ESPECTROFOTÓMETRO NANOVOLUMEN
NANOVOLUME SPECTROPHOTOMETER
SPECTROPHOTOMÈTRE NANOVOLUME

REF. - CODE - RÉF. - HJF001 (Z-6500) - HJF002 (Z-6500C)

Este manual es parte inseparable del aparato por lo que debe estar disponible a todos los usuarios del equipo. Le recomendamos leer atentamente el presente manual y seguir rigurosamente los procedimientos de uso para obtener las máximas prestaciones y una mayor duración del mismo.

This manual should be available for all users of these equipments. To get the best results and a higher duration of this equipment it is advisable to read carefully this manual and follow the processes of use.

Ce manuel est une partie indissociable de l'appareil et doit être mis à la disposition de tous les utilisateurs de l'équipement. Nous vous recommandons de lire attentivement ce manuel et de suivre scrupuleusement les procédures d'utilisation afin d'obtenir des performances maximales et une plus longue durée de vie de l'appareil.

LANGUAGE INDEX

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1. PRODUCT INTRODUCTION

The Zuzi Nanovolume Spectrophotometer is equipped with an 8-inch display, 1 HDMI interface, 1 network port, 1 type C port, and 2 USB interfaces. The built-in software does not require installation and a mouse, keyboard, printer, USB flash drive, wireless network card, and other USB devices can be connected.
The instrument has an absorbance module, which is suitable for detecting samples with high concentrations (such as dsDNA > 20ng/ul). It has two detection forms: micro-volume mode and cuvette mode, which can accurately measure micro-volume samples from 0.3 to 2μL with good repeatability. Low concentration detection is more stable, and the high concentration detection range is wider, 200 times that of a conventional UV-visible spectrophotometer, without the need for dilution or baseline calibration. The micro-volume mode requires less sample volume, with a minimum measurement volume of 0.3uL, and can be used to detect nucleic acids, proteins, and conventional full-wavelength scanning, while the cuvette mode can be used for traditional cuvette detection (such as cell solutions, microarray samples) and kinetic detection modules. All data is automatically saved for easy data statistics, and the software is easy to master.

1.1 Absorbance Module Detection Principle

After the spectrophotometer has made a blank control, the instrument will automatically record the spectral results of the blank reference solution and save them as the light intensity reference value for the wavelength. When detecting samples, the light intensity transmitted through the sample will be recorded. The absorbance of the sample is calculated according to the following formula by comparing the light intensity transmitted through the sample with that of the blank control:

$$Absorbance = -\log\left[\frac{Intensity_{sample}}{Intensity_{blank}}\right]$$

Thus, the absorbance at a specific wavelength can be calculated through the transmitted light intensity of the sample and the blank control.
The relationship between sample concentration and absorbance is determined by the Lambert-Beer (Lambert-Beer) law:

$$\mathbf{A = \varepsilon\, b\, c}$$

Where: A = Absorbance (A)

ε = Wavelength-dependent molar extinction coefficient (unit L/mol*cm)

b = Path length (unit cm)

c = Sample concentration (unit mol/L)

The reference solution, or blank solution, is typically those solvents that dissolve the targeted molecules, which should have the same pH and ionic strength as the sample solution.

1.2 Application Range of the Instrument

The Zuzi Nanovolume Spectrophotometer can be used to measure the following ranges:

1.2.1 Nucleic Acids:

- The concentration and purity of nucleic acid samples, including double-stranded DNA, single-stranded DNA, RNA, user-defined, OligoDNA, OligoRNA.
- Gene chip: capable of detecting nucleic acids and fluorescence dye concentrations simultaneously.

1.2.2 Protein:

- A280 measurement of protein sample concentration, including 1Abs=1mg/ml, BSA, HSA, MSA, Mouse IgG, Human IgG, Human IgE, Lysozyme, molar extinction coefficient ε/Molecular weight M, mass extinction coefficient.
- Peptides: including A205 and A215.
- Protein chip: capable of detecting proteins and fluorescence dye concentrations simultaneously.
- Kit method (Lowry method, BCA method, Bradford method, Pierce660 method): the software determines the protein concentration of the unknown sample by drawing a standard curve.

1.2.3 Conventional UV/Visible full-wavelength scanning:

Full-wavelength UV/Visible (190-910nm) scanning can be performed.

1.2.4 Cell solution (only Z-6500C model):

Measurement of the absorbance value of cell solution OD600 and determination of cell density.

1.2.5 Standard curve method:

In addition to the commonly used kit method, standard curves for other detection wavelengths can also be made to determine concentrations.

1.2.6 Colloidal gold:

Detection of the absorbance value of colloidal gold.

1.2.7 Kinetics (only Z-6500C model):

It can detect the trend of absorbance change with time at a certain fixed wavelength and can also simultaneously select multiple wavelengths for comparative analysis to study the kinetics of the detected substances.

1.3 Instrument parameters

1.3.1 Ultra-micro mode

Optical path: 1mm, 0.2mm, 0.1mm, 0.03mm, 0.02mm
Volume requirements: 0.3-2μL
Light source: Long-life xenon flash lamp (109 flashes)
Detector type: 3864-element linear siliconized CCD array
Test wavelength range: 190-910nm
Xenon lamp wavelength range: 185-2000nm
Wavelength accuracy: ±1nm
Wavelength resolution: 2nm (FWHM at Hg 254nm)
Absorbance accuracy: 0.002 Abs
Absorbance accuracy: 1% (0.988 Abs at 257nm)
Absorbance range: 0.04～800Abs (equivalent to 10mm optical path)
Concentration detection range (microwave base): 2～40000ng/μl (dsDNA); 0.06～1194mg/ml (BSA); 0.03mg/ml-584mg/ml (IgG); 0.02mg/ml-303mg/ml (Lysozyme).
Detection cycle: ≤ 3 seconds
Working voltage: DC 24V/2.5A Maximum power: 60W
Sample base: Stainless steel
Dimensions: 300mm×210mm×130mm Weight: 5 kg

1.3.2 Cuvette mode (only Z-6500C model)

Cuvette specifications: optical path 1mm, 2mm, 5mm, 10mm Light beam height: 8.5mm
Concentration detection range (10mm cuvette): 0.2 - 80 ng/μl (dsDNA); 0.006 - 2.38mg/ml (BSA); 0.003mg/ml-1.16mg/ml (IgG); 0.002mg/ml-0.61mg/ml (Lysozyme)
Absorbance accuracy: 1% (0.988 absorbance at 257nm)

2. INTRODUCTION TO DETECTION MODES

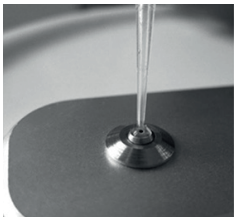
2.1 Ultra-micro Mode

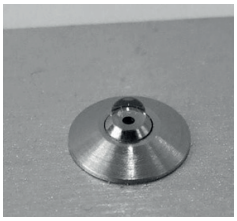
1. Blank: Use a pipette to transfer 0.3-2μl (quantified according to actual conditions) of buffer solution and drop it onto the detection base (material of the detection base is stainless steel and the center point is quartz). The lower detection head is the receiving end, and the upper detection head is the emitting end.
2. Sample Measurement: Use a pipette to transfer 0.3-2μl of the measured sample and drop it onto the detection base. For protein samples, a sample volume of 2.0μl is required for detection.
3. Due to the inconsistent tension of different samples, in order to better form the liquid column of the sample, the recommended sample detection quantity is as follows (users can adjust according to actual conditions):

Nucleic Acid Solution: 2.0μl Protein Solution: 2.0μl Other Samples: 2.0μl

2.1.1 Basic Operation of the Base

1. Lift the sample arm, use a pipette to aspirate 0.3□2μL of sample and drop it onto the base.

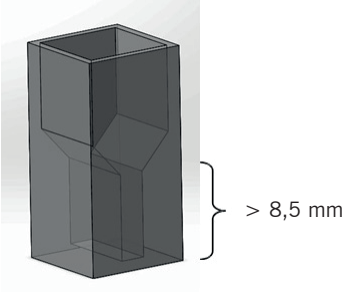




2. Lower the sample arm and start the absorbance value detection using the software on the computer. An automatic sample column will be pulled out between the two optical fibers, and then the detection will be carried out.
3. After the detection is completed, lift the sample arm, and use absorbent paper towels to wipe the samples on the upper and lower bases clean. This wiping of the sample can prevent the residue of the sample on the base.

2.2 Cuvette Mode (only Z-6500C model)

The instrument can use conventional (height 45mm) or custom (27mm) cuvettes with a light path of 10mm. When using cuvettes with a small light path (such as 5mm, 2mm, 1mm), we recommend using opaque cuvettes with no transparency around. Opaque cuvettes ensure that all light that passes through the sample reaches the detector. Transparent cuvettes allow light that has not passed through the sample to also reach the detector, which can lead to inaccurate detection, especially for low concentration samples.
Due to the height of the light beam, the height of the sample added inside the cuvette must be greater than 8.5mm. Please refer to the manufacturer's recommendations for the required sample volume.
The cuvettes provided with the instrument are 10mm light path conventional glass cuvettes, with a minimum sample volume of 1000μl.



2.2.1 Basic Operation of the Cuvette

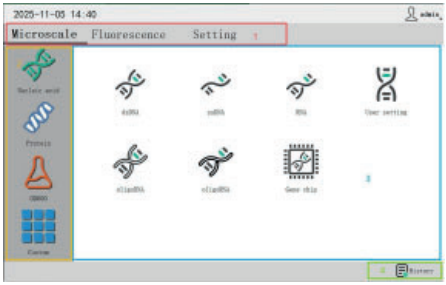
1. Add the sample to the cuvette, ensuring that the added sample volume is sufficient to cover the light beam. It is recommended that the liquid level be greater than 8.5mm.
2. Lift the sample arm, insert the cuvette into the cuvette detection chamber, and pay attention to the direction of the optical path on the instrument when inserting the cuvette.
3. The sample arm must be lowered when performing cuvette detection.
4. After the detection is completed, remove the cuvette, pour out the sample, and clean the cuvette.

Note: When using a cuvette for detection, the detection arm also needs to be lowered. When using the base for detection, it is recommended to remove the cuvette to ensure that the base arm can be placed in the correct position.

3. SOFTWARE INTERFACE INTRODUCTION

After the instrument is powered on, wait for about 2 minutes to enter the user login interface. The default administrator account is 'Username: admin Password: 123456'. Click 'Account Login' to enter the detection interface. If user management login is required, the administrator can set login permissions in the 'Settings' interface - 'User Module'.

3.1 Ultra-Micro Interface



3.1.1 Main Menu Bar (Area 1):

Microscale, Fluorescence (not displayed on Z-6500 and Z-6500C models), Settings.

3.1.2 Left Detection Type Bar (Area 2):

Nucleic Acid, Protein, OD600, Custom (including Full Wavelength, Standard Curve Method, Colloidal Gold, Kinetics).

3.1.3 Right Detection Item Bar (Area 3):

The detection items under each detection type are different. The detection items for nucleic acid are:

dsDNA, ssDNA, RNA, User Settings, oligoDNA, oligoRNA, Gene Chip;
The detection items for protein are: A280, Peptide, Protein Chip, Bradford, Lowry, Pierce660. The detection items for OD600 are: Cell Suspension.
The detection items for Custom are: Full Wavelength, Standard Curve, Colloidal Gold, Kinetics.

3.1.4 History Records (Area 4)

4. ULTRA-MICRO MODULE FUNCTION AND SAMPLE DETECTION

4.1 Nucleic Acid Module

The Zuzi Nanovolume Spectrophotometer can measure the concentration of nucleic acid samples and evaluate the purity of nucleic acids. Since nucleic acids have the highest Absorbance peak at 260nm for ultraviolet light, by measuring the absorbance of nucleic acid samples at 260nm, the software can directly give the concentration of nucleic acid samples through the concentration calculation formula (Lambert-Beer's Law), and by referring to the ratios of A260/A280 and A260/A230, the purity of nucleic acid samples can be evaluated.

4.1.1 Sample Dose Requirements

Ultra-Micro Volume (recommended): 0.3-2μL
Cuvette Volume (recommended): ≥1000μL

4.1.2 Measurement Range

Modo ultramicro:

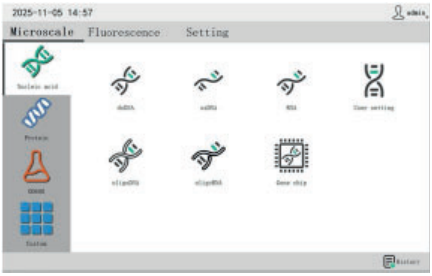
DS-DNA: 2-40000ng/μL
SS-DNA: 1.32-26400ng/μL
RNA: 1.6-32000ng/μL
Repeatability: Concentration 2-100 ng/μL: ±3ng/μL (dsDNA)
Concentration >100 ng/μL: ±3% (dsDNA)

Cuvette Mode:

Optical Path Length	Measurement Range (Abs)	dsDNA Concentration (ng/uL)
10 mm	0,004-1,6	0,2-80
5 mm	0,008-3,2	0,4-160
2 mm	0,02-8,0	1-400
1 mm	0,04-16	2-800

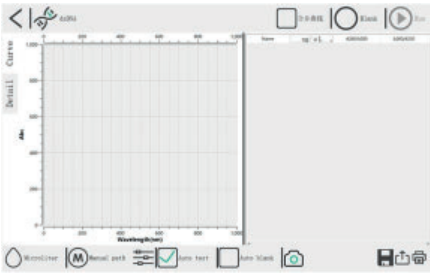
4.1.3 Measurement Settings

After powering on, select the default administrator account 'Username: admin Password: 123456', click 'Account Login' to enter the detection interface. The default setting is the ultra-micro module under the nucleic acid type interface, as shown in the figure below:



4.1.3.1 First select the item to be tested:
dsDNA, ssDNA, RNA, User Settings, oligoDNA, oligoRNA, Gene Chip.

4.1.3.2 Select dsDNA, ssDNA, RNA, and enter the detection interface. The settings and methods are the same. Taking dsDNA as an example, as shown in the figure below:



Click this button to switch between ultra-micro and cuvette modes.

Click this button to switch between automatic and manual optical path.

If manual optical path is selected, then choose this icon, in the pop-up dialog box select the required optical path (0.02/0.03/0.1/0.2/1.0mm).

Select this option (tick) to enable automatic detection function, that is, close the detection arm to enable automatic detection; if not selected (not ticked), the automatic detection function is disabled, that is, close the detection arm and need to click the detection button manually.

Select this option (tick) to enable automatic blank detection function, that is, close the detection arm to automatically detect blank; if not selected (not ticked), the automatic blank detection function is disabled, that is, close the detection arm and need to click the blank button manually.

Click this button to open the camera.

Click this button to save the current program. For more information, see “Data Storage”.

Export files to USB. You need to insert a USB flash drive before exporting.

Print button (optional).

Tick this box and then select the curves you want to merge for display.

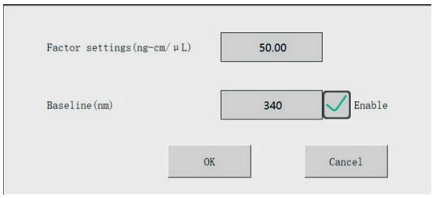
This button is the blank detection button. Before measuring the sample, you need to measure the blank first, and then measure the sample.

This button is the sample detection button.

Return to the previous level interface. If manually saved, the record will be saved with the default name.

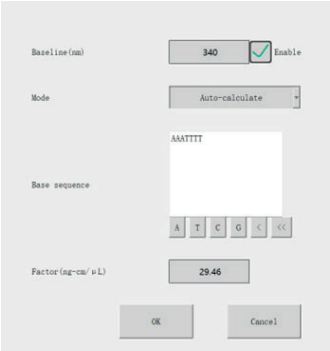
Notes:
1. Click Chart/Detailed Report to switch the display mode.
2. In the history record interface, double-click the sample name in the result display area to change it.
3. In the history record, the sample name cannot be changed again.

4.1.3.3 Select User Settings, enter the coefficient and tick whether to enable the reference wavelength in the pop-up dialog box, click OK to enter the detection interface. The settings and operation steps in the detection interface refer to the dsDNA detection interface.

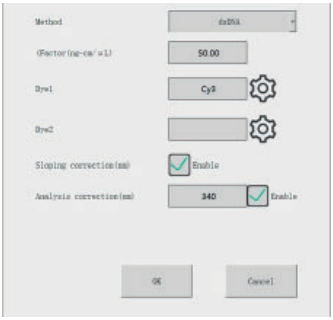


4.1.3.4 Select oligoDNA, oligoRNA to enter the setup interface, you need to select A/T/C/G or A/U/C/G keys, enter the nucleotide sequence, the software will automatically calculate the coefficient and display it in the coefficient area. After confirming the set parameters, click OK to enter the detection interface. For the settings and operation steps of the detection interface, refer to the dsDNA detection interface.

The following figure shows the setup interface for oligoDNA.



4.1.3.5 Select gene chip to enter the setup interface. The following figure shows the setup interface for the gene chip.



- Detection method: Select one of the following for detection: dsDNA, ssDNA, RNA, oligoDNA, oligoRNA, or user-defined.
- Coefficient: When user-defined, enter the relevant coefficient.
- Dye 1/Dye 2: You can choose one or two dyes.
- Dye unit: You can choose pmol/uL, uM, or mM.
- Dye slope correction wavelength (nm): You can choose whether to enable dye slope correction.
- Analysis wavelength correction wavelength (nm): The default is 340 nm. You can change the wavelength or choose whether to enable it.

After confirming the set parameters, click OK to enter the detection interface. For the settings and operation steps of the detection interface, refer to the dsDNA detection interface.

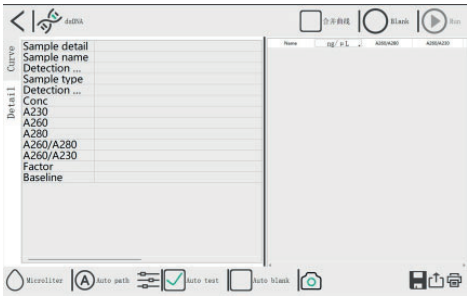
4.1.4 Detection steps

After completing the settings, start the detection in the detection interface. The ultra-micro steps are as follows:
1. Use a pipette to aspirate the nucleic acid solvent, drop it on the base, close the detection arm, and click “Blank”.
2. Use a tissue to wipe the solvent away.
3. Drop the sample onto the base, click “Detect” (if “Automatic detection” is enabled, there is no need to click the “Detect” button, the system will automatically detect).

4. After a few seconds, the detection results will be displayed, including the values and spectra.

The steps for cuvette detection: Refer to Section 2.2 for the selection and use of cuvettes.

4.1.5 Result display



4.1.5.1 The result display area will show: sample name, concentration (unit), A260/A280, A260/A230.
- 260/280 - The ratio of absorbance at 260 nm and 280 nm, this value is used to determine the purity of DNA and RNA. The purity of DNA is about 1.8, and the purity of RNA is about 2.0. If this ratio is too small, it indicates the presence of protein, phenol, or other contaminants, which have a significant absorbance at 280 nm.
- 260/230 - The ratio of absorbance at 260 nm and 230 nm, this is a secondary indicator of nucleic acid concentration. The ratio of pure nucleic acids is usually higher than the 260/280 ratio, generally between 1.8-2.2. If the ratio is low, it indicates that there are contaminants in the nucleic acids.

4.1.5.2 If you need to view detailed information about the results, select detailed report on the left panel, as shown in the following figure:

4.2 Protein module

The Zuzi Nanovolume Spectrophotometer can detect protein concentration. Utilizing the highest absorbance peak of protein at 280 nm in the ultraviolet light, for pure proteins, the concentration of the protein sample at 280 nm can be directly calculated by the software using the concentration calculation formula (Lambert-Beer's law), and the concentration of the protein sample can be obtained.

4.2.1 Sample dosage requirements

Ultra-micro volume (recommended): 0.3-2 μL
Cuvette volume (recommended): ≥1000 μL

4.2.2 Measurement range

Ultra-micro mode

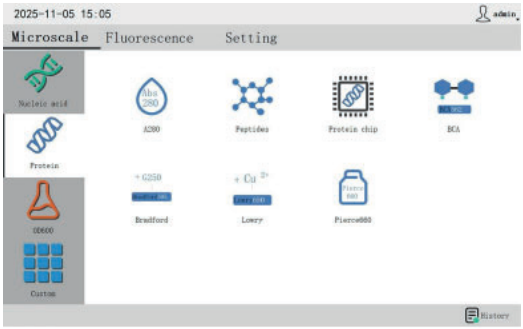
1 Abs=1 mg/mL: 0.04-800 mg/mL
BSA: 0.060-1194 mg/mL
HSA/MSA: 0.075-1509 mg/mL
Mouse IgG: 0.025-519 mg/mL
Human IgG: 0.03-584 mg/mL
Human IgE: 0.028-563 mg/mL
Lysozyme: 0.02-303 mg/mL
Repeatability: 0.0-3 mg/mL: ±0.09 mg/mL (BSA)
>3 mg/mL: ±3% (BSA)

Cuvette Mode

Path Length	Measurement Range (Abs)	Protein Concentration (BSA) (mg/mL)
10 mm	0,004~1,6	0,006~2,38
5 mm	0,008~3,2	0,012~4,77
2 mm	0,02~8,0	0,03~11,94
1 mm	0,04~16	0,06~23,88

4.2.3 Measurement Settings

Select the protein type on the main interface, as shown in the figure below:

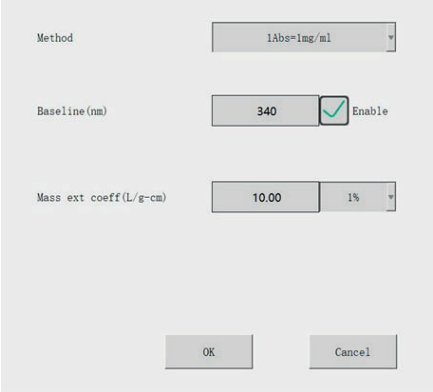


4.2.3.1 First, select the project to be tested: A280, peptide, protein chip, BCA, Bradford, Lowry, Pierce660.
Notes: 1Abs=1mg/ml is used to measure the protein with an absorbance of approximately 1.0 at a concentration of 1mg/mL and a path length of 10mm;
BSA, HSA, MSA, Mouse IgG, Human IgG, Human IgE, Lysozyme are used to measure pure bovine serum albumin, human serum albumin, mouse serum albumin, mouse immunoglobulin G, human immunoglobulin G, human immunoglobulin E, and lysozyme, respectively; BCA, Bradford, Lowry, Pierce660 are quantitative kits for protein measurement.

4.2.3.2 Select A280, enter the setting interface:
- If you choose to test with 1Abs=1mg/ml, BSA, HSA, MSA, Mouse IgG, Human IgG, Human IgE, Lysozyme, confirm that other parameters are correct, and then click OK to directly enter the testing interface.
- If the chosen testing method is molar extinction coefficient ε/molecular weight or mass extinction coefficient, it will directly connect to the sub-menu, input the molar extinction coefficient ε and molecular weight M, or mass extinction coefficient of the sample. After clicking the OK button, enter the testing interface. The settings and operation steps of the testing interface refer to the dsDNA testing interface.

The following figure shows the setting interface of A280.

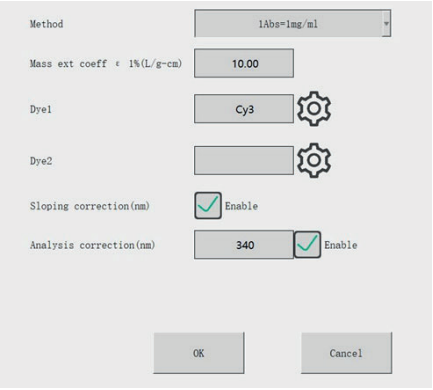
- Testing methods: 1Abs=1mg/ml, BSA, HSA, MSA, Mouse IgG, Human IgG, Human IgE, Lysozyme, molar extinction coefficient ε/mol wt, mass extinction coefficient.
- Reference Wavelength (nm): The default baseline wavelength is 340nm, and the baseline wavelength is enabled. You can change the baseline wavelength whether it is enabled.
- Mass Extinction Coefficient: Select 1% or 0.1%.



4.2.3.3 Select peptide, enter the setting interface. Select the testing method (A205, A215), confirm the parameters, and then click the “Confirm” button to directly enter the testing interface. The following figure shows the setting interface of peptide.

4.2.3.4 Select protein chip, enter the setting interface. The following figure shows the setting interface of the protein chip.

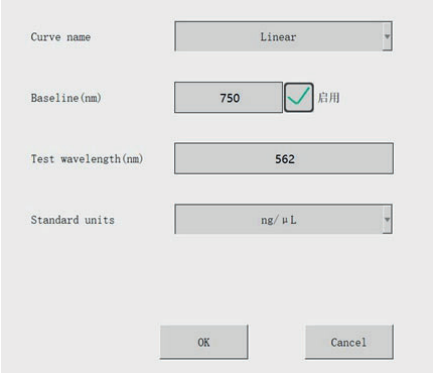
- Testing methods: 1Abs=1mg/ml, BSA, HSA, MSA, Mouse IgG, Human IgG, Human IgE, Lysozyme, molar extinction coefficient ε/molecular weight, mass extinction coefficient.



If the selected detection method is the molar extinction coefficient ε/molecular weight M or mass extinction coefficient, it will directly link to the sub-menu, and it is necessary to enter the molar extinction coefficient ε and molecular weight M, or mass extinction coefficient related to the sample. Other detection methods (1Abs=1mg/ml, BSA, IgG, Lysozyme, etc.) have default mass extinction coefficients and do not require input.
- Mass extinction coefficient: enter or display the 1% mass extinction coefficient.
- Dye 1/Dye 2: you can select one or two dyes.
- Dye units: you can choose pmol/uL, uM, mM.
- Dye slope correction wavelength (nm): you can choose whether to enable it.

Analysis wavelength correction wavelength (nm): the default is 340nm, you can change the wavelength or choose whether to enable it.
After confirming the set parameters, click OK to enter the detection interface. Refer to the dsDNA detection interface for the settings and operation steps of the detection interface.

4.2.3.5 BCA, Bradford, Lowry, Pierce660 are four protein kit methods, respectively suitable for BCA method, Bradford method, Lowry method, and Pierce660 method to determine protein concentration. When the user selects one of these methods, the instrument defaults to a fixed wavelength: BCA method at 562nm, Bradford method at 595nm, Lowry method at 650nm, and Pierce660 method at 660nm. A standard curve must be made before the sample measurement. Their setting methods are the same, and the BCA setting interface is used as an example below.



- Curve type: linear, interpolation, quadratic polynomial, cubic polynomial.
- Reference wavelength (nm): The displayed is the default reference wavelength, and the reference wavelength is enabled. You can also change the reference wavelength and choose whether to enable the reference wavelength; it is recommended to use the default reference wavelength and enable it.
- Detection wavelength (nm): The displayed is the detection wavelength, which cannot be changed.
- Standard solution unit: you can choose ng/μL, μg/μL, μg/mL, mg/mL, ng/mL.

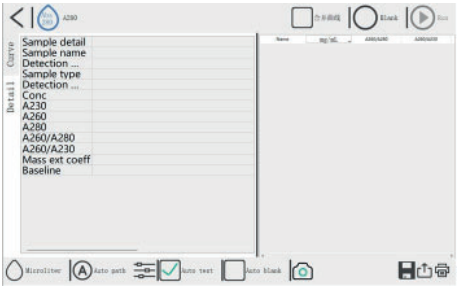
4.2.4 Detection steps

The operation of the A280 and peptide module is referred to as the nucleic acid detection steps (refer to 4.1.4).
The operation of the protein chip module is referred to as the gene chip detection steps (refer to 4.1.3.5).
The method of creating a new standard curve or selecting a known curve in the kit (BCA, Bradford, Lowry, Pierce660) is referred to as the standard curve method (refer to 4.4.3).

4.2.5 Result display

4.2.5.1 The result display area will show: sample name, concentration (unit), A260/A280, A260/A230.

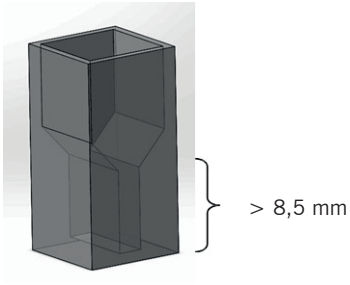
4.1.5.2 If you need to view the detailed information of the results, select Detailed Report on the left panel, as shown in the following figure of the A280 sample detail.



4.3 OD600 module (only Z-6500C model)

OD600 is used to measure cell broth, i.e., using a spectrophotometer to detect the light scattering of the cell suspension (only used in cuvette mode.)

4.3.1 Sample dose requirements



Because of the beam height, the height of the sample added to the cuvette must be more than 8.5mm. Please refer to the manufacturer's recommendations of the cuvette to determine the required sample volume.

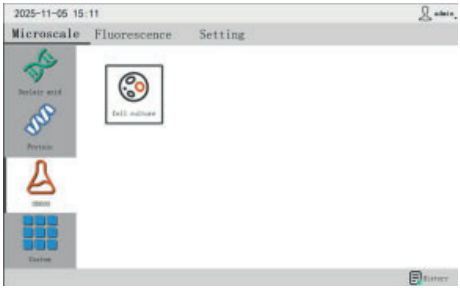
Optical path	Measurement range (absorbance)	Sample volume (constant cuvette)
10 mm	0,004~1,6	above 1000 µl
5 mm	1,6~3,2	above 500 µl
2 mm	3,2~8,0	above 200 µl
1 mm	8,0~16	above 100 µl

4.3.2 Measurement Range

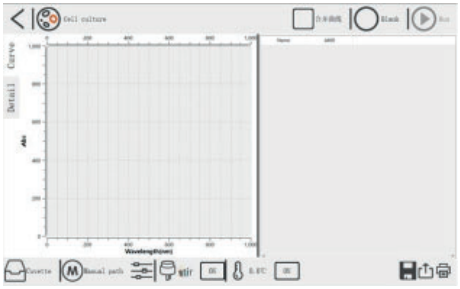
Absorbance range of cell culture: 0Abs ~ 1.6Abs
Repetibility: 0 Abs ~ 1,6 Abs : ±0,1

4.3.3 Measurement Settings

Select the OD600 type on the main interface, as shown in the figure below:



Click cell culture to enter the detection interface.



You can enter the cell culture settings. Absorbance calibration settings, other detection wavelength settings, cell count conversion coefficient settings, reference wavelength settings, and whether to start, etc., can be set according to user needs.

Click the icon to enter the settings interface, set the stirring intensity and stirring time; click the switch button to turn on/off stirring (optional).

4.3.4 Measurement Steps

1. Use an appropriate buffer as a blank control. Typically, pure water is used as a blank control. Insert the cuvette according to the optical path marked on the instrument and close the lid. Click ‘Blank’.
2. Remove the blank control, place the cuvette containing the test sample in a dark room, close the lid, and click ‘Detect’.
3. The detection results, values, and spectra will be displayed a few seconds later.
4. After the detection is complete, remove the cuvette, pour out the sample, and clean the cuvette.

4.4 Customization

The “Custom” module contains four detection items: Full Wavelength, Standard Curve, Colloidal Gold, and Kinetics. Users can select the corresponding detection item for detection according to their detection needs. The settings and detection methods are as described in the above document.

4.4.1 Detection Items

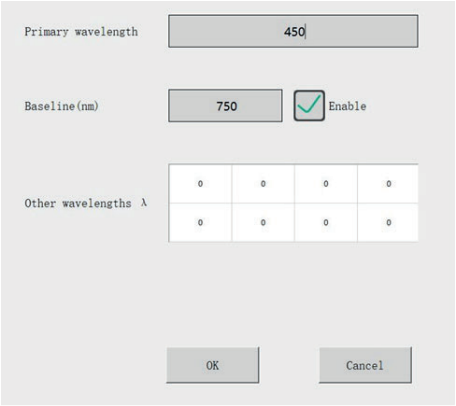
Select the Custom type on the main interface, as shown in the figure below:

4.4.2 Full Wavelength

Full wavelength detection includes ‘185-500’ and ‘greater than 500’ two modules. ‘185-500’ module: Detection wavelength range 185-500nm, use this module.
‘greater than 500’ module: Detection wavelength range greater than 500nm, use this module.

4.4.2.1 Select ‘185-500’, enter the settings interface.

Users can set the main detection wavelength, reference wavelength, and whether to enable the reference wavelength, and other 8 detection wavelengths. Click OK to enter the detection interface.



4.4.2.2 Select ‘greater than 500’, enter the settings interface.

Users can set the main detection wavelength, reference wavelength, and whether to enable the reference wavelength, and other 8 detection wavelengths. Click OK to enter the detection interface. The detection wavelength and reference wavelength entered must be greater than 500nm.

4.4.2.3 Detection Steps

After the settings are completed, start the detection in the detection interface. The following are the steps for ultra-micro detection:

1. Use a pipette to aspirate the blank and drop it on the base, close the detection arm, and click 'Blank'.
2. Use a tissue to wipe away the solvent.
3. Add the sample to the base and click 'Detect' (if 'Automatic Detection' is enabled, there is no need to click the 'Detect' button, the system will automatically detect).
4. The detection results, values, and spectra will be displayed a few seconds later.

Cuvette detection steps: Refer to section 2.2 for the selection and use of cuvettes.

4.4.2.4 Display of Results

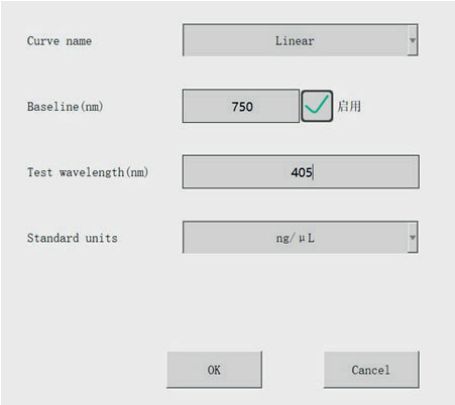
The result area will display: sample name, absorbance at the main detection wavelength, and absorbance at other detection wavelengths.

The detailed report will display: sample details, sample name, detection time, sample type, detection platform, wavelength and corresponding absorbance, reference wavelength and its absorbance value.

4.4.3 Standard Curve Method

4.4.3.1 Select the standard curve method and enter the settings interface.

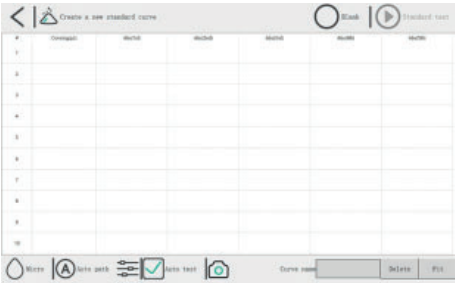
Users can select curve types: linear, interpolation, quadratic polynomial, cubic polynomial; whether to enable reference wavelength; detection wavelength, the wavelength setting range is 190-910nm; standard material unit: ng/μL, μg/μL, μg/mL, mg/mL, ng/mL.



4.4.3.2 Standard Curve Selection

Select a saved standard curve: select the required standard curve and click confirm to enter the detection page.

Create a new standard curve: click the '+' in the upper right corner to enter the new standard curve interface, as shown in the figure below.



- Select ultra-micro volume/colorimetric plate mode, automatic path length/manual path length.
- Enter the sample concentration in the 'Concentration' list,
- Absorbance detection: each concentration can have up to 5 parallel samples, and data with deviations can be deleted by clicking on the corresponding data and selecting 'Delete'.
- After the detection is completed, enter the 'Curve Name', click 'Fit', and the standard curve is successfully created.

4.4.3.3 Detection Steps
Select 'Curve Name' to enter the detection interface and follow the subsequent operation steps of ultra-micro volume detection (refer to 4.1.4).

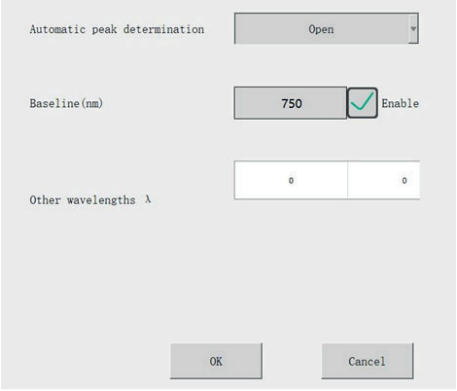
4.4.3.4 Detection Results
The result area will display: sample name, concentration, absorbance at the corresponding wavelength, and status (in or out).
Note: 'in' indicates within the curve range; 'out' indicates not within the curve range.

The detailed report will display: sample details, sample name, detection time, sample type, detection platform, concentration and corresponding wavelength absorbance, standard curve name, standard curve formula, reference wavelength, and status.

4.4.4 Gold Nanoparticles

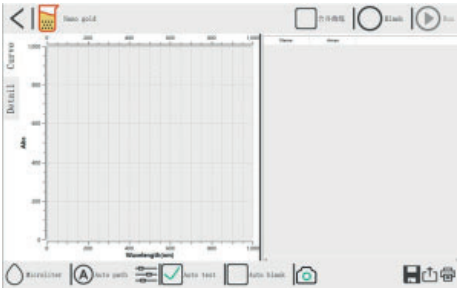
4.4.4.1 Select gold nanoparticles and enter the settings interface. If automatic peak detection is turned off, the default detection wavelength is 525nm (can be changed); if automatic peak detection is turned on, the software will automatically detect the peak between 500-550nm and display it.

Users can set whether to enable automatic peak detection, main detection wavelength (when automatic peak detection is turned off), up to 2 other detection wavelengths, reference wavelength, whether to enable reference wavelength, and other detection wavelengths.



4.4.4.2 Detection Steps

After the settings are completed, start detection in the detection interface. Refer to the dsDNA module for the operation method.



4.4.4.3 Detection Results

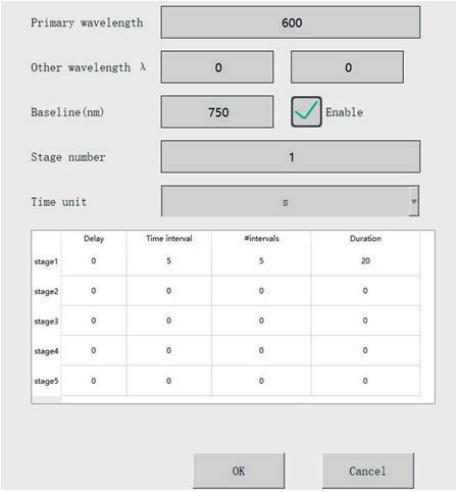
The result area will display: sample name, Amax/A (set wavelength), and absorbance at other wavelengths.

The detailed report will display: sample details, sample name, detection time, sample type, detection platform, Amax/A (set wavelength), corresponding maximum peak, reference wavelength, and its absorbance.

4.4.5 Kinetics (only Z-6500C model)

4.4.5.1 Select kinetics and enter the settings interface. Kinetic detection is only applicable to colorimetric plate mode.

Users can set the main detection wavelength, 2 other detection wavelengths, reference wavelength, whether to enable it, the number of stages (1-5), time unit (seconds, minutes), delay per stage, time interval, number of detections, and the automatically calculated duration. Click OK to enter the detection interface.



4.4.5.2 Detection Steps

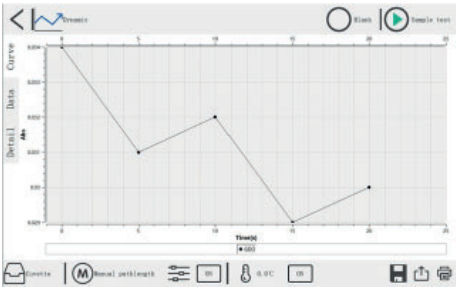
After completing the settings, start the detection on the detection interface. During the detection process, you can choose to pause or stop.

Cuvette detection steps: Refer to section 2.2 for the selection and use of cuvettes.

4.4.5.3 Detection Results

Curve: Shows the kinetic spectrum of up to three wavelengths.

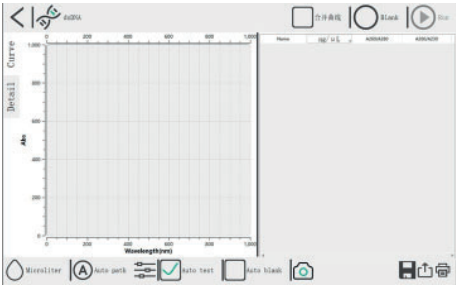
Data: Displays the sample name, stage, detection time, and absorbance corresponding to the wavelength in a list form.
Detailed report: Sample details, sample name, detection time, sample type, detection platform, cuvette path length, current stage number, detection time, absorbance corresponding to the wavelength, reference wavelength, and absorbance of the reference wavelength.



Note: When the number of stages is ≥2, if the delay time per stage is 0, the first data of each stage will overwrite the last data of the previous stage.

5. DATA STORAGE

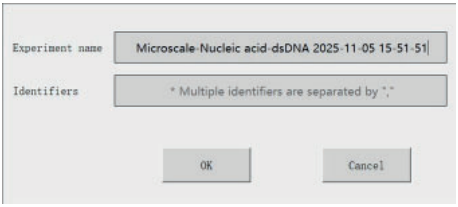
5.1 Save, Export and Print



5.1.1 Save

1) In the detection interface, click  , a save interface will pop up.

Double-click the dialog box to bring up the keyboard. The default format for the experiment name is detection mode-detection type-detection module-time-number, and the experiment name cannot be duplicated; identifiers can be used in notes and search.
Note: After clicking 'Save' and confirming, a history record will be generated. If you click 'Save' again, the displayed.
Interface will still be the default, not the previous naming. Confirming again will generate another history record.

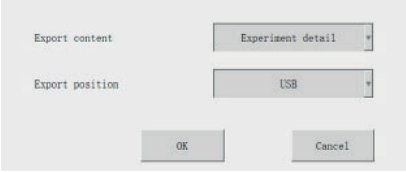


2) If you do not click the 'Save' button and directly click  , the program will be automatically saved with the default naming.

5.1.2 Export

1) Exporting in the detection interface can only be done for a single sample and is mainly used for exporting the original data and images of a single sample.
- Export to USB: Insert a USB flash drive in advance, select the detection results of the required sample in the detection interface, click , an export page will pop up. Users can choose to export 'Experiment Details/Original Data/Images', and select 'USB' as the export location. After confirming, the interface will prompt 'Operation completed'. Return to the main interface, click Safe ejection , a prompt indicating successful operation will appear, and then you can remove the USB flash drive.
- Export to Local: This means exporting to the instrument's memory, which can be used for file transfer within the local area network.

2) History Record Interface: Can export the results of 1 or more experiment groups. Suitable for batch export of experiment details and original data, not suitable for batch export of images.
- Export to USB: Insert a USB flash drive in advance, select 1 or more experiment groups to be exported from the left list area, click the icon on the interface, and select 'Experiment Details/ Original Data' for export. Select 'USB' as the export location, confirm, and the interface will prompt 'Operation completed'. Return to the main interface, click Safe ejection , a prompt indicating successful operation will appear, and then you can remove the USB flash drive.
- Export to Local: This means exporting to the instrument's memory, which can be used for file transfer within the local area network.



5.1.3 Print (Optional)

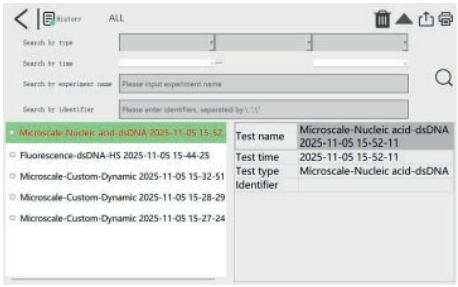
1) In the detection interface, you can only print the results of a single sample. First click the button to save the experiment group, then select the required sample to print, click , and after printing is completed, the interface will prompt 'Operation completed'.

2) In the history record interface, the printout is the results of the entire experiment group. Select the experiment group to be printed from the left list area, click the icon , the printer will start printing, and after printing is completed, the interface will prompt 'Operation completed'.

3) Printing Paper: Thermal printing paper with a width of 57mm.

5.2 History Records

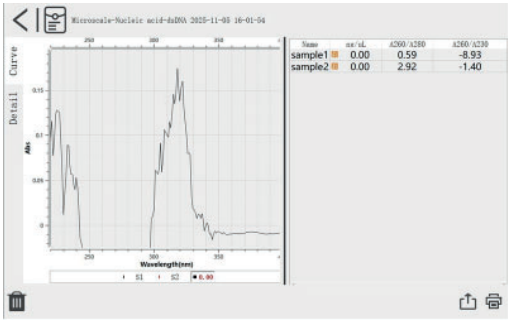
Click History in the main page to enter the history record interface to query and retrieve historical records. The history record interface is divided into a search box, a list area, and a detail area.



- Search box: Can be searched by detection type, detection time, experiment name, and identifier; some fields are optional.
- List area: Displays the historical records, which can be selected. Clicking on a record will make it red font, and double-clicking on the name will jump to the record.
- Detail area: Displays the details of the red font records in the list area, including experiment name, experiment time, detection type, and identifier. The experiment name can be changed again by double-clicking on it.

	Return to the previous interface.
ALL	Select all records in the current list area; click again to deselect all.
	Delete the selected records.
	Open/close the search box.
	Click to start the search.
	Export the selected experiment group.
	Print the currently selected historical records, refer to 5.1.3 (optional).

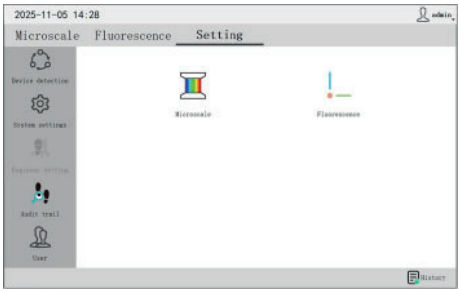
Selecting a specific experiment group in the list area will jump to the following records:



6. SETTINGS

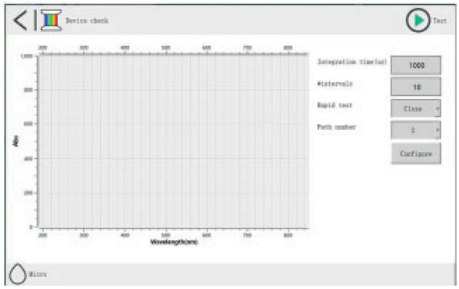
6.1 Device Detection

Click ‘Settings’ - ‘Device Detection’ to set the instrument. This module is for engineers to check the settings, please do not modify the parameters at will.



6.1.1 Ultra-micro

- Click ‘Test’ to view the instrument’s spectral intensity (commonly used for engineers’ after-sales use).
- Ultra-micro rapid detection can be turned on or off as needed.



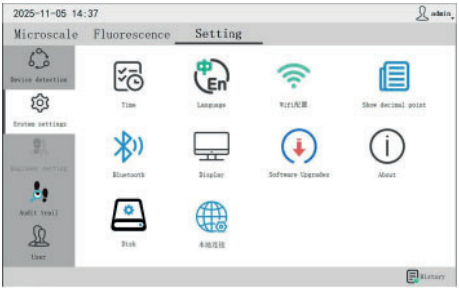
Off: All five optical paths will be detected, with the five optical paths being 1mm, 0.2mm, 0.1mm, 0.03mm, and 0.02mm.
On: Under the premise of being turned on, the number of optical paths can be selected as needed.
Selecting ‘2’ represents selecting detection optical paths of 1mm and 0.2mm (default). Selecting ‘3’ represents selecting detection optical paths of 1mm, 0.2mm, and 0.1mm.
- Clicking on ‘Ultra-micro Mode’ at the bottom left can switch to ‘Cuvette Mode’.

6.1.2 Fluorescence (not applicable to Z-6500 and Z-6500C models)

Click to detect to view the fluorescence intensity (commonly used for engineers’ after-sales use).

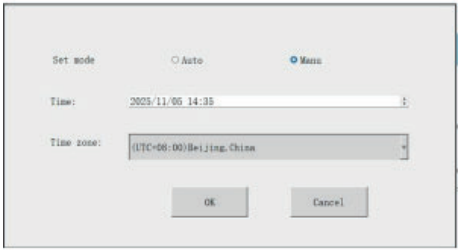
6.2 System Settings

Click ‘Settings’ - ‘System Settings’ to perform time, language, network settings, decimal point display, Bluetooth, display, software update, and other settings.



6.2.1 Time

Click time, select manual to set time and time zone.



6.2.2 Language

The software supports eight languages: Chinese, English, French, German, Spanish, Russian, Japanese, and Korean. Click language to switch languages. The change takes effect after restarting after changing the language.

6.2.3 Software Update

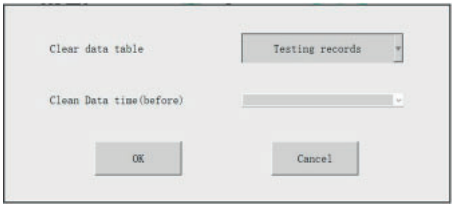
Insert the USB flash drive (with the upgrade package) in advance, click the upgrade button, and a prompt 'Upgrading...' will appear on the interface. After the upgrade is complete, a prompt 'Upgrade completed' will appear. After the upgrade is complete, restart the instrument.

6.2.4 About

You can learn about the software version number and other instrument information by clicking 'About'.

6.2.5 Disk Management

After the instrument has been used for a while and the memory is nearly full, you can clear the memory and release space by selecting the 'Disk Management' option.



1) First, save the experimental data in advance, and in the interface, select 'Detection Records' or 'SD Card' in the 'Clear Data Items' selection.

2) Please select the data clearing time. In the calendar that appears, select the date to be cleared, and the instrument will delete the relevant records before that date.
Note: Save the experimental data in advance before deleting records.

7. SHUTDOWN

You can directly turn off the power switch on the instrument.

8. APPENDIX

Detection Module	Range	Status
dsDNA: High sensitivity	Core range: 1ng/mL-500ng/mL	in
	Extended range: 0.5ng/mL-1ng/mL, 500ng/mL-600ng/mL	extend
dsDNA: Broad range	Core range: 0.01ug/mL-5ug/mL	in
	Extended range: 5ug/mL-10ug/mL	extend
1×dsDNA: High sensitivity	Core range: 1ng/mL-500ng/mL	in
	Extended range: 0.5ng/mL-1ng/mL, 500ng/mL-600ng/mL	extend
1×dsDNA: Broad range	Core range: 0.01ng/uL--5ng/uL	in
	Extended range: 5ng/uL--10ng/uL	extend
RNA: High sensitivity	Core range: 25ng/mL-500ng/mL	in
	Extended range: 20ng/mL-25ng/mL, 500ng/mL-1000ng/mL	extend
RNA: Broad range	Core range: 0.1ug/mL-5ug/mL	in
	Extended range: 0.05ug/mL-0.1ug/mL, 5ug/mL-6ug/mL	extend
RNA: Extended range	Core range: 1 ng/uL--50 ng/uL	in
	Extended range: 0.5ng/uL-1ng/uL, 50 ng/uL-100 ng/uL	extend
microRNA	Core range: 5ng/mL-500ng/mL	in
	Extended range: 2.5ng/mL-5ng/mL, 500ng/mL-750ng/mL	extend
RNA Integrity & Quality	IQ value: 1-10	/
Oligo: ssDNA	Core range: 5ng/mL-1000ng/mL	in
	Extended range: 1ng/mL-5ng/mL, 1000ng/mL-1200ng/mL	extend
Protein	Core range: 1.25ug/mL-25ug/mL	in
	Extended range: 1ug/mL-1.25ug/mL, 25ug/mL-26ug/mL	extend
Protein: Broad range	Detection range: 0.1mg/mL~20mg/mL	in