Labotronics

Multi-Mode Microplate Reader

LB-10MMM

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Index

1. Safety Measures

1.1 Important information for safe use

Users should have a clear main idea on how to use this instrument before operating, kindly read this manual carefully before operation.

Any improper operation may cause injury or electric shock. Kindly read the manual carefully and operate safely according to the guidelines.

This instrument is intended to be used in Scientific Research only.

Instruments should not be discarded at will. When discarded, the product must be sent to an appropriate facility for recovery and recycling.

1.2 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 affect the scheduled use life of the Instrument, and the protection provided.

Before using the device, read the Manual carefully. These units are designed for use in laboratory environments. The device must be used by skilled personnel with the appropriate training.

Warning: Biological contamination!! All samples for testing, quality control, and calibration are regarded as infectious, and any part contact with samples will also need to be treated as infectious. Kindly wear gloves when operating this device.

Warning: Avoid injury. Keep your body or any part of your body away 15cm (or more) from the instrument when running.

Except for the part which can be opened by the user according to the manual, the user is forbidden to disassemble the instrument.

Before powering on, guarantee the voltage used should be according to the voltage needed, and the rated load of the electrical outlet should not be lower than the demand.

If the electric line is damaged, you should replace it with the same type. You should ensure there's nothing on the electric line and you should not put the electric line in the ambulatory place.

The Instrument should be put in a place of dry, less dust, no water and no sun or strong lamp. What's more, the place should have good ventilation, no corrosive gas or strong disturbing magnetic field, far away from central heating, camp stove and other hot resource.

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

Pull the connector plug from the socket at once in the following cases:

- There is some liquid flowing into the Instrument.
- Drenched or fire burned.
- **Abnormal operation:** Such as abnormal sound or smell.
- Instrument dropping or outer shell damaged.
- In case of Malfunction.

2. Introduction

Multi-Mode Microplate Reader LB-10MMM offers absorbance, fluorescence, and luminescence detection mode. Features PID temperature control technology and 10-inch touch screen interface with LCD control buttons. With advance software it ensures convenient data collection and analysis of multiple algorithm functions.

3. Features

- Offers multiple microplate technologies and detection modes
- High quality detection performance with accurate and reliable analysis
- Flexible and changeable upgrade compatible unit for best experience
- Incubation with PID temperature control technology for stability
- 10-inch touch screen interface with LCD control buttons
- Advance software with android system for convenient operation
- Code scanning function for easy data processing and import
- Supports up to 384 well microplate for flexible operation
- Ideal unit to meet various application requirements

4. Specifications

<table>
<tr><td>Model No.</td><td>LB-10MMM</td></tr>
<tr><td>Microplate capacity</td><td>6 to 384 microplates</td></tr>
<tr><td>Shaking mode</td><td>Linear, annular, double annular</td></tr>
<tr><td>Incubation temperature</td><td>RT + 4 to 45°C</td></tr>
<tr><td>Temperature uniformity</td><td>± 0.5°C @37°C</td></tr>
<tr><td>Detection modes</td><td>Absorbance, Luminescence, Fluorescence</td></tr>
<tr><td>Absorbance</td><td>
<table>
<tr><td>Wavelength range</td><td>200 to 1000 nm, 1 nm step</td></tr>
<tr><td>Wavelength accuracy</td><td>2 nm</td></tr>
<tr><td>Wavelength repeatability (SD)</td><td>0.2 nm</td></tr>
<tr><td>Half width</td><td>< 2.5 nm</td></tr>
<tr><td>Measuring range</td><td>0 to 4 OD</td></tr>
<tr><td>Resolution</td><td>0.0001 OD</td></tr>
<tr><td>Accuracy @ 450 nm</td><td>96-precision mode: ± (1.0 %+ 0.003 Abs) @ (0.0 to 2.0 Abs]</td></tr>
<tr><td></td><td>±2.0 % @(2.0 to 3.0 Abs]</td></tr>
<tr><td>Repeatability @ 450 nm</td><td>CV < 1.0 % or SD < 0.003 fast (0.0 to 3.0 Abs)</td></tr>
<tr><td></td><td>CV < 0.5 % or SD < 0.003 accurate (0.0 to 3.0Abs)</td></tr>
</table>
</td></tr>
</table>

	Linearity @ 450 nm: R2 ≥ 0.999 @ (0.0 to 3.0 Abs) Stray light: 0.1% @ 220 nm Light source: Xenon lamp Detector: PD
Luminescence	Wavelength detection range: 200 to 850 nm Detection limit: 15 amol/hole 5 amol/hole (Photon PMT) Linear range: 6 logs Cross talk: ≤ 0.005 % Detector: PMT
Fluorescence	EX Wavelength range: 200 to 1000 nm EM wavelength range: 270 to 850 nm Filter: 3 groups: EX470/EM525, EX523/EM564, EX624/EM692 Detection limit: 13:00 PM Linear dynamic range: 6 logs

	<table><tr><td>Reading</td><td>Top reading mode</td></tr><tr><td>Light source</td><td>Xenon lamp</td></tr><tr><td>Detector</td><td>PMT</td></tr></table>
Display	10-inch color touch screen display
Storage	10 GB
Power supply	AC 100 to 240 V, 50 to 60 Hz
Dimension (W×D×H)	420×550×386 mm
Packaging dimension (W×D×H)	800×780×800 mm
Net weight	33 kg
Gross weight	70 kg

5. Applications

Multi-mode microplate reader is used for quantification of different biological and chemical assays across cytology, biotechnology, medical, research, forensics, pharmaceuticals etc.

6. Instrument Introduction

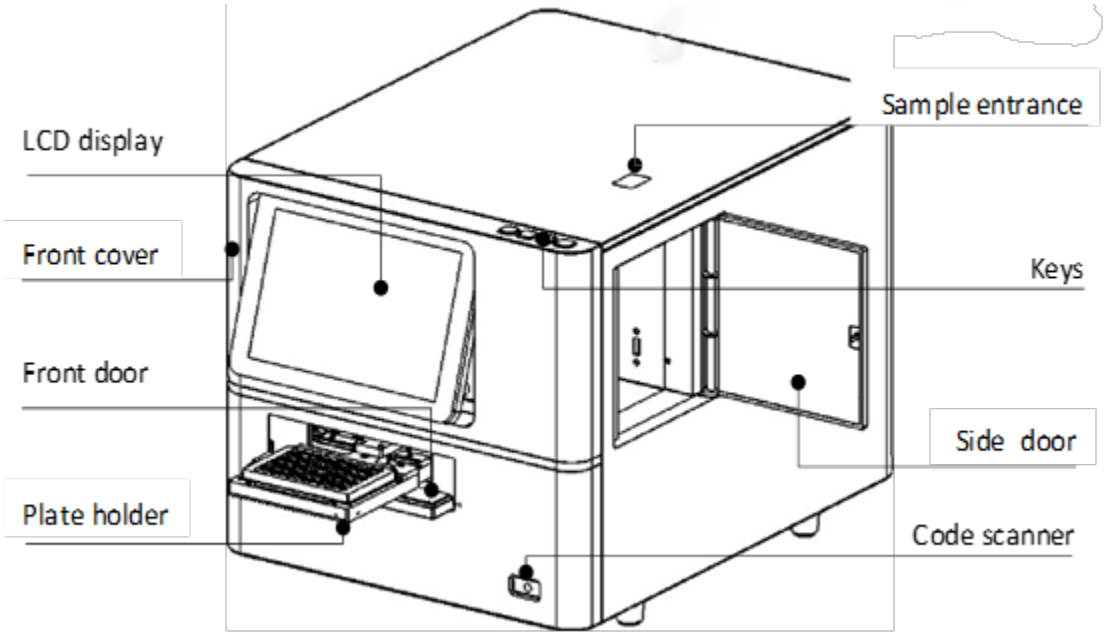


Figure-1

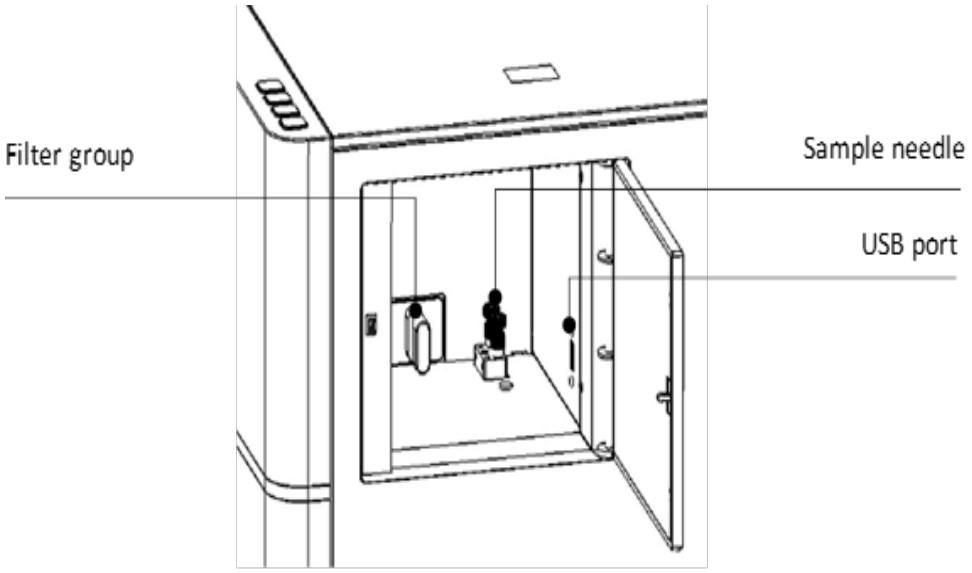


Figure-2

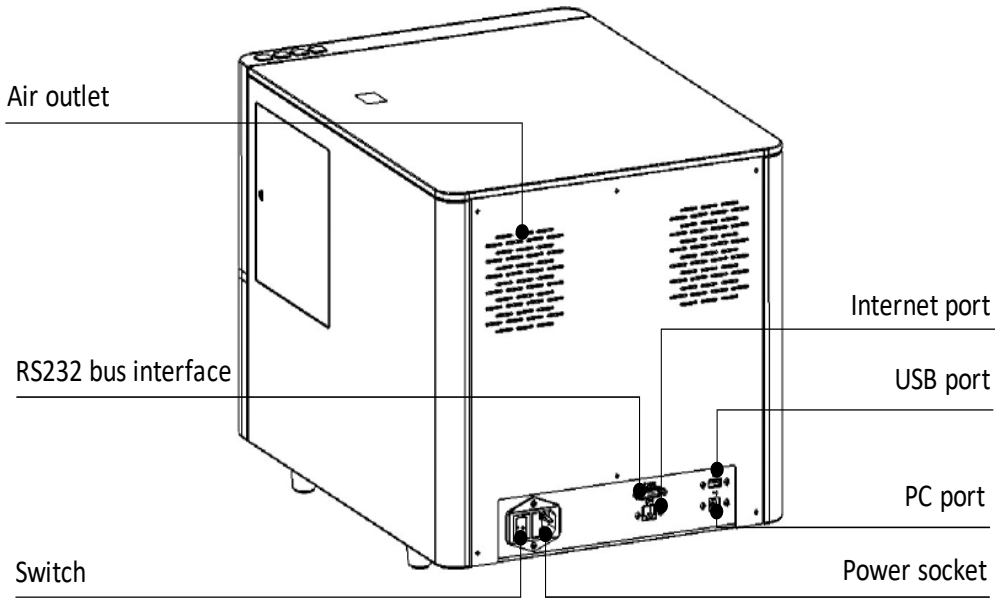

Air outlet
Internet port
RS232 bus interface
USB port
PC port
Switch
Power socket

Figure-3

7. Installation

7.1 Opening check

The **LB-10MMM** is thoroughly tested before shipping, but kindly check again when you receive the instrument. Note if the following damage exists:

1) The outer package is upside down or damaged.
2) The outer package has no obvious moisture stains.
3) The outer package has marks of impact.
4) The outer package has signs of being opened.

If the outer packing is intact, kindly open the packing case and check it in the presence of the authorized staff:

- According to the packing list, confirm that all ordered accessories have been included.
- Check the instrument's appearance for any damage.

7.2 Installation requirement

1) **Working condition:** Locate the instrument on a flat dry and clean worktable. When placed on the table, keep 15cm space for the back, left and right sides to enable putting or connecting wires; keep the front side with enough space for plate holders in and out.
2) **Working environment:**
   a. Clean air free from corrosion steam or smoke.
   b. Temperature should be within the range of +10°C ~ +40°C.
   c. Relative humidity should be within the range of 10% ~ 80% to avoid condensation.

   Note: Keep the instrument away from destructive gas or liquid!

7.3 Installation steps

1) Place the instrument and package lightly on the operation site, unpack the carton, take out the upper package, and then take out the instrument and place it on the work table.
2) Open the side door and press the button on the head of the locking pin with your finger to release the locking. Keep the pressing state, and upward to pull out the locking pin. Then plug the dustproof plug from the accessories to the installation hole of the locking pin, to play the role of dustproof and light avoidance.

   Note: The locking pin plays a limiting role in ensuring that the microplate bracket is in a fixed state during the instrument transportation. Kindly pull out the locking pin before the instrument is used.

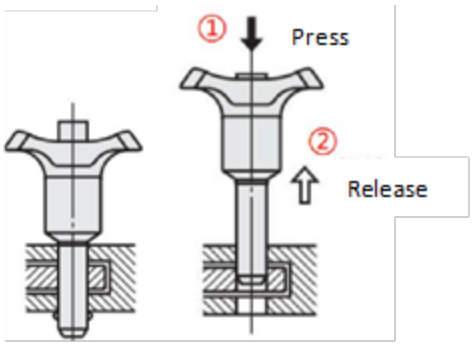


Figure-4

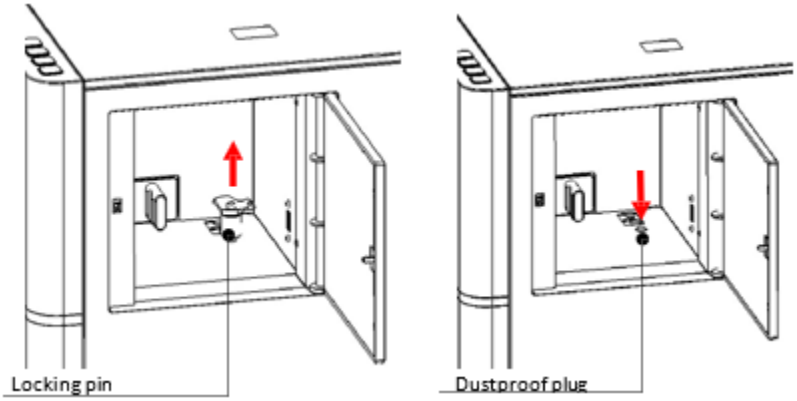


Figure-5

3) Switch the **"I/O"** button to "O" at the back of the instrument. Take out the power cable, insert the plug into the power socket at the back of the instrument, and then connect the other end of the power cable to the power supply with the voltage of AC100 ~ 240V.
   Warning: Don't connect the instrument to the power socket without a ground wire.

8. Software Operations

8.1 Start the instrument

After installing the instrument according to installation, turn on the power switch to start the instrument and enter the self-checking interface as **Figure 6**. At this time, the instrument will automatically complete the self-check and calibration. If there is a fault alarm, kindly refer to the Troubleshooting.

Figure-6 Self-checking interface

The user login interface will appear after self-checking, see **Figure 7**.

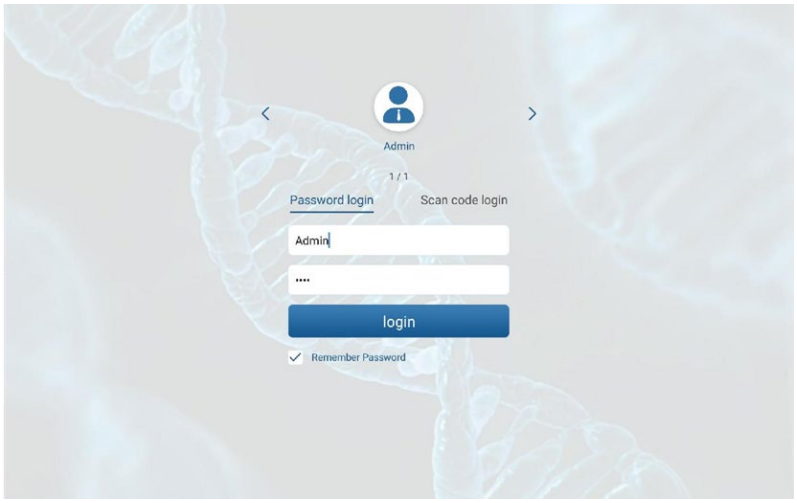


Figure-7 Login interface

Lists the permissions of the three types of users

Name	Permissions content	Remark
Admin	User administrator permissions, all permissions related to user operations. Users cannot log in after forgetting the password;	Unique account, fixed name, initial password 0000
Advanced user	Administrator defined by Admin, the function operation is the same as that of Admin, or the permissions and functions of the administrator are less than or equal to that of Admin. The permissions and functions operation range are defined by Admin. The permissions are fixed before delivery and the password is reset by Admin when forgotten.	Manage account group
User	Can only operate, cannot do anything else, the lowest level of permission, current permission is fixed before delivery.	User Account Group

Note:
Kindly keep the manager's password to avoid unnecessary losses.

Click Account to enter the Account-Admin interface, see **Figure 8**. By default, the change password interface is displayed, see **Figure 9.**

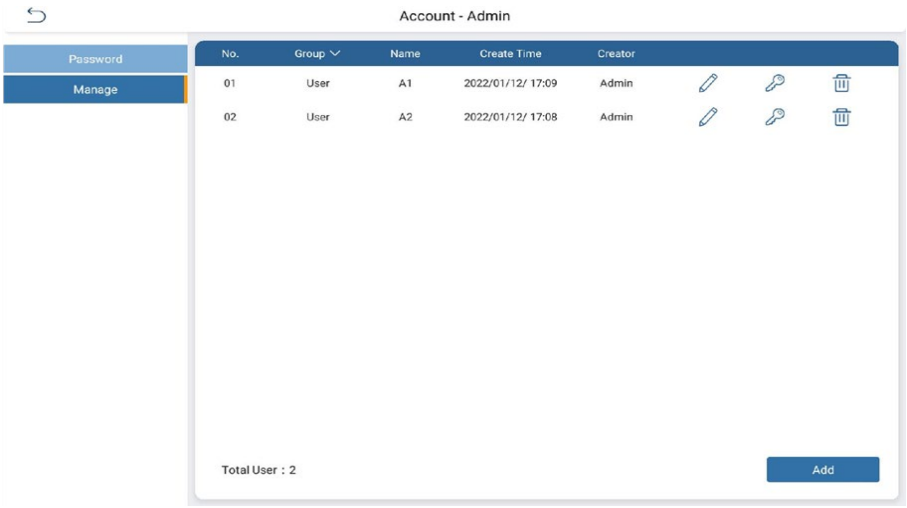


Figure-8 Account-Admin interface

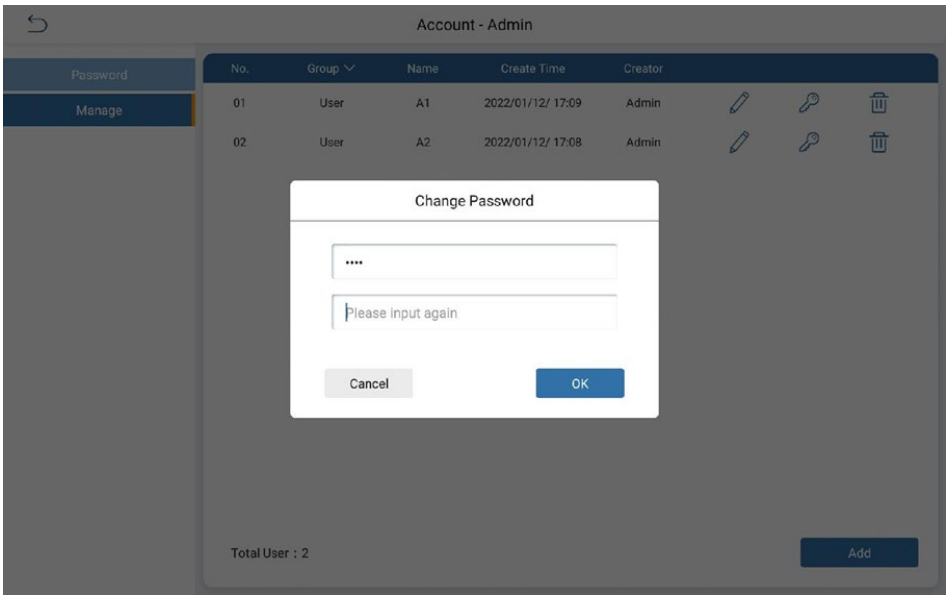


Figure-9 Change password interface

After you select a user and enter the password, the system's main interface is displayed, as **Figure 10**.

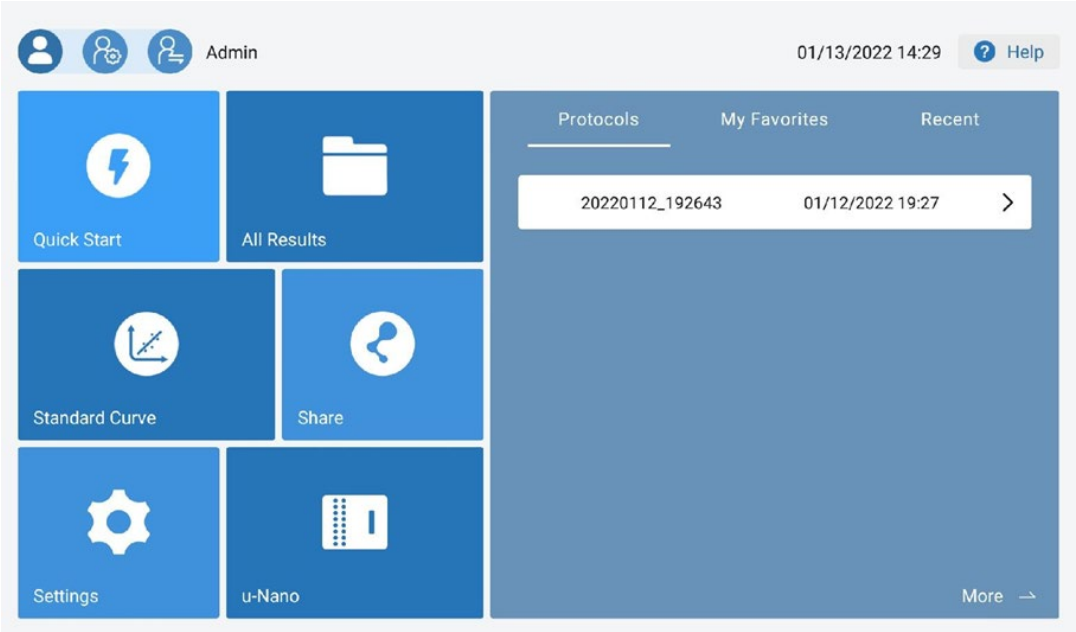


Figure-10 Main interface

In this case, you can log out by pressing the button in the upper right corner, return to the user interface, and log in again.

The files in this software are divided into three categories: protocol file (P), result file (R) and standard curve file (SC). The table below lists the file functions on the main interface.

File Functions

Name	Type	Function
All results	Key	There is only the result file (R), which contains the running data
Standard curve	Key	There is only the standard curve file (SC), which is saved from the results
Share	Key	It includes protocol (P), result (R), standard curve (SC), Tab switch
Protocol	Key	There is only the protocol file (P), which includes layout, setting, and algorithm parameters, without running data; Click **"More"** to view all protocol files;
My favorites	Key	There are only protocol files (P) in it. Click "More" to view all protocol files
Recent	Key	There may be either protocol (P) or results (R), which refers to the most recent operation of the 6 protocol/result files, in chronological order, with the most recent time at the top, with no "More" button.

8.2 Protocol settings

Click **"Quick Start"** on the main interface to pop up a new protocol selection box. Users can select protocol parameters according to experimental requirements, as **Figure 11**.

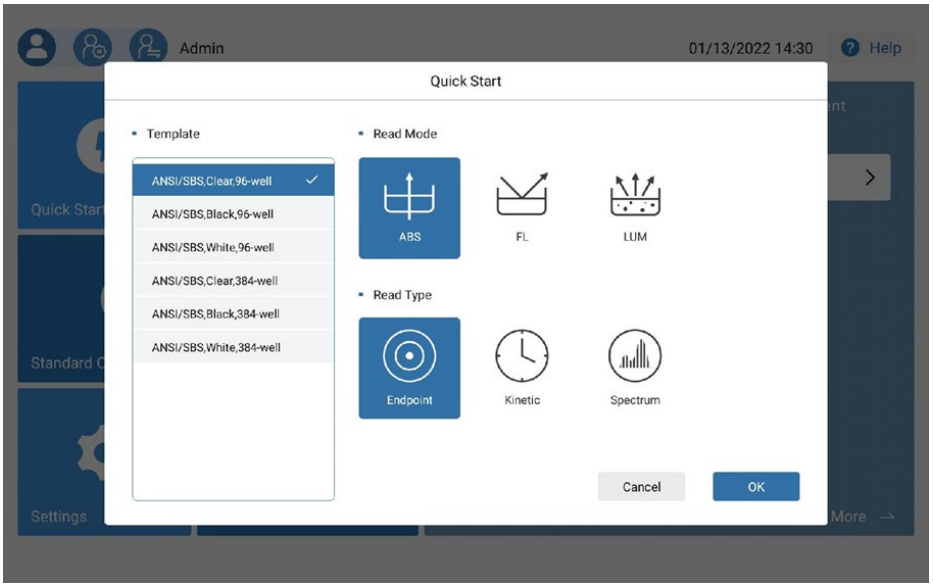


Figure-11 Quick start interface

After selecting protocol parameters, click **"OK"** to enter the protocol interface, as **Figure 12**. It mainly consists of a title bar, main display area, menu bar and option bar.

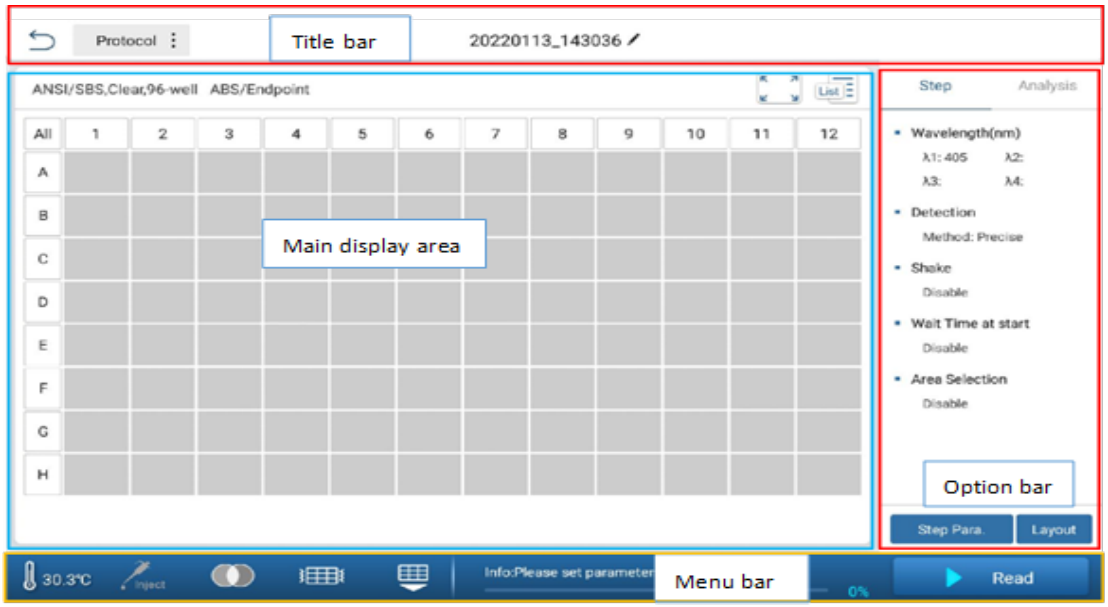


Figure-12 Interface framework

There are three read modes: ABS, FL, and LUM. The ABS mode has three read types: EndPoint, Kinetic, and Spectrum. FL and LUM only have two read types: EndPoint and Kinetic. The basic difference between Endpoint and Kinetic is that Endpoint only takes one read, whereas the Kinetic is a cycle read, with a minimum of two reads and a maximum of 99. Where the specific number of reads is determined by the setting of time reading in Kinetic, the spectrum is read in the wavelength range of 200-1000nm according to specified rules. The table below shows the relationship between read modes and read types.

Relationship between read modes and read types

	EndPoint	Kinetic	Spectrum
ABS	1. General 2. Shake 3. Advanced 4. Area Selection	1. General 2. Detection 3. Shake 4. Advanced 5. Area Selection	1. General 2. Shake 3. Advanced 4. Area Selection
FL			
LUM	1. Injector 2. General 3. Shake 4. Advanced 5. Area Selection	1. Injector 2. General 3. Detection 4. Shake 5. Advanced 6. Area Selection	

8.2.1 Title bar

The title bar is used to return to the previous page, protocol operations, name and modify files, as **Figure 13**.

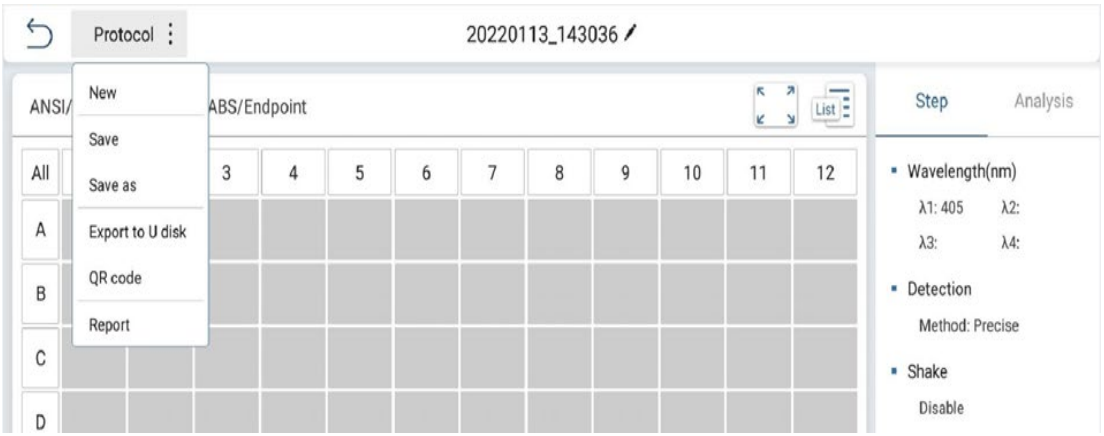


Figure-13 Title bar

The below table describes the functions of the title bar
Functions of the title bar

Name	Functions
	Click and a prompt box will pop up asking the user whether to exit the current interface; click **"OK"** and another prompt box will pop up "Do you want to save the current protocol?"; click **"OK"** to save and exit; click **"No"** to exit without saving.
	Click to display the input box to modify the current name. The input box contains a maximum of 15 characters, including upper/lower case letters, digits, and symbols "-" and "_".
Protocol	Click to display operation options, including New, Save, Save as, Export to U disk, QR code.
New	Click and the selection box as **Figure 11** will pop up.
Save	Click to save the current protocol/results.
Save as	Click to pop up the save protocol name input box, if the current protocol has been executed, then the pop-up box with another "without data" option.
Export to U disk	Click to determine whether to insert the U disk first, if no, it will prompt, if yes, the selected protocol will be exported to the U disk.
QR code	Click to generate a QR code for the data on the left of the standard curve.

Click the **"modify name"**, and the input box for modifying the protocol name will pop up, as **Figure 14**. The red text indicates that the protocol has a repeated name; otherwise, it will not be displayed.

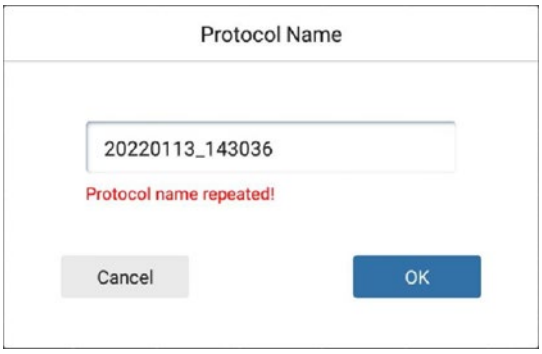


Figure-14 Input box for protocol name

8.2.2 Main display area

The main display area consists of two parts: The operation bar and the display area. The default display area is a 96-well plate, consisting of 8 rows (A-H) × 12 columns (1-12). Click A-H to select all the wells in the row, click 1-12 to select all the wells in this column, and click the blank block above A to select all the wells of the plate. The template includes 96-well plates and 384-well plates. The table below lists the relationships between microplates and their names. There is no zoom function if the microplates are smaller than 96 well.
The operation bar can view Kinetic or Spectrum data, run logs, and the data list.

Relationships between microplate and name

Well plate	Name
96 well plate	ANSI/SBS, clear,96-well
	ANSI/SBS, black,96-well
	ANSI/SBS, white,96-well
384 well plate	ANSI/SBS, clear,384-well
	ANSI/SBS, white,384-well

The content of the main display area varies according to the type of the current interface. **Figure 15** shows the finished interface when the protocol is running Endpoint.

Figure-15 Protocol finished interface endpoint

After the protocol is finished, the heat diagram is shown in **Figure 16**. Only the Endpoint has a heat diagram.

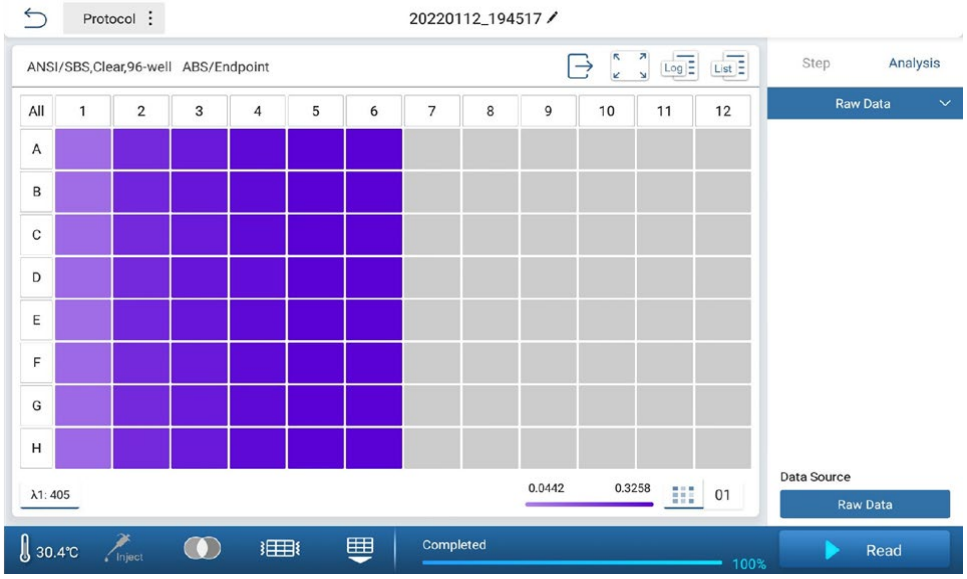


Figure-16 Heat diagram interface after the protocol is finished

Figure 17 shows the interface when the protocol is finished when Kinetic or Spectrum is running.

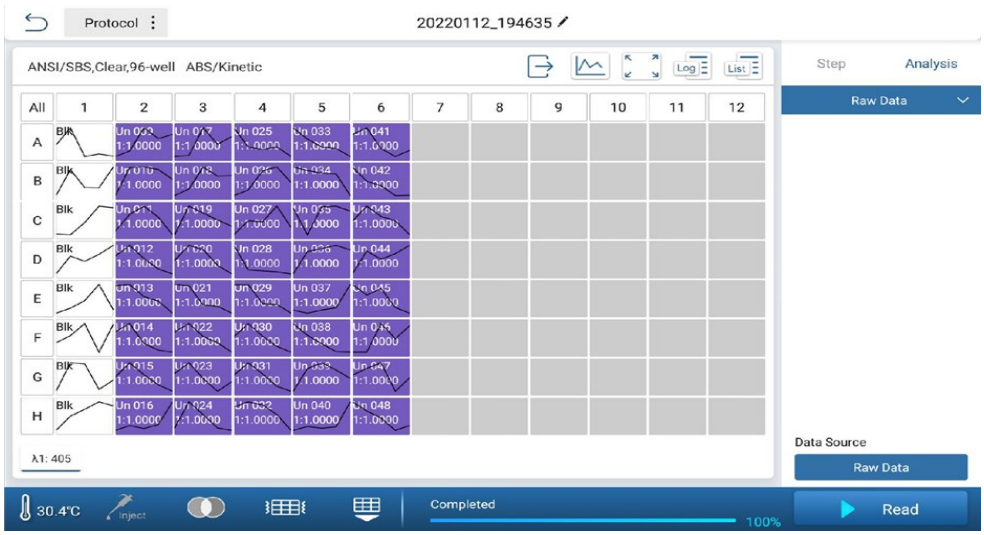


Figure-17 Protocol finished interface (Kinetic)

8.2.3 Option bar

In the options bar, switch between step and analysis at the top, and parameter display, set, and layout buttons at the bottom, as **Figure 18**.

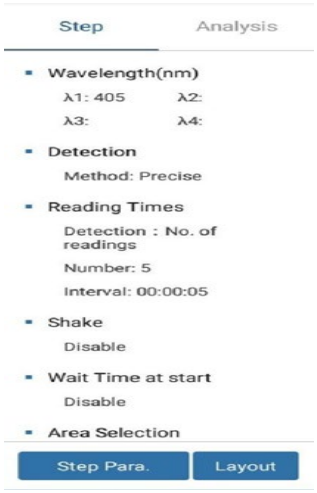


Figure-18 Option bar

It is mainly used to set the parameter information of the protocol running. There are three read modes: ABS, FL and LUM. Three read types for ABS: EndPoint, Kinetic and Spectrum, while the other two only have two read types: EndPoint and kinetics.

8.2.4 Menu bar

The lower part is the menu bar, as **Figure 19**. Including incubator, inject, filter, shake, plate in/out, running information, and Read button.

Figure-19 Menu bar

Menu bar function

Name	Function
	Click to pop up the incubator setting box.
	Click to pop up the inject setting box.
	Click to pop up the filter setting box.
	Click to execute shaking, lasting 1 second.
	When the plate of the current instrument is out, click the plate into, otherwise click plates out.
	Click to start reading, and the protocol becomes the stop button.

When you click the incubator button, the incubator temperature input box and keyboard will pop up. Enter the incubator temperature, as **Figure 20**.

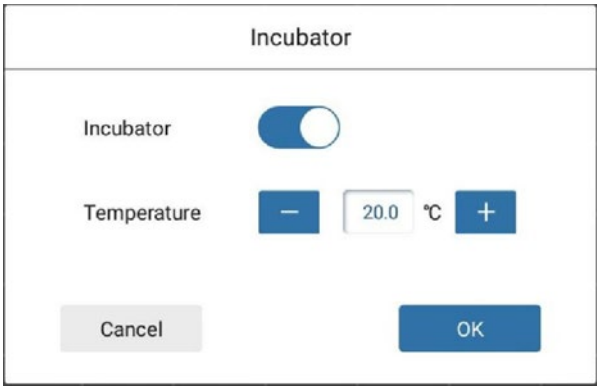


Figure-20 Enter incubator temperature

The incubator function is a global variable. The Table below lists the specific functions of the incubator setting interface.

Incubator interface function

Name	Function
Incubator	On or off incubation, off by default.
Temperature	Input the incubation target temperature, ranging from RT+4℃to 45℃.
OK	Click to save the current Settings.
Cancel	Return button.

If the instrument does not have an automatic sample injector module(optional), the button is gray and unavailable. When the injector button is available, click to pop up the injector interface, as **Figure 21** and **Figure 22**.

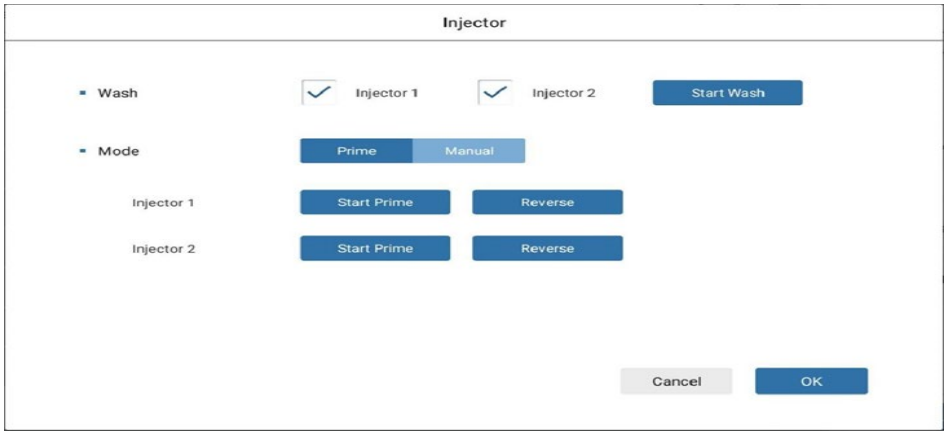


Figure-21 Injector interface 1

Figure-22 Injector interface 2

Functions of injection interface

Name	Function
Wash	Select at least one injector to be washed.
Mode	Select the injector mode, Prime or Manual is optional, default Prime. In Prime, the volume of wash and reverse is fixed.
Start Wash	Click to start washing.
Start	Click to start the injection.
Reverse	Click to reverse part of the liquid.

When you click the filter button, the filter setting interface pops up, as **Figure 23**, shows the information about the current filter and the filter that can be replaced.

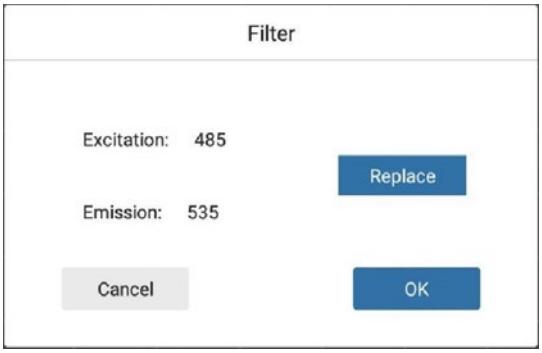


Figure-23 Filter interface

Functions of filter interface

Name	Function
Excitation	Display the wavelength of excitation light.
Emission	Display the wavelength of emission light.
Replace	Click the instrument scanning module to scan the code. The user can scan the QR code of the new filter, and the interface will display the parameters of the new filter. Users can manually replace the filter.

The Microplate Reader has four physical buttons, namely "Start", "Stop", "Plate in/ Out", and "LCD" to flip the display. The physical buttons are only available on the plate interface.

8.3 Step parameter setting

8.3.1 ABS general setting

The general setting interface of Endpoint and Kinetic for ABS is the same, as in **Figure 24**. On the left is the check box to confirm whether to enable the wavelength. If it is enabled, the corresponding graph box will be displayed. The graph box will change according to the input color. Enter range is 200-1000 nm, λ1 defaults to 405nm, λ2 to 450nm, λ3 to 492nm, and λ4 to 630nm, user can change the wavelength as required. Detection is divided into fast and precise, the default precise mode

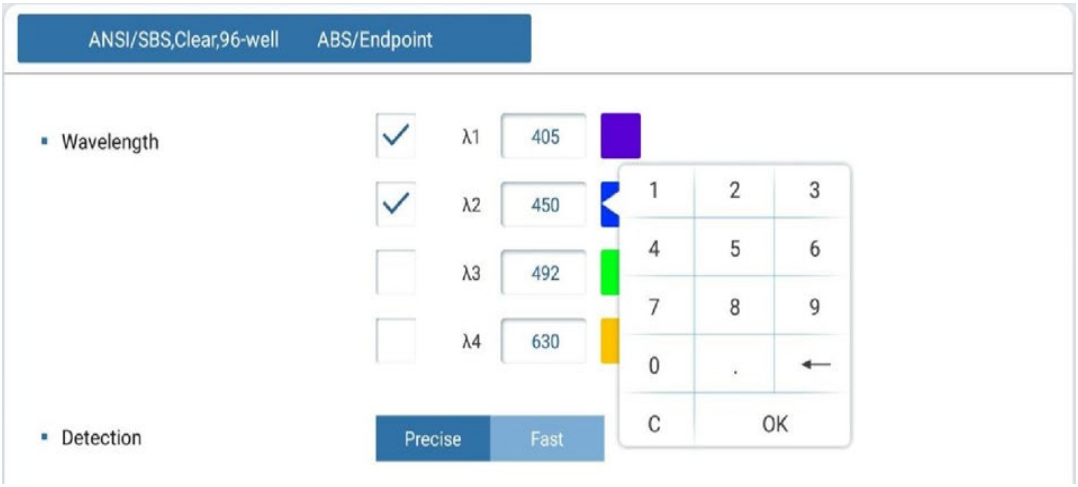


Figure-24 General setting interface of endpoint and kinetic for ABS

The general setting interface of the spectrum for ABS is shown in **Figure 25**. Enter the start wavelength and end wavelength. The color of the graph box on the right changes according to the wavelength. The default value is 200nm for the start and 300nm for the end. The value ranges from 200 to 1000nm. The default step is 10, it can be changed as required.

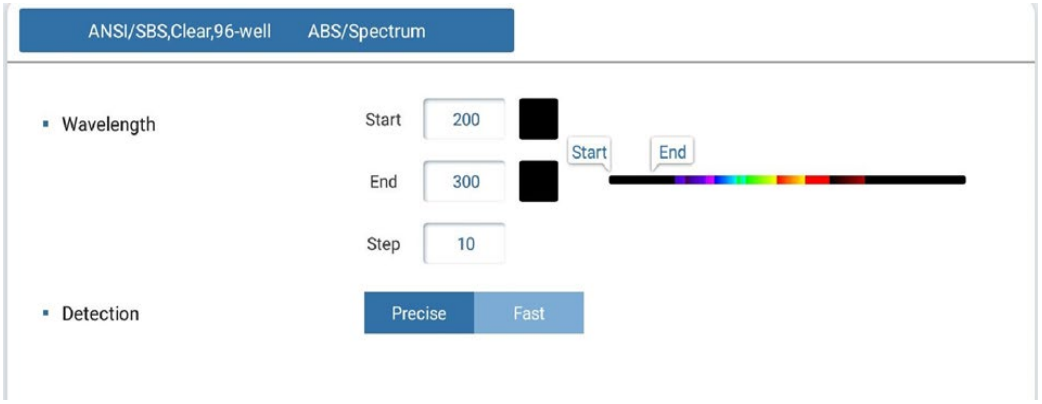


Figure-25 The general setting interface of spectrum for ABS

8.3.2 FL general setting

The general setting interface of Endpoint and Kinetic for FL is the same, as in **Figure 26**.

Figure-26 The general setting of endpoint and kinetic for FL

Function of the general setting interface of endpoint and kinetic for FL

Name	Function
Wavelength	Display the excitation wavelength EX and emission wavelength EM of the instrument, which cannot be changed.
Detection	Can select Precise, Normal or Fast, the default is Precise. When selecting Precise, it needs to enter the number of times, the default is 20, and the range is 1-150.
PMT Gain	Optional Automatic/Low/Medium Low/Medium High/High, default automatic.
Settle Time	Settle time can be entered, default 150ms, range 5-999ms.
Integration Time	Integration time can be entered, default 40us, range 5-1000us.

8.3.3 LUM general setting

The general setting interface of Endpoint and Kinetic for LUM is the same, as in **Figure 27**, and **Figure 28**. **Figure 29** shows the interface for selecting no reagent/reagent 1/ reagent 2 for the injector, and **Figure 28** shows the interface for selecting both reagents for the injector.

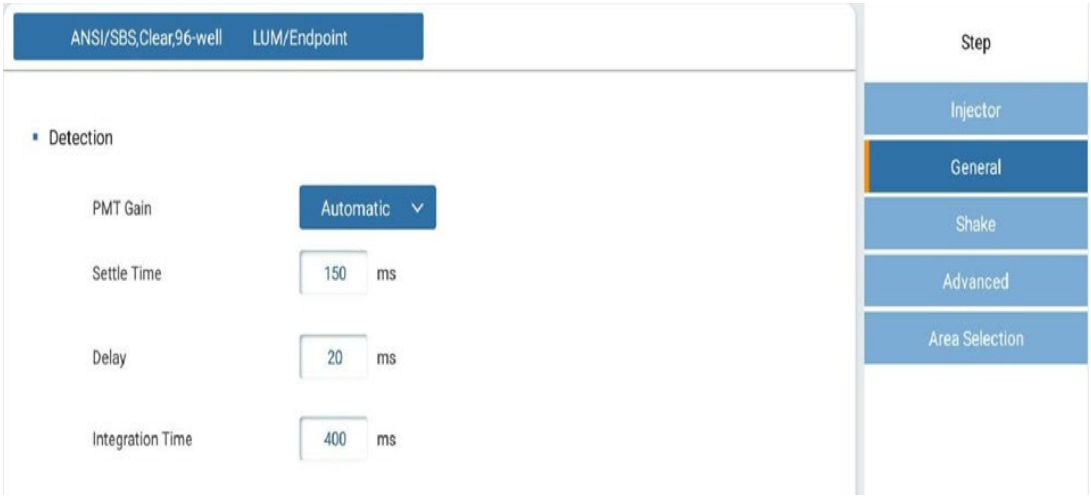


Figure-27 The general setting interface 1 of endpoint and kinetic for LUM

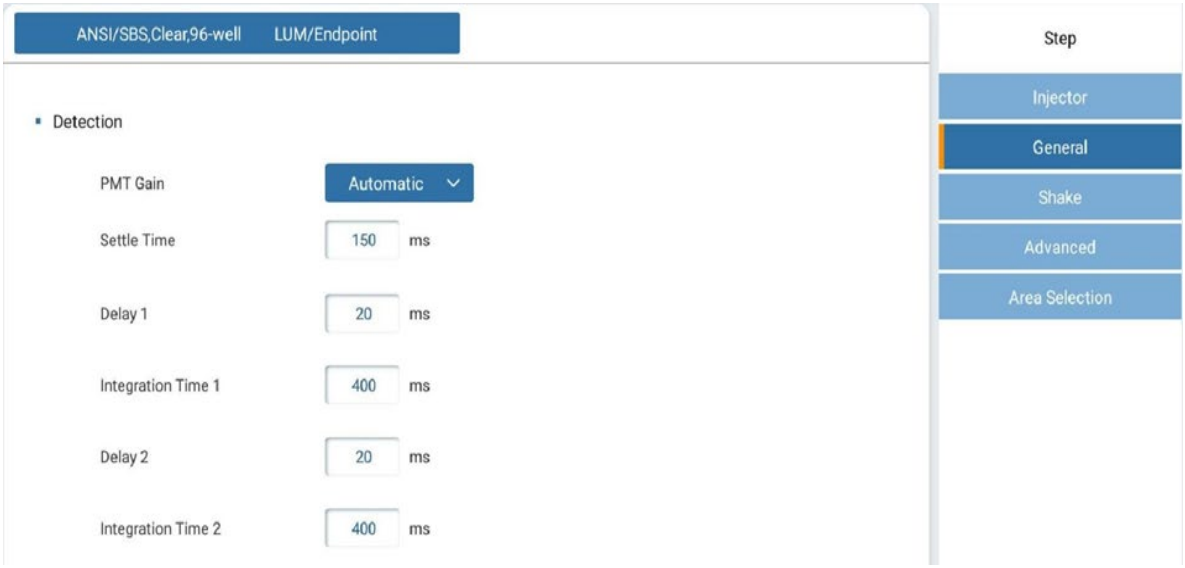


Figure-28 The general setting interface 2 of Endpoint and Kinetic for LUM

The injector is specific to the LUM, as **Figure 29** to **Figure 30**. Input injector volume, default is 100μL. When both injectors are selected, the injector integrals are divided into injector volume 1 and injector volume 2, ranging from 5 to 500. Input injector speed, default 200uL/s. When both the injectors are selected, the injector speed is divided into injector speed 1 and injector speed 2, ranging from 5 to 500.

Figure-29 Injector reagent 1

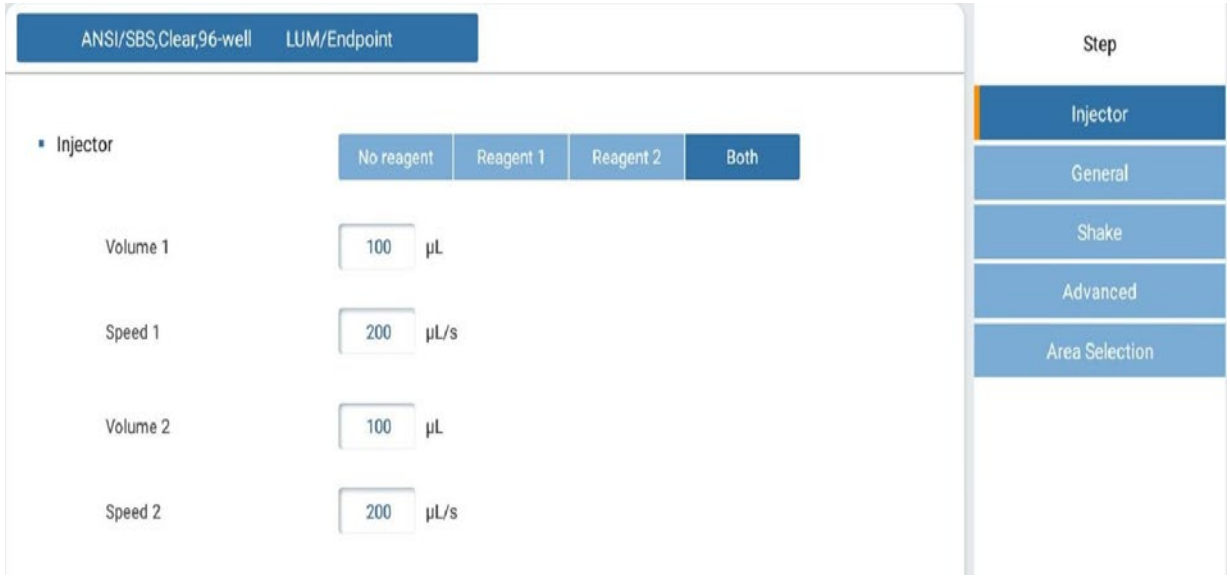


Figure-30 Both injector reagents

8.3.4 Read setting

Click **"Read"** to enter the Kinetic parameter setting interface. The Kinetic Settings are divided into total time and number of readings, as shown in **Figure 31** and **Figure 32** respectively. When the total time is selected, the calculation of reading number: Rounding the value of time/ interval and then adding 1.

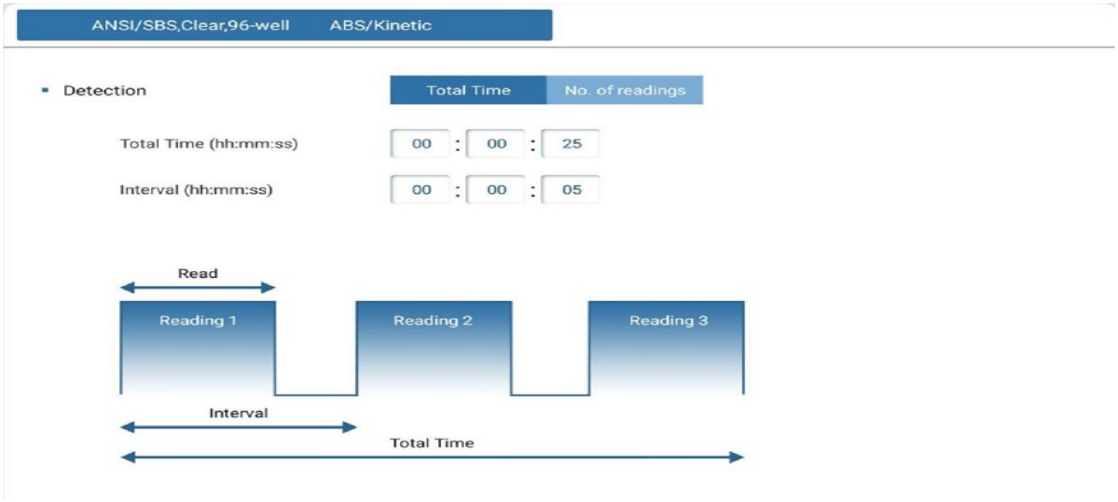


Figure-31 Kinetic-Total Time setting

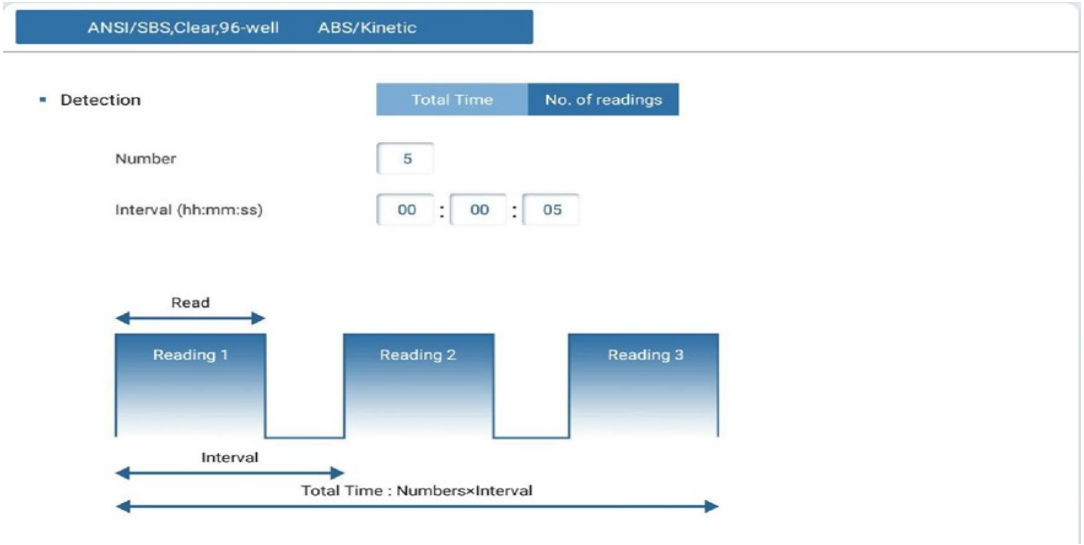


Figure-32 Kinetic -No. of readings setting

The table below lists the parameters to be set.

The function of Kinetic option columns

Name	Function
Total Time/No. of readings	Enable the total time to control the Kinetic cycle or according to the total number.
Total time	The maximum time is 99:59:59.
Number	The maximum number is 99.
Interval	The interval time between Kinetic, the maximum is 99:59:59.

8.3.5 Shake

Click Shake to enter the shake interface, as shown in **Figure 33**.

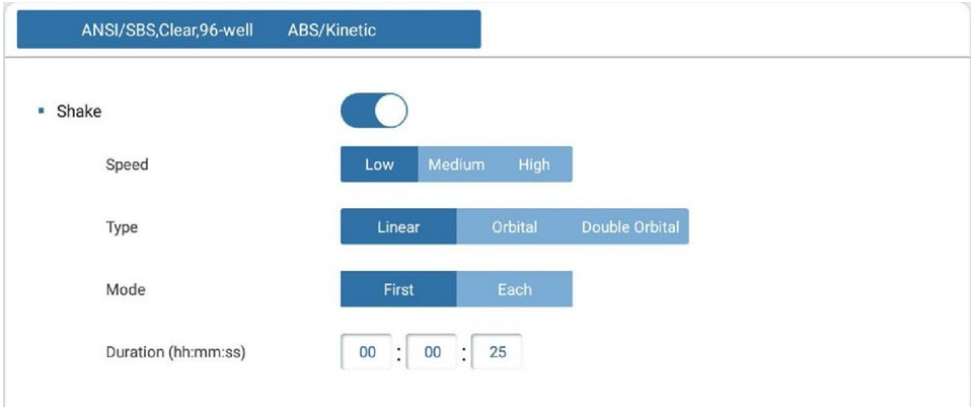


Figure-33 Shake interface

Default shake settings

Name	Default settings
Shake	The default value is off.
Speed	The default value is not display. When shake is on, the default value is low. It can select low/medium/high.
Type	The default value is linear. Linear/Orbital/Double Orbital is optional.
Mode	The default value is first time. It can select first time/each time. Only Kinetics has this function, Endpoint and spectrum do not have this function.
Duration	When the shake is on, the default value is 00:00:25. The value ranges from 00:00:01 to 23:59:59.
Way	The default is plate, plate/well can be selected; Only LUM has this function, and ABS, and FL do have not this function.

8.3.6 Advanced

Click the advanced button to enter the advanced setting interface. Currently, the sub-option is closed. The advanced screen is displayed, as shown in **Figure 34**. Wait Time at the start is on by default when LUM and the rest are off by default. For LUM, the default time is 00:01:00, ranging from 1min to 30min. For others, the default time is 00:00:25, ranging from 00:00:01-01:59:59.

Figure-34 Advanced setting interface

8.4 Layout

Click the **"Layout"** button in the sidebar to switch to the layout interface, as shown in **Figure 35**.

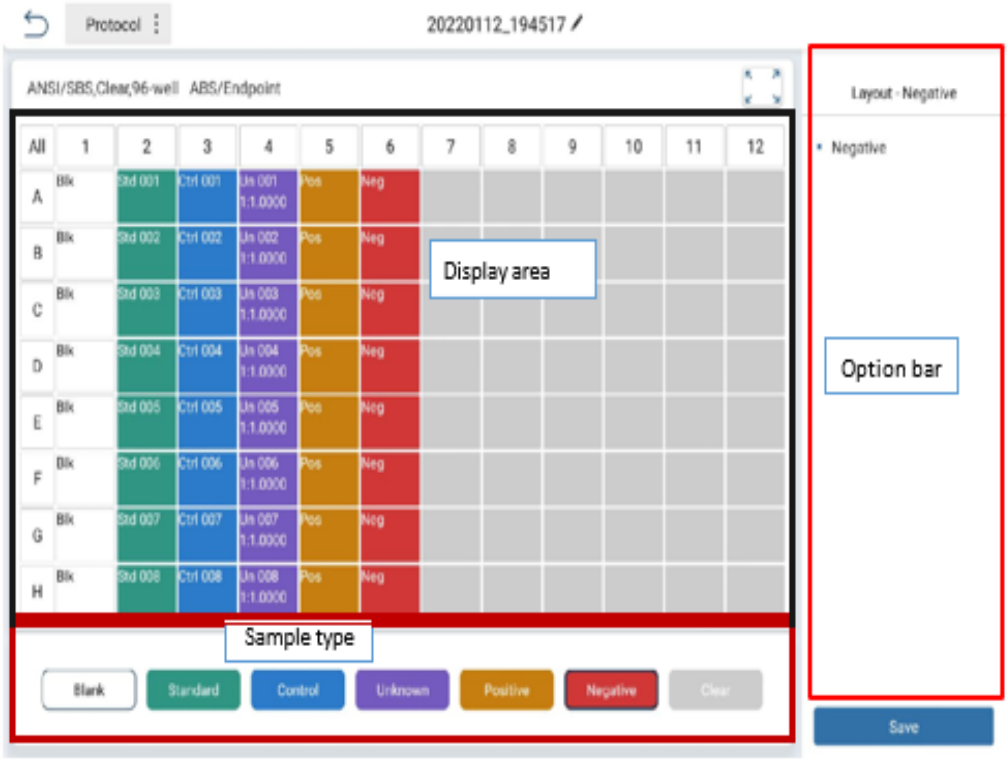
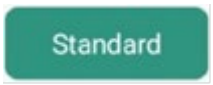
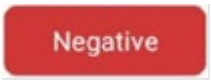
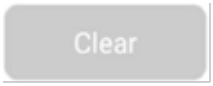


Figure-35 Layout interface

Different colors correspond to different options, and different options include different operational functions. Sample types mainly include blank, standard, quality control, unknown, negative, positive and clear. These seven types are in single mode and displayed with stroke display after selection.

Sample types of function

Name	Function	Icon
Blank	Blank is replicas (replicates). By default, the name corresponds to the group name and number. The "Blank Subtraction" in the calculation is the average of all blank sample subtraction from the selected group.	
Standard	Standard is mainly used to place standard samples standard curves can be made by standard reagents. The concentration of the standard must be set in advance. It can be set as a single well or replicates.	
Control	Control is used to place quality control samples. For user further operation analysis use, the default is replicated.	
Unknown	Used for placing solution samples of unknown concentration. Can be single wells or replicates. Unknown product has a dilution parameter option for setting the dilution ratio.	
Negative	Negative samples are used for the classification of special samples, default are replicates	
Positive	Positive samples are used for the classification of special samples, default are replicates	
Clear	This parameter is used to clear the well status and set the well status to None. When a new protocol file is created, the default state of all wells is "None".	

8.5 Analysis interface

When the user clicks the **"Analysis"** button in the sidebar, the options bar will switch to the analysis interface, as **Figure 36**. The main display area includes the operation bar and the display area. The switch box is the data analysis area, and the option bar is the algorithm parameters and calculation type.

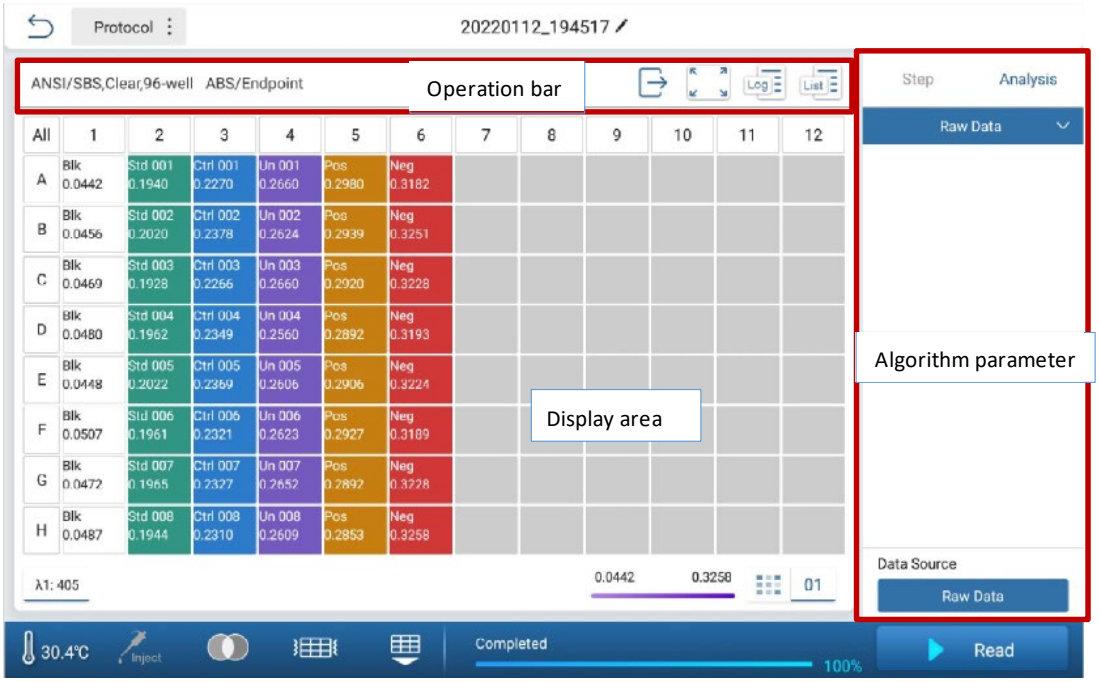


Figure-36 Main interface of result

Function of data analysis

Name	Type	Function
Raw Data	Drop-down menu	Click to display the algorithm that can be selected.
Data Source	Key	Click to select the data source, the data source includes the raw data and blank subtraction data.

"Raw Data" is an item that cannot be deleted. The three modes of Endpoint, Kinetic and Spectrum have their corresponding algorithm processes, and the algorithm cannot be deleted.

When click the existing calculation method in the data analysis area, the display area and the option bar on the right of the interface will jump to the corresponding content. For example, if select the standard curve calculation method in the data analysis area, the standard curve interface is displayed, and parameter settings of the standard curve are displayed in the option bar on the right.

8.6 Algorithm

Users can choose the algorithm to calculate and analyze the raw data.

8.6.1 Endpoint

In the calculation analysis of the results, it should be made clear that all algorithms operate on intra-group data, and a group is a whole. The Endpoint method includes blank subtraction, basic calculation, standard curve, quality control, and classification.

Restriction relation of the endpoint method

Name	Restriction condition
Blank Subtraction	Blank samples must be set
Standard Curve	The standard sample must be set, and the concentration of the a standard sample is not always 0.
Quality Control	Quality control must be set up
Classification	Negative and positive samples must be set

Specific algorithm of the endpoint method

Name	Algorithm
Blank Subtraction	1) Blank subtraction. 2) The read values of all blank wells in the sample group are averaged. Subtract this average value from all samples within the group.
Basic Calculation	Data-to-data calculations 1) Select data as A. 2) Select one of the operators +, -, *, / between A and B. 3) Select data as B. Get the calculation result.

Standard Curve	1) Linear The read values of the standard samples were linearly fitted by the least square method. 2) Linear (through origin) The read values of the standard samples were linearly fitted by the least square method. And must be through the origin. 3) Logistic(4PL) Use 4PL fitting to calculate. 4) Quadratic, Cubic, Quartic Polynomial Polynomial fitting calculation method, the core is the least square method. 5) Point to Point The data points are wired from point to point directly. 6) Cubic Spline Multiple linear systems of equations. 7) Logit/log The core is the least square method.
Classification	1) Select the data source (concentration or absorbance). 2) Input values K_1, K_2,K_3. 3) The critical value is calculated according to the formula $K_1 \times NC+K_2 \times PC+K_3$ (where NC is the average value of negative sample reading, and PC is the average value of positive sample reading). 4) Input values K_4. 5) According to the weakly positive formula: $\pm K_4\%$* critical value, calculate the range of weakly positive. 6) According to the positive formula: > critical value, calculate the positive range.
Quality Control	1) Select the data source (concentration or absorbance). 2) Set target value and deviation value. Calculate the values of the upper and lower limits according to the target value and deviation, and then check whether the read data is within the range of the upper and lower limits. If so, it will be displayed.

8.6.2 Kinetic

Kinetic algorithms include blank subtraction, basic calculation, and kinetic analysis.

Kinetic algorithms restrict relation

Name	Restriction condition
Blank Subtraction	Blank samples must be set
Kinetic Analysis	Kinetic readings must be performed

The specific algorithm of the kinetic

Name	Algorithm
Blank Subtraction	1) Blank subtraction. 2) The real value of all blank wells in the sample group is averaged; Subtract this average value from all samples within the group.
Basic Calculation	Data-to-data calculations 1) Select data as A. 2) Select one of the operators +, -, *, / between A and B. 3) Select data as B. Get the calculation result.
Kinetic Analysis	1) Average, SD and CV Select a reading range and take the kinetic read data of each wavelength. Get average, SD and CV. 2) Integral to get the area of the curve Set reading range and take the kinetic read data of each wavelength; Calculate the area of line segments according to the calculation method of trapezoidal area (if it is multiple line segments, disassemble to calculate). 3) Baseline subtraction. Select a baseline, all reading values minus the baseline value • Select a reading range and take the kinetic read data of each wavelength. • Set baseline points (from the beginning to a baseline point or from a baseline point to the end) to get a baseline. • Take the average of the baseline. • All the absorbances minus the average. 4) Maximum Rate • Select the readings range and take the kinetic read data of each wavelength. • Set the window value. • Set the units. • Calculate the reading difference between points (the reading at the last point minus the reading at the previous point) and divide by time. All results can be maximized according to the window partition. 5) Select Single Reading Set the readings and select a single reading. 6) Select Reading Range Set the reading range and take the kinetic read data of each wavelength. 7) Maximum (Peak) The maximum value of each curve

8.6.3 Spectrum

Spectrum algorithms restrict relation

Name	Restriction condition
Basic Calculation	Readings must have
Blank Subtraction	Blank samples must be set
Spectral Analysis	Must be in spectrum running mode

The specific algorithm of the spectrum

Name	Algorithm
Blank Subtraction	Blank subtraction. The readings of all blank wells in the sample group are averaged; Subtract this average value from all samples within the group.
Basic Calculation	Data-to-data calculations Select data as A. Select one of the operators +, -, *, / between A and B. Select data as B. Get the calculation result.
Spectral Analysis	1) Spectral Maximum (select spectrum range) • Select spectrum range; Select threshold. • Find out the absorption peak with the maximum wavelength, which is greater than the threshold. 2) Spectral Normalization (select spectrum range) Set the spectral range, take the maximum absorption peak as number 1, and the remaining values are converted into percentages based on this baseline. 3) Ratio within Spectrum Set two wavelength values, λ1 and λ2, which can be selected in the spectral range. Take the value of λ1/λ2. 4) Select Wavelength Range Set the start and end wavelengths and read the measurements in the wavelength range. 5) Select Single Wavelength. Set the wavelength value and read the measured value at that wavelength.

8.7 Algorithm parameter

The algorithm parameters are the specific setting parameters of the algorithm, which will change according to the change of the selected algorithm. The following are the algorithm parameters. Blank Subtracting does not need to set algorithm parameters, so it will not be introduced.

8.7.1 Standard curve

Figure 37 shows the algorithm parameter setting interface when a standard curve is selected.

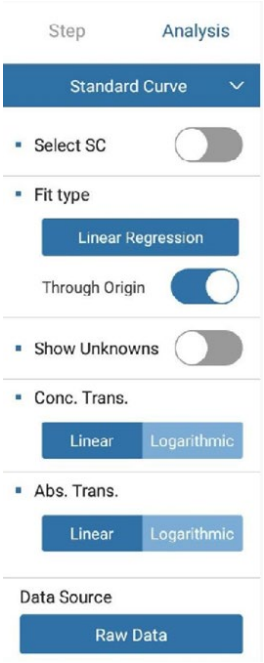


Figure-37 Standard curve algorithm parameter interface

The algorithm parameter function of the standard curve

Name	Function
Fit type	Click to display the type of selection interface of the standard curve, as shown in **Figure 37.**
Show Unknowns	Click to display the reading point of the unknown sample in the figure and click again to disappear.
Through Origin	The standard curve must be through the origin when clicking it.
Conc. Trans.	Transfer the concentration of the readings to a linear or logarithmic display.
Abs. Trans.	Transfer the absorbance of readings to a linear or logarithmic display.

Figure 38 shows the interface for selecting a standard curve type. On this page, you can select a standard curve type, including linear regression, 4PL, quadratic polynomial, cubic polynomial, quartic polynomial, point-to-point, cubic spline, and Logit/log.

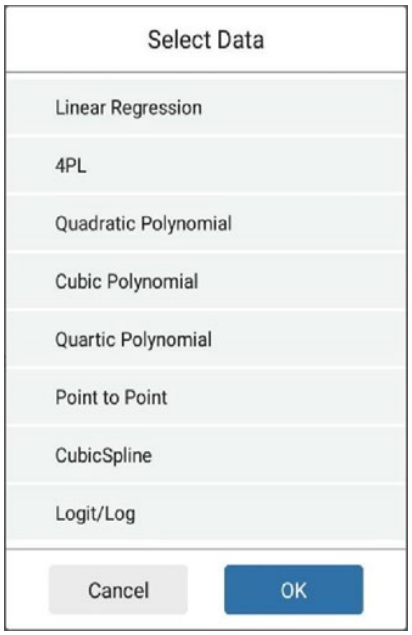


Figure-38 Selecting interface of standard curve type

Functions of display area on the standard curve interface

Name	Function
	Click on the pop-up operation items, saved to SC and QR code
Saved to SC	Click saved the standard curve to SC
QR code	Click to generate the standard curve to the QR code
	Click on Zoom to restore the initial value
	Click to switch to the list interface
	Click to select wavelength to perform the standard curve analysis

8.7.2 Kinetic

When choosing kinetic, calculation parameter settings vary according to different types of selection. the selection interface of kinetic calculation type as shown in **Figure 39**, including average, integral, baseline subtraction, select single reading, select reading range, maximum rate, and maximum (peak) seven types of calculation, is single selection mode.

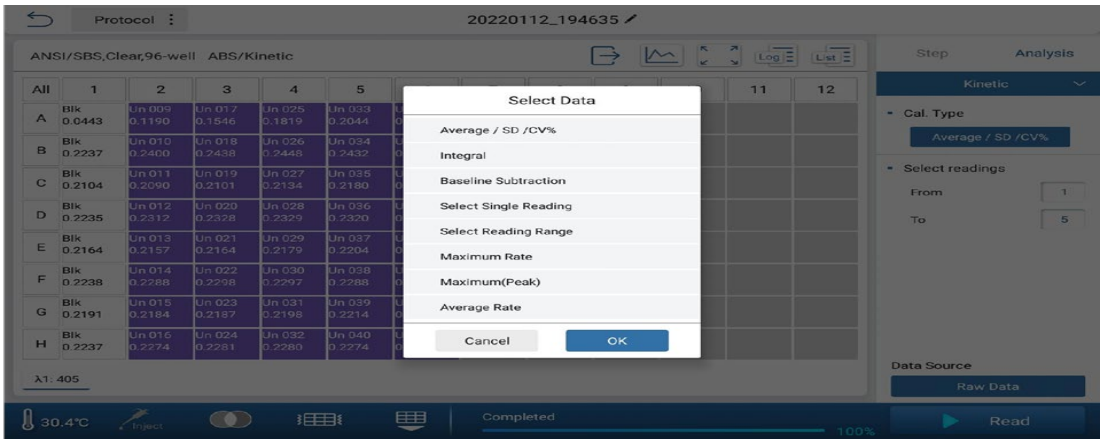


Figure-39 Kinetic calculation type

8.7.3 Spectral analysis

When spectral analysis is selected, calculation parameter settings vary according to the selection type. **Figure 40** shows the selection interface of spectral analysis calculation type, which includes five calculation types, namely spectral maximum, spectral normalization, ratio within the spectrum, select wavelength range and select single wavelength. It is a single selection mode.

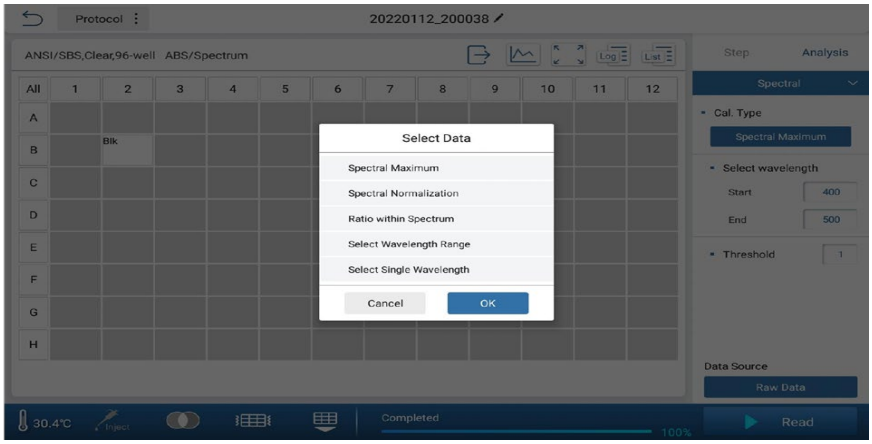


Figure-40 Selection interface of spectral analysis calculation type

8.7.4 Basic calculation

When the basic calculation is selected, **Figure 41** shows the calculation parameter setting interface. Click to pop up the calculation type selection interface, including A+B, A-B, A*B, and A/B.

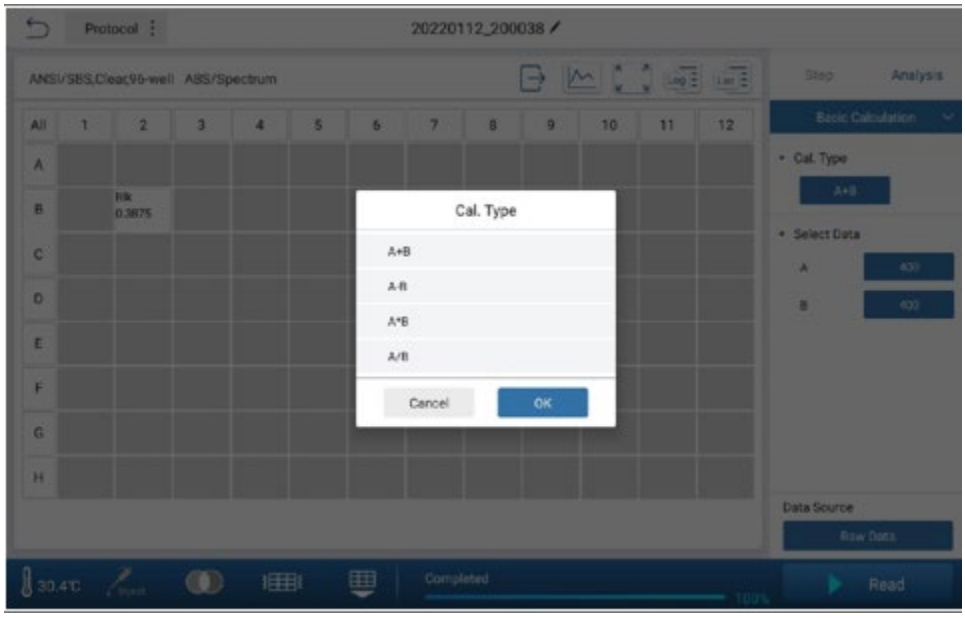


Figure-41 Calculation type selection interface

Figure 42 shows the interface for selecting basic calculation data. The raw data and all calculated steps are displayed on the left, and all optional values in the data are displayed on the right. The selection type is single.

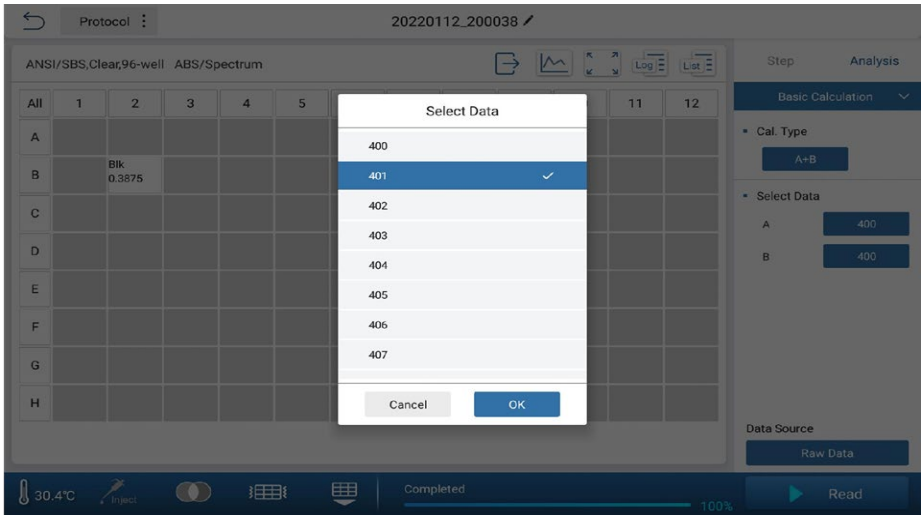


Figure-42 Data selection interface of basic calculation

8.7.5 Quality control

When quality control is selected, the calculation parameter setting interface is shown in **Figure 43**.

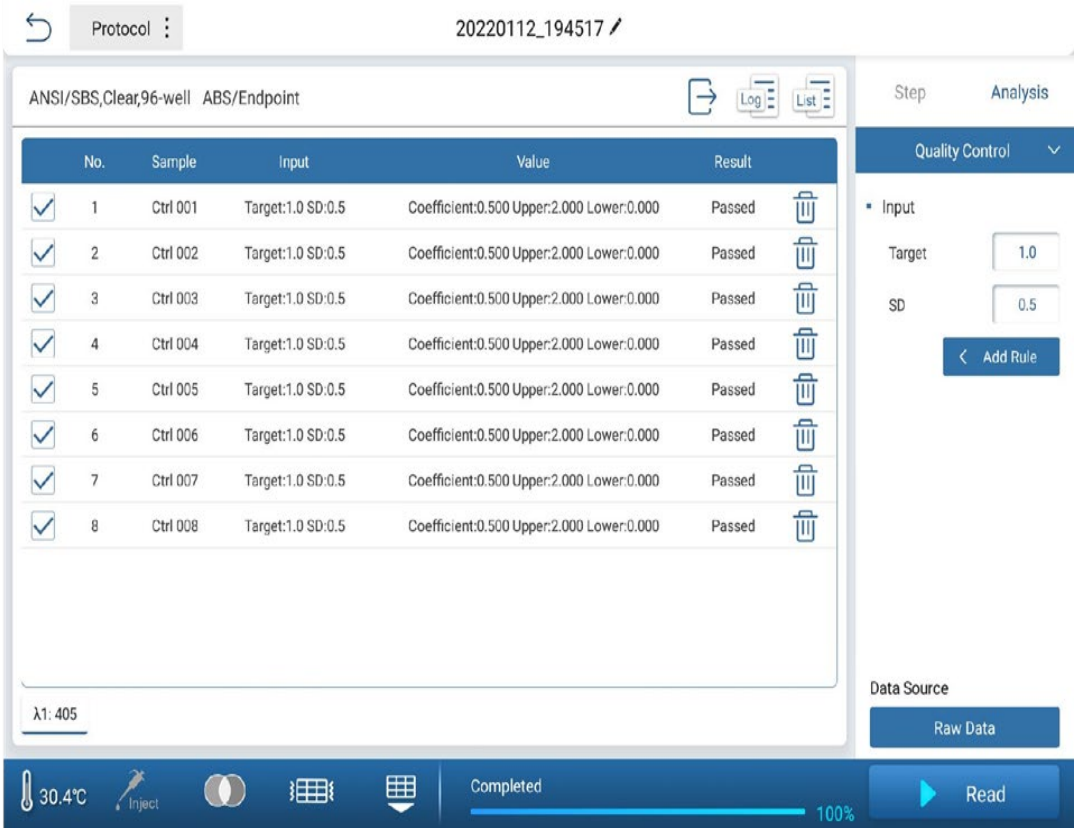


Figure-44 Parameter setting interface of quality control

Function of calculation parameters of quality control

Name	Function
Target	Click to enter the target value, default 1.000, range 0-999999, up to three decimal places.
SD	Click to enter the SD value, default 0.500, range 0-999999, up to three decimal places.
Add Rule	Click to add rules, and all values in the display area will judge whether each sample conforms to the set rules according to the set rules.

8.7.6 Classification

When classification is selected, the calculation parameter setting interface is shown in **Figure 45**.

Figure-45 Parameter setting interface of classification

The function of calculation parameters of classification

Name	Function
Data Type	The value can be absorbance or concentration
K_1	Click to enter K1 values, default 1, range 0-999999, Up to three decimal places.
K_2	Click to enter K2 values, default 0, range 0-999999, Up to three decimal places.
K_3	Click to enter K3 values, default 0, range 0-999999, Up to three decimal places.
K_4	Click to enter K4 values, default 1, range 0-999999, Up to three decimal places.
Positive	Select the positive judgment sign.

In classification, the type will be displayed in the upper right corner of each data well in the display area. The positive icon is "++", the weakly positive icon is" + ", and the negative icon is "−", as shown in **Figure 45**.

8.8 u- Nano Plate (Optional)

This microplate is an optional part. Click the **"u-Nano"** button on the main interface to pop up the reading type selection box, which can select Nucleic acid, Protein, or UV-VIS, as shown in **Figure 46**.

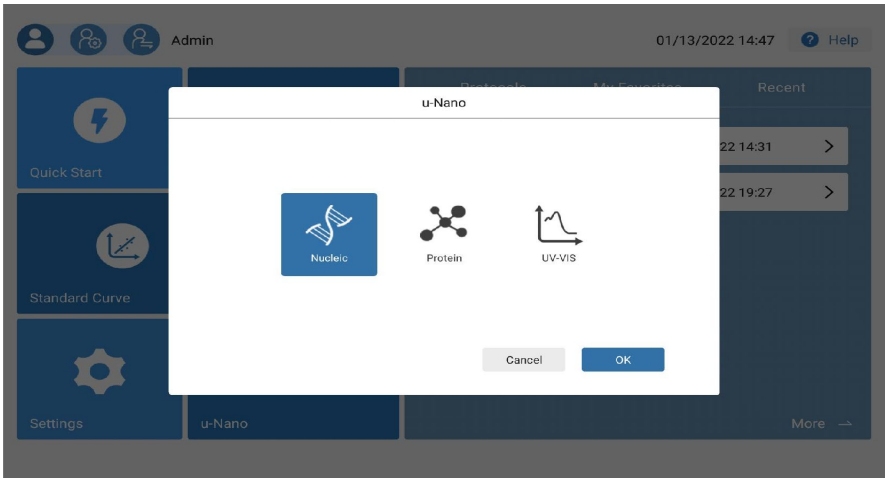


Figure-46 Reading type of u-Nano

8.8.1 Nucleic acid

Select nucleic acid on the u-Nano interface and click OK to enter the nucleic acid reading interface and create a protocol. The main display area of the nucleic acid interface is shown in **Figure 47** and **Figure 48**. On the left is the well-location layout of the u-Nano plate: Row (A-H) * Column (3-4).

Figure-47 Nucleic acid interface (multi-wavelength)

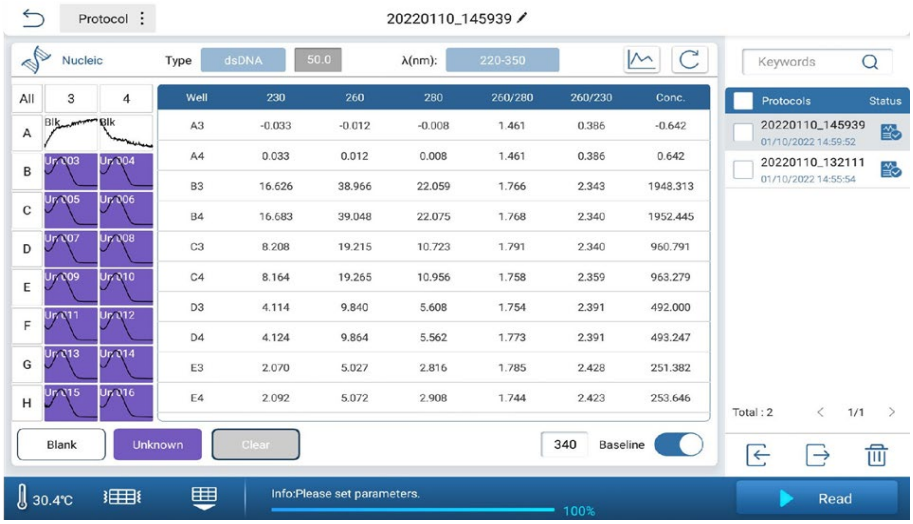


Figure-48 Nucleic acid interface (Spectrum)

Function of nucleic acid interface

Name	Function
	Click to prompt whether to exit, if click **"Yes"** to prompt whether to save the current file, then click **"Yes"** to save and exit to the main interface, if click **"No"** to not save and exit to the main interface.
Protocol	Click the button to pop up the operation of the currently selected protocol, including save, save as, export USB disk, QR code, and report; When clicking save as, if the protocol has been run, a prompt box will pop up with whether to save the data option, otherwise, there is no option to save the data; The export format of the report is Xls, and the export format of protein and UV-VIS is the same.
	Click the pop-up modify input box, can modify the current protocol name.
Upload	Click to upload the current protocol to FTP. If the upload is not enabled in settings, the button will not be displayed. The function of the protein and UV-VIS is the same.
Type	Click to select the type of nucleic acid reading, including dsDNA, ssDNA, RNA, and Others; Among them, the coefficient of dsDNA is 50.0, ssDNA is 33.0, RNA is 40.0, the default value of Others is 25.0, users can manually input, the input range is 0.01-99.99.
λ(nm)	The reading mode can be selected from "multi-wavelength (230,260,280)" or "spectrum (220-350nm)".

	Click to view the graph of the selected well, only when the reading mode is spectrum, the button will be available;
	Click to refresh the current interface data.

Functions of the main display area of nucleic acid

Name	Function
Left wells	When not running, the well shows the sample name; When running multi-wavelength, the well displays the name and data; When running the spectrum, the well shows the name and curve Minimap; The operation of the row, column, single selection and area selection of well is consistent with that of 96 well.
Blank	Select this button, and then select the well of the u-Nano plate then set the well to blank type.
Unknown	Select this button and then select the well of the u-Nano plate, then set the well to an unknown type.
Clear	Select this button and then select the well of the u-Nano plate to clear the well setting, and there will be a prompt when clearing.
Baseline	Can set whether to open baseline, optional range of 220-350nm.
Well	Display well, display well list.

When reading the spectrum of nucleic acid, select the well and click the curve button to display the curve, as shown in **Figure 49.**

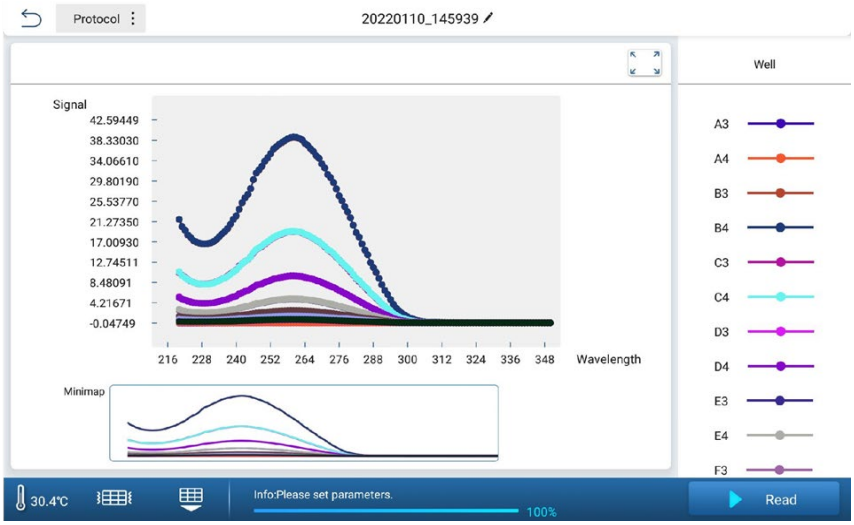


Figure-49 Curve interface

The functions of the control area of protein and UV-VIS are consistent.

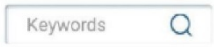
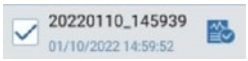
Functions of the control area

Name	Function
	**Note:** In u-Nano plate mode, the volume is small and easy to evaporate, so the incubation function cannot be set
	Click and the instrument shakes once
	When the plate is in the instrument, the plate out operation is performed; Otherwise, the plate in operation is performed
	Click to run the protocol, and the key becomes the stop key

On the right of the nucleic acid interface is a list of all nucleic acid files, including executed (with data) and unexecuted (without data). The executed icon is displayed next to the data, as shown in **Figure 50**. The file interface functions of protein and UV-VIS are consistent.

Figure-50 File interface

The function of the file interface

Name	Function
	Search based on input
	Select the protocol to operate
	Displays the file name and the creation date
	Shows whether the protocol has been executed, the icon indicates that it has been executed, with running data
Total : 16	Display the total protocol number
	Previous page, current/total page, next page
	Click, the box pops up, and display U disk specified directory, Udisk:\Feyond\ username \Nucleic. The user can select the protocol and import it. The folder name of Protein is Protein, and the folder name of UV-VIS is Uv.
	Click to export the currently selected protocol to the USB disk, where the directory is U disk: \ Feyond\ username\ Nucleic. If there is no USB disk, it will prompt. The folder name of Protein is Protein, the folder name of UV-VIS is Uv, and the folder name of Cuvette is Cuv.
	Click the pop-up prompt box to ask the user whether to delete the selected protocol, click yes to delete, the selected protocol refers to the check box selected.

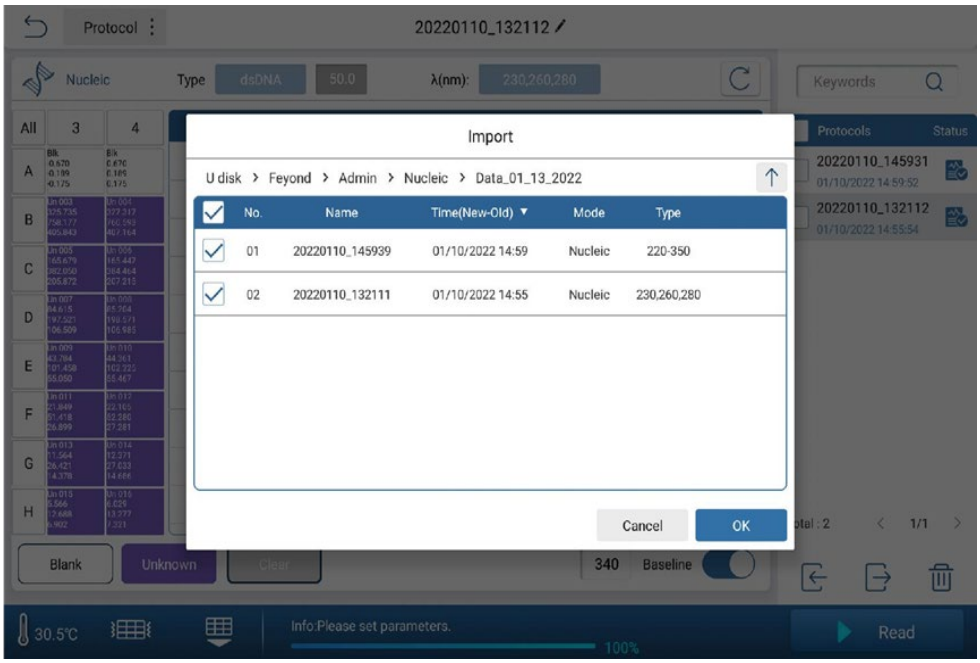


Figure-51 Import protocol

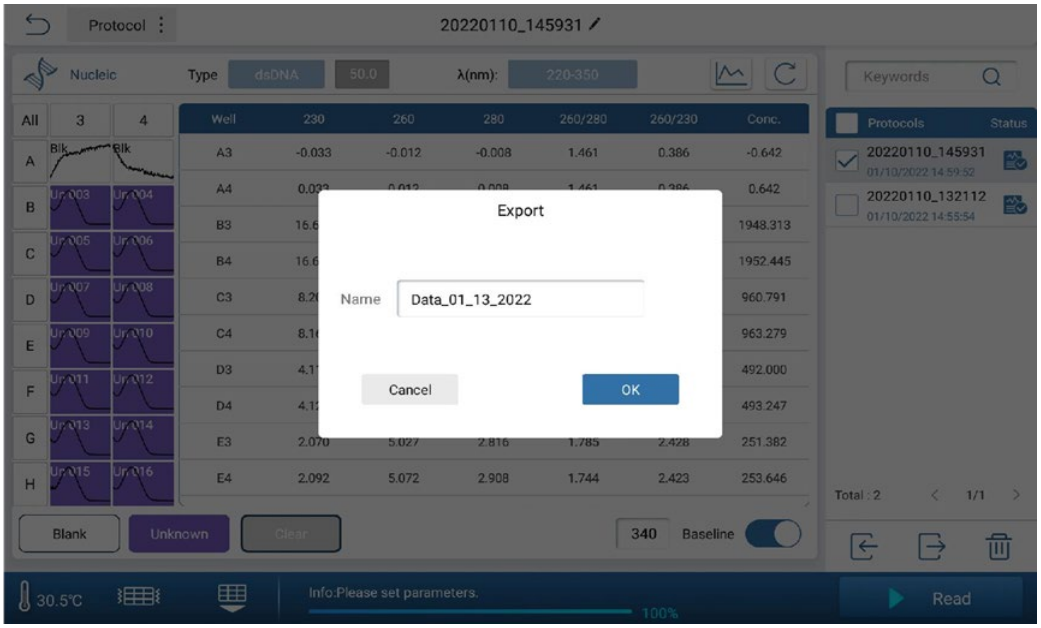


Figure-52 Export protocol

8.8.2 Protein

Select the protein in the u-Nano interface and click OK to enter the protein reading interface, as shown in **Figure 53** and **Figure 54**, where protein reading can be performed.

Figure-53 Protein interface (Multi-wavelength)

Figure-54 Protein interface (Spectrum)

Protein reading types, including A280, BSA, IgG, Lysozyme, others; The coefficient of A280 is 10.0, BSA is 6.7, IgG is 13.7, Lysozyme is 26.4, and the default value of Others is 25.0. It can manually enter, the range is 0.01-99.99, as shown in **Figure 55.**

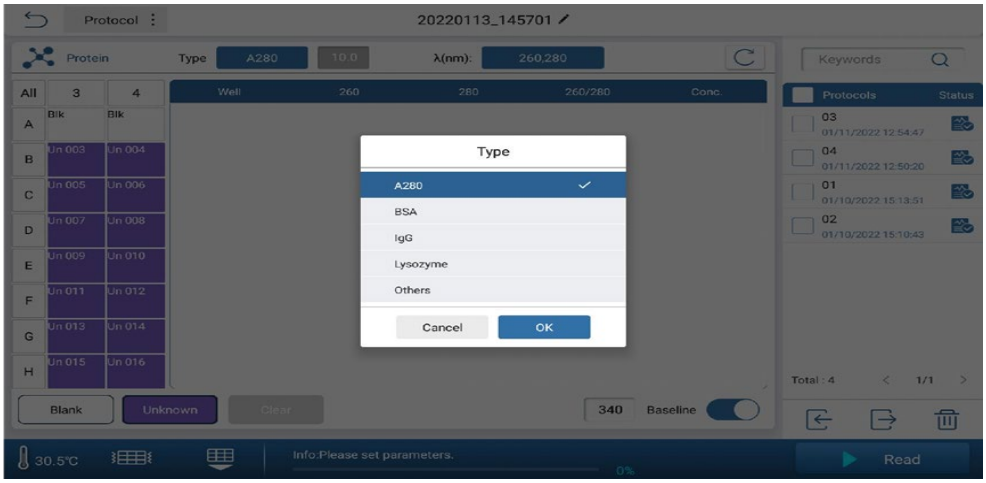


Figure-55 Protein reading type

8.8.3 UV-Vis

Select UV-VIS on the u-Nano interface and click OK to enter the UV-VIS reading interface, as shown in **Figure 56**. λ(nm) Set the start wavelength, end wavelength, and step. The start wavelength must be smaller than the end. The default start value is 200, and the default end value is 350. The step value can be 1/5/10. The default value is 1. You can set whether to open the baseline. The baseline wavelength can be set from the test wavelength range.

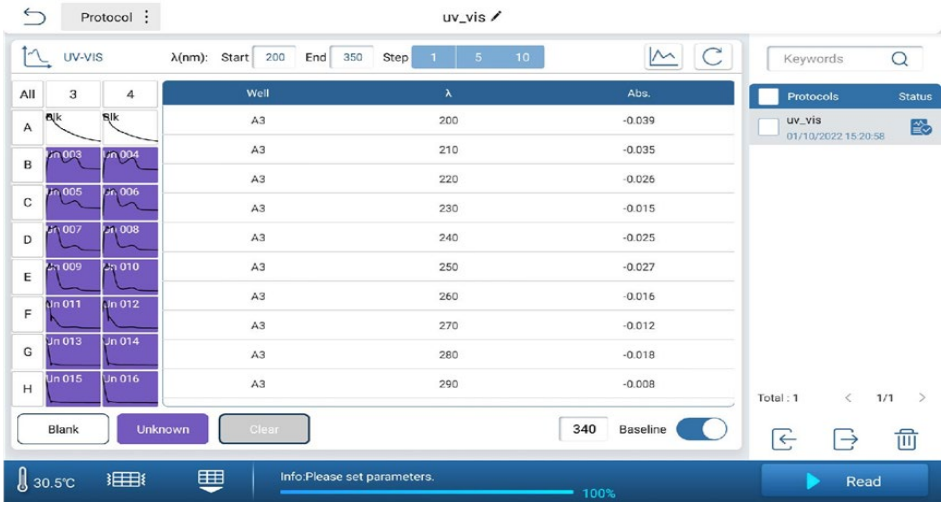


Figure-56 UV-Vis interface

8.9 Report export

After the results are processed, the processed data and raw data can be exported by the Report interface. Click **"Protocol"** in the upper left corner, and then click **"Report"** to enter the main interface of the report as shown in **Figure 57**. is for quick export

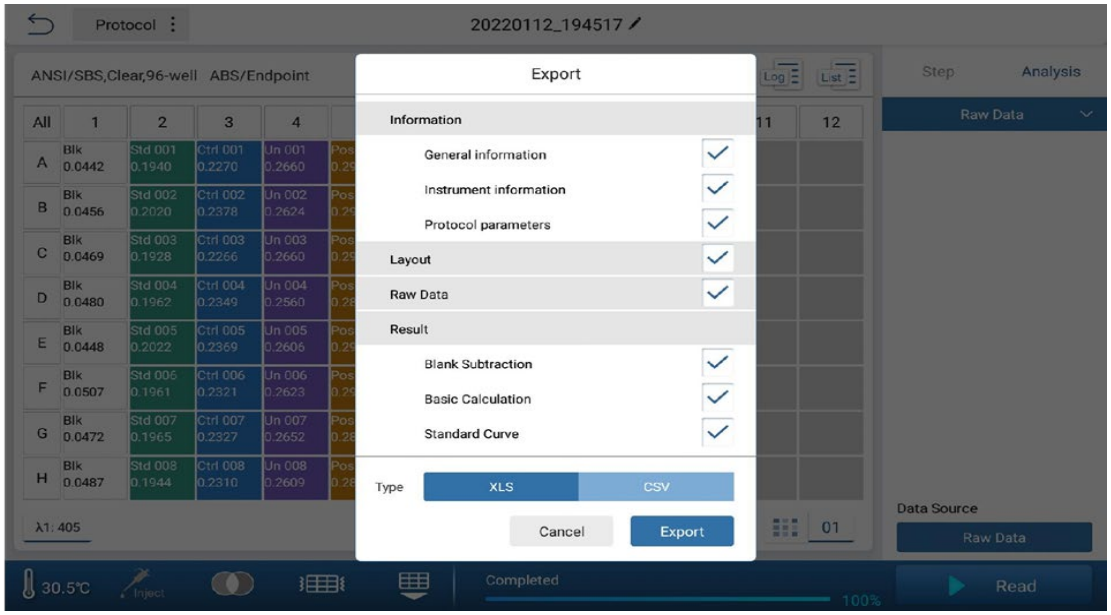


Figure-57 Report export

In the File Type column, it can select the file format to export. Currently, two text formats are available:

- Xls
- Csv

On the right of Export content, select the content to be exported by clicking. If √ is displayed on the right, the option is selected. Click **"Export"** to export the data to the U disk.

The export content varies depending on the protocol setting and the result processing.

8.10 Power off

When power off the device,

Note:

Remove the microplate kit from the instrument and enter back the microplate holder into the instrument.

Turn off the power switch at the back of the instrument to complete the power off.

9. Maintenance

1) Keep the storage environment dry and clean to prevent moisture and corrosion away from strong electromagnetic interference sources.
2) The instrument was already calibrated before leaving the factory. The user is not allowed to disassemble and adjust.
3) Continuous emergency turning on/off is not allowed.
4) Make sure to apply the device with the correct input voltage scope.
5) Ensure the instrument power off correctly when needed.
6) Keep the instrument away from dust.
7) Remove the overflowing solution right away in case of any damage, then clean it with deionized-distilled water every day.
8) If the surface has been contaminated with a biohazard, sterilize it with a mild disinfectant.
9) Clean instrument enclosure regularly.
10) Clean the plate holder when necessary.
11) Sterilize the instrument when re-installing or maintaining.

Storage and transportation

1) Storage at room temperature -10℃ ~ 45℃, relative humidity less than 80%, without corrosive gas and with good ventilation.
2) Keep away from heavy shock, vibration, and humidity during transportation.

10. Troubleshooting

No.	Trouble description	Possible reason	Solution
1	The Microplate Reader cannot be started	Power supply failure	1) Check if the instrument is energized. 2) If the power plug is loose. 3) Check the voltage
2	"Communication timeout" during self-checking	The instrument is not working	Restart the instrument and try again.
3	"E913, E923, E933, E943" during self-checking	Insufficient light intensity	
4	"E912, E922, E932, E942" when self-checking	Light intensity is too strong	
5	"E911, E921, E931, E941" when self-checking	Excessive dark current	
6	"E612, E622, E632, E642" when self-checking	Detection module failure	
7	"E402, E403, E415, E425, E435,E445" when self-checking	Motor failure	
8	"E011~E056" when self-checking	Incubation failure	
9	Test results are greatly deviated or all are zero	Xenon lamp damaged	Restart the instrument and try again.
10	Microplate holder cannot in or out	Blocked by something	Check whether obstacles around the plate holder or whether the plate cover is raised.
11	Crash noise occurred during running	The microplate is not in place, or the plate cover fell off	1) Check the microplate state. 2) If the noise is still there when running without a plate, restart the instrument.
12	Test results unstable	Light path failure	Check if the plate is placed well if liquid spilled out and whether the front door works well, then re-start the instrument.
13	Stop running during the detection	Communication breakpoint	Press **"stop",** restart the detection

11. Accessories

Optional accessories

S. No	Accessory Name
1	Microplate
2	Injector