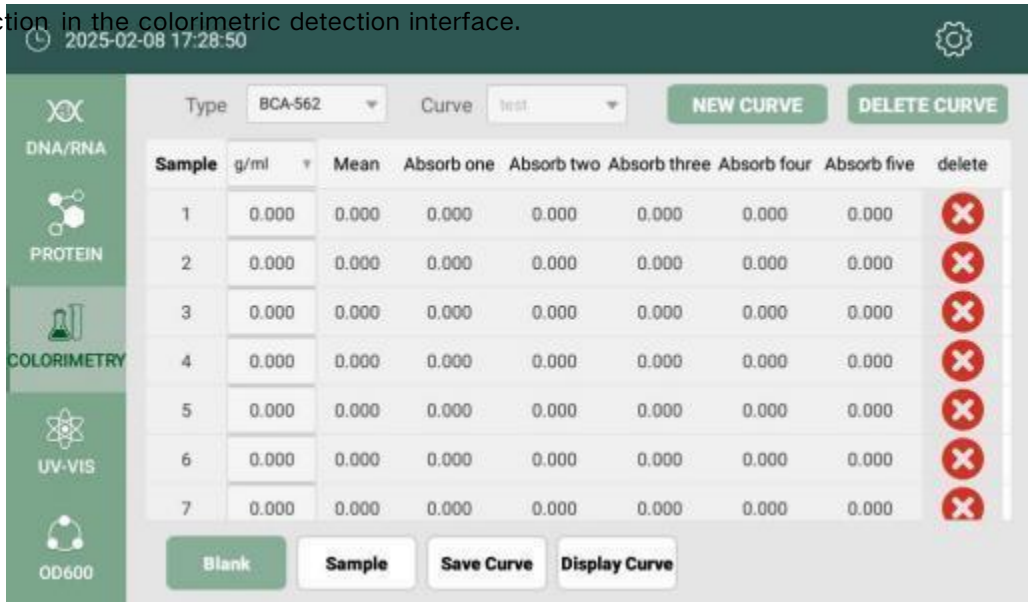


Figure 5.2 Standard Curve Interface for Colorimetric Method

(1) Create a New Curve:

1 Click the button: **NEW CURVE** to open a dialog box. Enter the name for the new curve and click "Confirm" to display the interface as shown below:

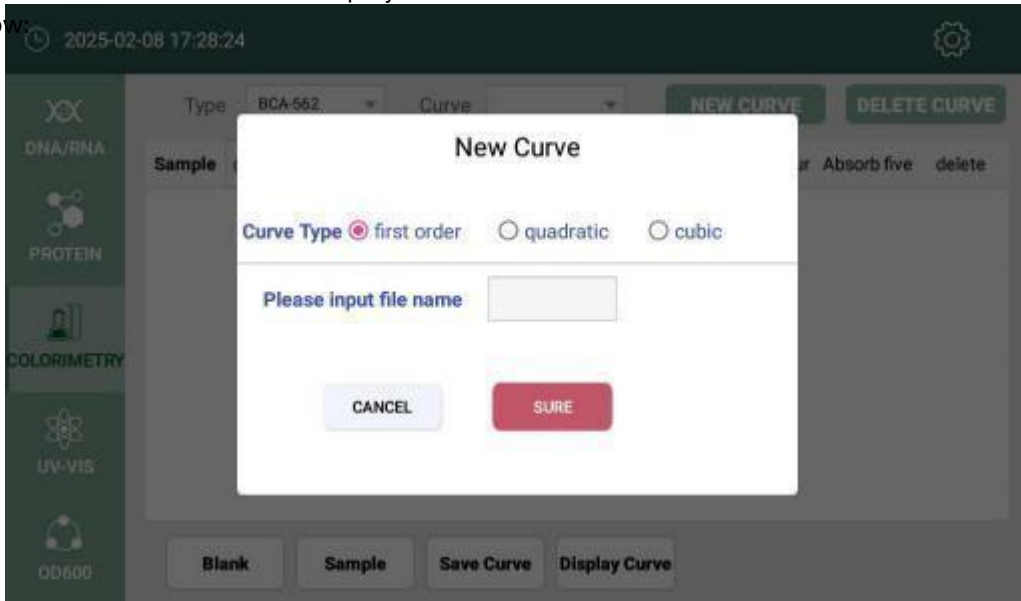
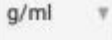


Figure 5.3 Colorimetric method new curve interface




**Figure 5.4 Entering Concentration Values in the Standard Curve Screen**

2 Click the button:  to select the unit for the standard sample. Enter the corresponding concentration values for the standard samples in the input field. The order of input for standard sample concentrations is not required; it only needs to match the concentration values with the samples added during detection.


3 In the interface shown in Figure 5.4, click on the name of a standard sample to select it. The background of the selected standard sample will turn blue. Then, follow the sequence of blank and sample detection to measure the absorbance of the standard sample. Repeat the same steps to measure the absorbance of other standard samples.

Each standard sample's absorbance value can be measured up to five times consecutively, and the average value is used as the sample point for the standard curve. To delete a standard sample, click on the sample name or press and hold a location in the row other than the sample name to select it, then click the Delete button on the right.

4 After completing the detection of all standard samples, click  to store the newly created curve.

**Note: The newly created curve must be saved to appear in the dropdown menu of curves in the detection interface.**

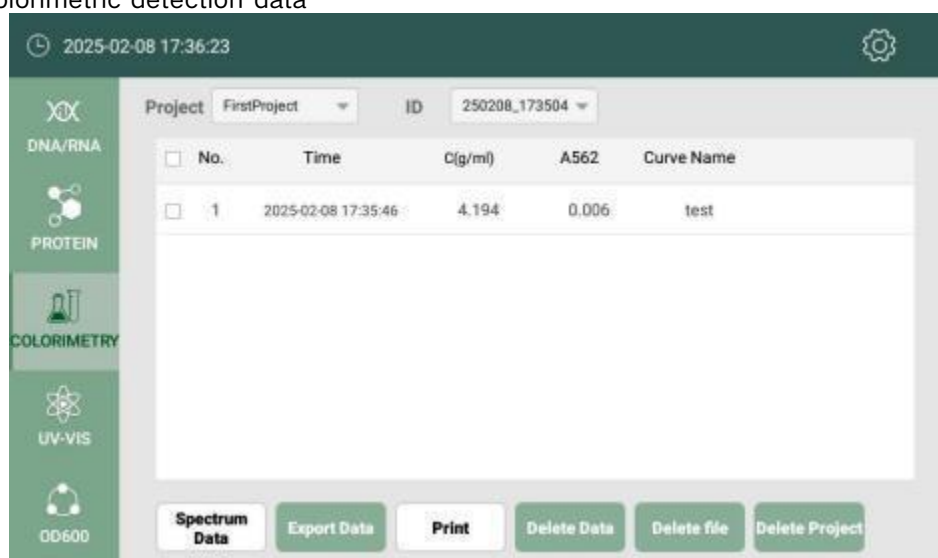
(2) Other Button Descriptions:

1  : Click this button to display the currently established curve, as shown in the figure below:



**Figure 5.5 New Curve**

#### 5.4 Colorimetric detection data



**Figure 5.6 Colorimetric Detection Data Interface**

## 6. Uv-Vis full wavelength scanning

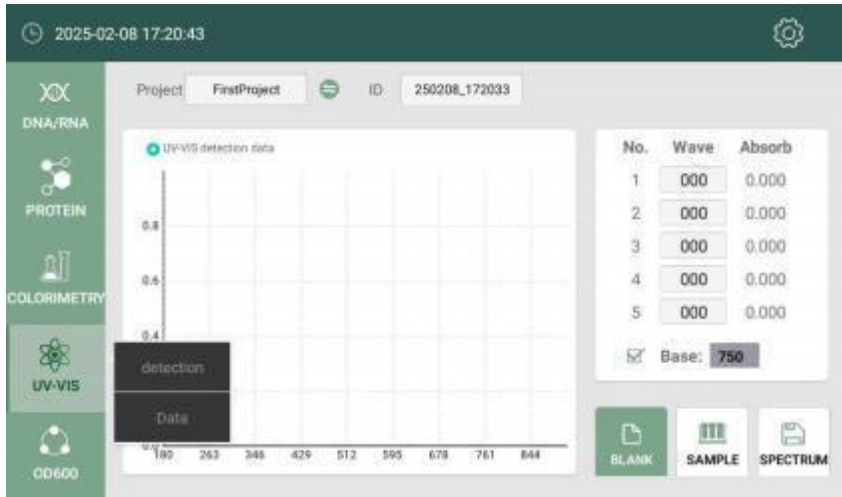
### 6.1 Overview

The Uv-Vis function allows the instrument to measure the absorbance of samples from 180–910nm like a normal UV-Vis spectrophotometer.

The Uv-Vis function allows the instrument to measure the absorbance of samples from 180 to 910nm in the same way as a normal UV-Vis spectrophotometer. The Uv-Vis function allows the instrument to automatically select the detection range according to the range of the absorbance value of the test solution, and is capable of detecting the absorbance equivalent to a maximum of 300 at a 10mm range.


### 6.2 Uv-Vis Detection

In the main interface, click the “Uv-Vis” icon to enter the following interface:



**Figure 6.1 Initial interface of Uv-Vis detection**

(1) The main layout of this interface is the same as the initial interface for nucleic acid testing, with a few different layouts highlighted here:

- 1 Click the button: , when the proofreading is finished, click the sample, and Figure 6.2 pop-up screen will appear.



**Figure 6.2 Viewing Absorbance at Characteristic Wavelengths**

② As shown in Figure 6.3, the characteristic wavelength can be entered into the input box as desired, and the absorbance at that wavelength will be displayed after the sample is detected. The wavelength must be entered before the sample is tested, but not after.

No.	Wave	Absorb
1	230	3.605
2	260	9.428
3	000	0.000
4	000	0.000
5	000	0.000

Base: 750

**Figure 6.3 Viewing Absorbance at Characteristic Wavelengths**

(2) Operation steps:

- ① Set the project name, sample number and characteristic wavelength;
- ② Use the buffer to establish a blank control: take 2ul of blank solution and add it to the lower base, put down the upper base and click “ blank ” ;
- ③ Wipe the blank solution on the base with a clean dust-free cloth;
- ④ Take 2ul of sample and add it to the lower base, put down the upper base and click “ Sample Detection ” to test;

**Note: The sample for each test must be freshly added.**

- ⑤ After the detection is completed, the sample on the upper and lower bases must be wiped off with a clean, dust-free cloth before the next sample can be detected.

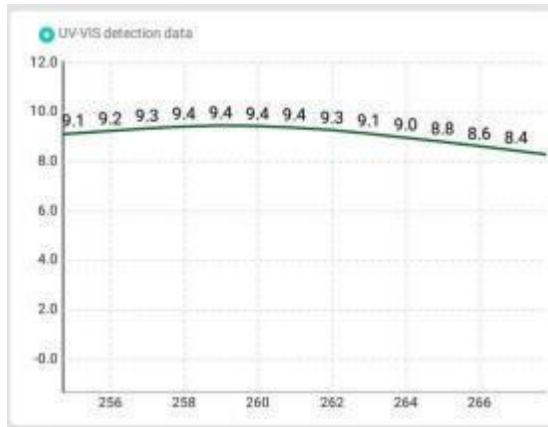
### 6.3 Uv-Vis Detection Data

No.	Time	W1	W2	W3	W4	W5
1	2025-02-08 17:22:10	230/-0.014	260/-0.007	0/0.000	0/0.000	0/0.000
2	2025-02-08 17:22:40	230/3.605	260/9.428	0/0.000	0/0.000	0/0.000

**Figure 6.5 Uv-Vis Detection Data**

The main layout of this interface is the same as the data interface of Nucleic Acid Detection, and the operation and function of the buttons with the same name are the same, please refer to the chapter of Nucleic Acid Detection for details.

It should be noted that, if you need to view the absorbance of other wavelengths, please zoom in or out to display the absorbance of the wavelength at the position of the wavelength shown in the graph, as shown in the following figure, because the LCD screen supports multi-touch control:



**Figure 6.6 Uv-Vis full wavelength data**

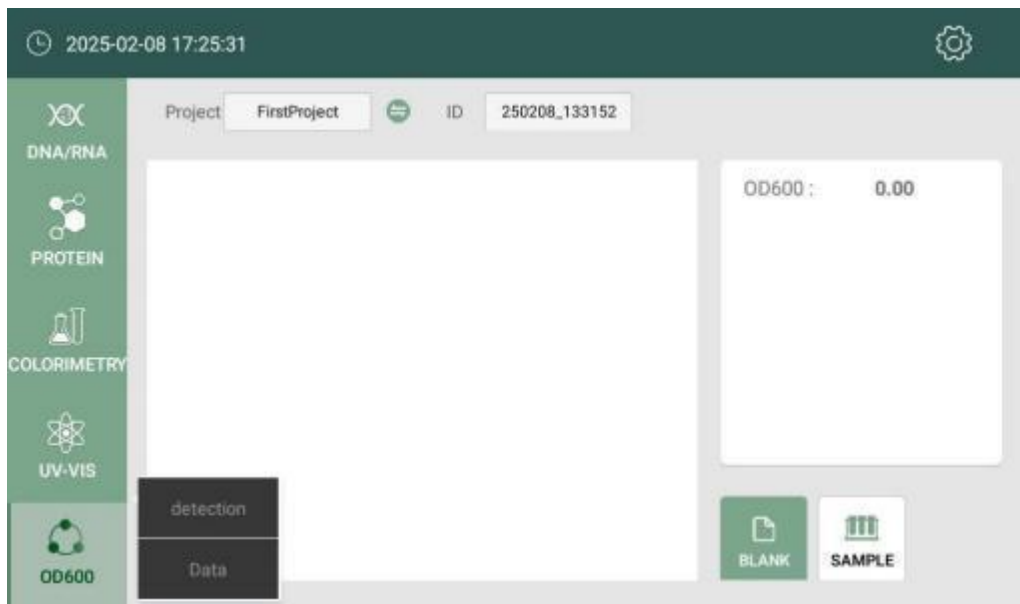
## 7. OD600

### 7.1 Overview

OD600 refers to the absorbance of a solution at 600nm.

One of its important applications is to utilize the absorbance of bacteria to measure the concentration of a bacterial culture solution to estimate the growth of bacteria.

### 7.2 OD600 Detection



**Figure 7.1 Initial boundaries for OD600 detection**

Operation steps:

- 1 Set the name of the item, the sample number is normally given automatically by the system;
- ② Blank: the blank can be air, empty cuvette or cuvette with blank solution, depending on the experimental requirements;
- ③ After the blank is completed, the detection solution is added to the cuvette, and the amount of solution added is 2ml~3ml;
- 4 Click "Sample" to test, and the measurement result will be displayed on the right side of the interface.

### 7.3 OD600 Detection Data

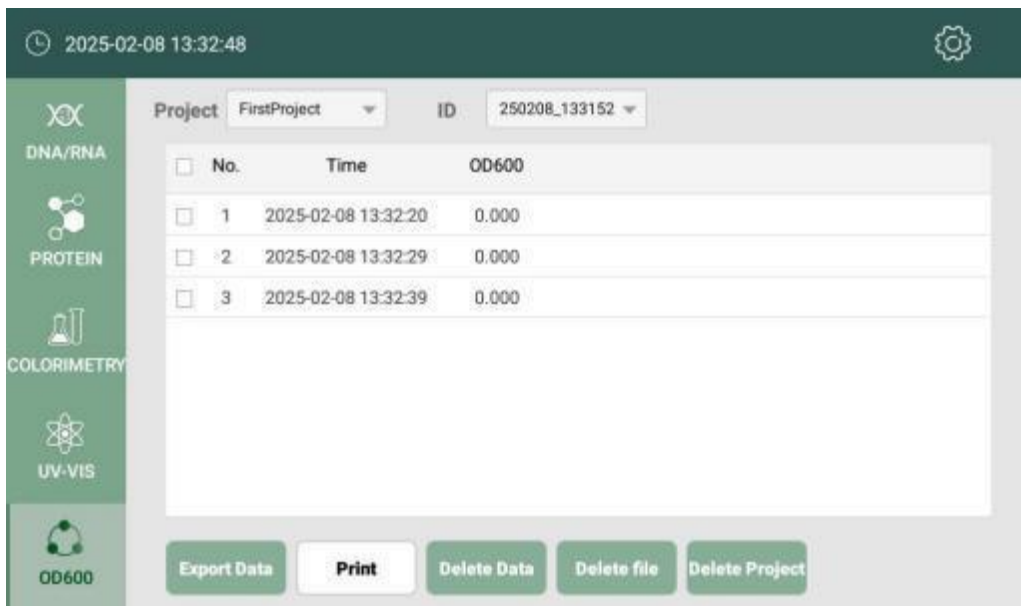


Figure 7.2 OD600 Detection Report Interface

## 8. System Settings

Click the “Settings” icon in the main interface to enter the following system settings interface.

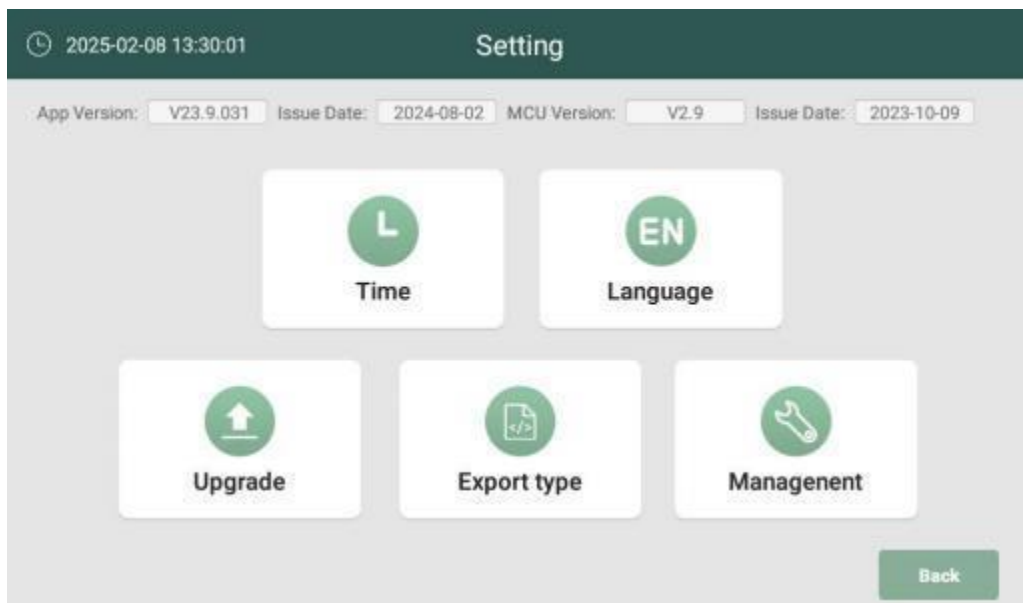
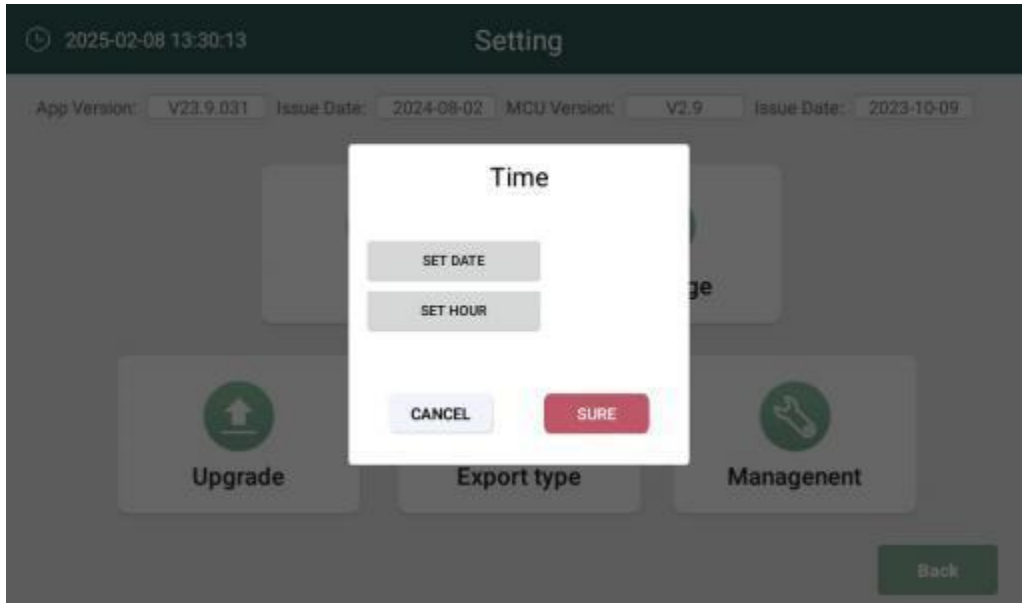


Figure 8.1 System Settings

### 8.1 Time Setting

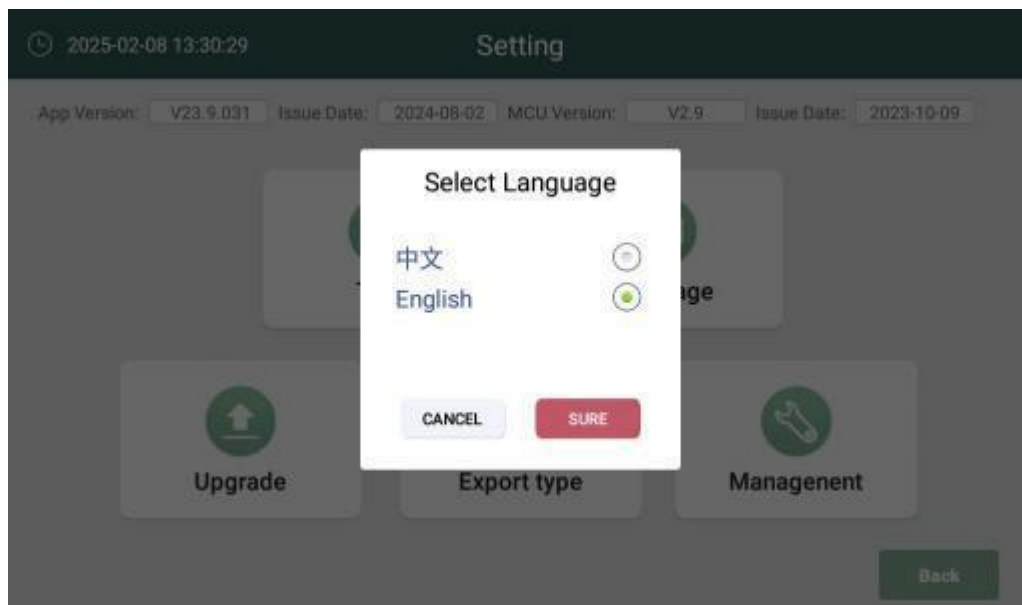
Click “Time” icon to enter the main interface of system time setting.



**Figure 8.2 Time Setting**

### 8.2 Language Selection

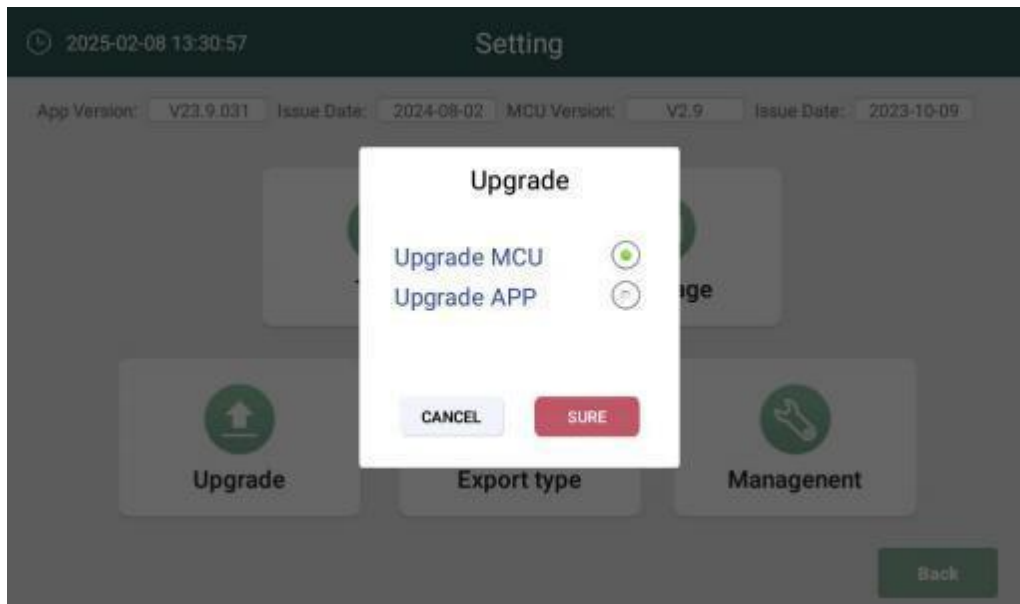
Click “Language” icon to bring up the language selection dialog box, select the desired language and click “OK” to complete the language selection.



**Figure 8.3 Language Selection**

### 8.3 Upgrade

Put the upgrade software in the root directory of the USB flash drive, insert the USB flash drive into the computer, and then click the “Upgrade” icon, the dialog box shown in Figure 8.4 will pop up, if you want to upgrade, click Install. The installation is finished and the system is upgraded.



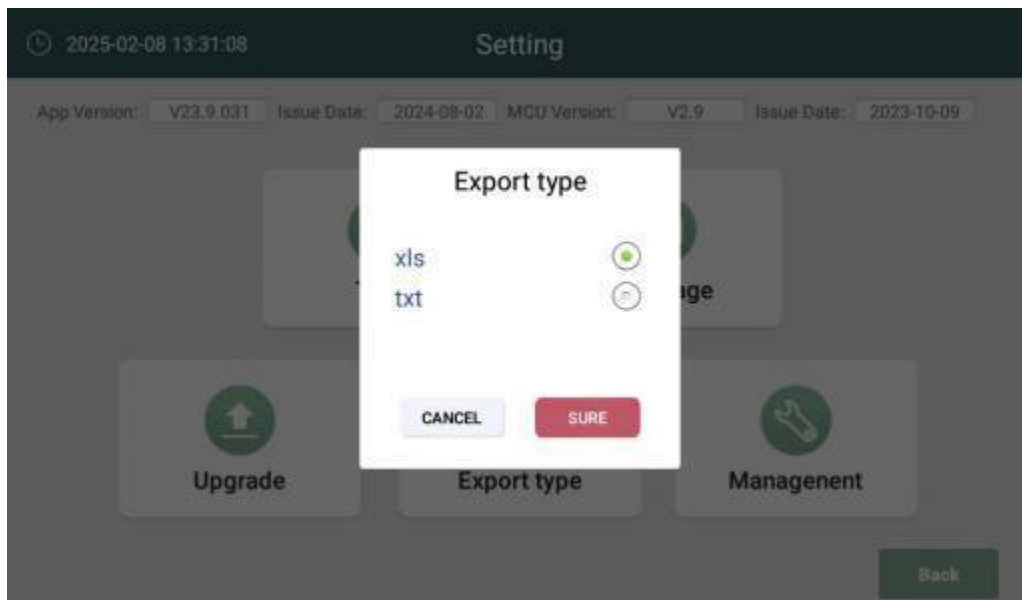
**Figure 8.4 Upgrade**

#### 8.4 Maintenance

The maintenance function is only used in the production and maintenance process, the interface is not involved in the user's use, and professional technicians are required to enter the maintenance interface after inputting the password to carry out debugging and maintenance of the instrument, which will not be explained in detail here.

#### 8.5 Formats

The machine provides two kinds of data formats, namely \*.xls and \*.txt, users can choose the appropriate format according to their needs.



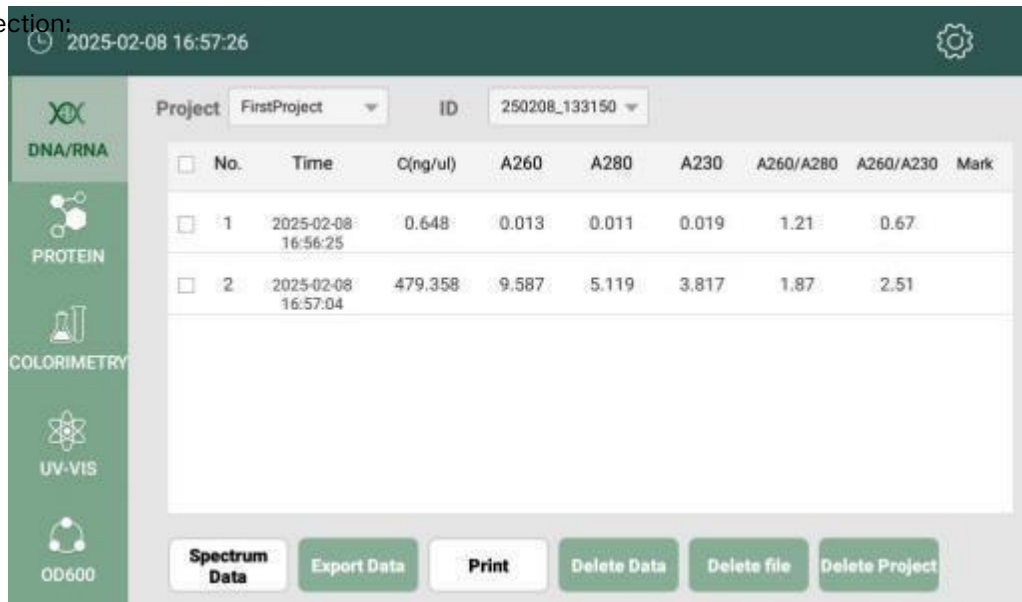
**Figure 8.5 Format Settings**

#### 9. Option Function

New optional functions are added.

## 9.1 Printer Function

Each module has a printer function. The following is an example of nucleic acid detection:



**Figure 9.1 Print display**

Plug in the printer usb before power on, connect to the printer, after powering on the test samples, check the data to be printed, click the batch print button, you can print the test data. The data can be printed at the same time.

## 9.2 Battery powered

The user can choose whether or not to have a battery-powered system. The version with batteries can be charged and discharged and can be used normally without being plugged in.

## V. Failure Analysis and Handling

### Failure analysis and handling methods:

NO.	Failure phenomena	Analysis of causes	Methods of Handling
1	Instrument will not start	1.Power not on 2.Bad switch 3.Bad power adapter	1. Check power supply, re-plug power supply 2. Replace the switch 3. Contact supplier or manufacturer
2	Inaccurate nucleic acid detection results	1.Liquid column not formed 2.Contaminated base 3.Other	1. Refill sample, ensure column formation 2. Scrub the base several times with pure water 3. Contact supplier or manufacturer
3	OD600 module failed	Bad connection between data cable and motherboard	Contact supplier or manufacturer
4	Insufficient Light Alarm	1.Failure of analysis module 2.Broken optical fiber	Contact supplier or manufacturer
5	Touch screenjumps	Power supply not grounded	Provide an effectively grounded power supply
6	Communication timeout	Analysis module communication does not respond	1. Restart the instrument 2. if not resolved, contact supplier or manufacturer
7			
8			

## Performance Checklist

<b>Name of Instrument</b>	Ultraviolet-visible spectrophotometer	<b>SKU</b>	NP3000
<b>Date of Detection</b>		<b>NO.</b>	YN-N01-

NO.	Project Name	Detection Method	Standard Requirement	Test Result
1	Spectrophotometer Wavelength Range	dsDNA Reagent Detection	190-900nm	<input type="checkbox"/> Qualified
2	Spectrophotometer Wavelength Accuracy	dsDNA Reagent Detection	± 1nm	<input type="checkbox"/> Qualified
3	Spectrophotometer Absorbance Precision	dsDNA Reagent Detection	0.003Abs (1mm Optical Path Length)	<input type="checkbox"/> Qualified
4	Spectrophotometer Absorbance Accuracy	dsDNA Reagent Detection	± 1%	<input type="checkbox"/> Qualified
5	Spectrophotometer Absorbance Range	dsDNA Reagent Detection	0.04~300Abs	<input type="checkbox"/> Qualified
6	Spectrophotometer Concentration Detection Range	dsDNA Reagent Detection	2~15000ng/uL	<input type="checkbox"/> Qualified
7	Spectrophotometer Detection Time	dsDNA Reagent Detection	< 6s	<input type="checkbox"/> Qualified
8	OD600 Absorbance Range	Standard Filter Detection	0~4.000Abs	<input type="checkbox"/> Qualified
9	OD600 Absorbance Stability	Standard Filter Detection	[0,3] ≤0.3% , [3,4] ≤2%	<input type="checkbox"/> Qualified
10	OD600 Absorbance Repeatability	Standard Filter Detection	[0,3] ≤0.2% , [3,4] ≤2%	<input type="checkbox"/> Qualified
11	OD600 Absorbance Accuracy	Standard Filter Detection	[0,2] ≤0.005A , [2,3] ≤1% , [3,4] ≤2%	<input type="checkbox"/> Qualified
12	Voltage Resistance 1500V	Voltage Resistance Tester	No Breakdown, No Flicker	<input type="checkbox"/> Qualified
13	Ground Leakage Current	Leakage Current Tester	≤0.75mA	<input type="checkbox"/> Qualified
14	Basic Functions	Visual Inspection	Valid	<input type="checkbox"/> Qualified
15	Appearance Requirements	Visual Inspection	Compliant	<input type="checkbox"/> Qualified
16	Appearance Labeling	Visual Inspection	Compliant	<input type="checkbox"/> Qualified
17	Continuous Operation Test	Visual Inspection	36 Hours of No Malfunction	<input type="checkbox"/> Qualified
<b>Detection Result</b>				
<b>Memo:</b>				
<b>QC:</b>		<b>Confirmed by:</b>		

## PACKING LIST

NO.	Project Name	SPEC.	Unit	QTY	Confirm	Memo
1	Micro-Volume Spectrophotometer	NP3000	Unit	1		
2	Power Adapter	12V 4A	Unit	1		Elbow Three-Prong Plug with Grounding
3	Power Cable		Unit	1		
4	USB Drive		Unit	1		
5	Dust-Free Paper		Box	1		
6	User Manual		Unit	1		
7	Warranty Certificate		Unit	1		
8	Certificate of Conformity		Unit	1		

Person in Charge:

Loading

Date: