Operation Manual V1.0

SMARTREADER [™] MULTIMODE



This Product is for Research Use Only



Thank you for purchasing the SmartReader[™] MultiMode. This user manual details the instrument's features, specifications, as well as complete operating instructions; please read it carefully before operation. Keep this user manual for later use.

Important:

Please keep the box and packaging material for this instrument. If service is required, the box will be needed to ship the instrument to our Service Department.

Initial Inspection

Please inspect the instrument as well as all included accessories when you first open the packaging. If you find anything damaged or missing, please contact Benchmark Scientific or your local distributor immediately.

BENCHMARK SCIENTIFIC / ACCURIS INSTRUMENTS

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Safety Warnings and Guidelines

1. Important information for safe use

Users should understand how to use this instrument before operating. Please read this manual carefully prior to operation.



Any improper operation may cause injury. Please read this manual carefully and operate safely according to the guidelines.

2. Operation and Maintenance

The operation and maintenance of the instrument should comply with the basic guidelines and warnings below. Incorrect operation or maintenance will have detrimental effects on the life, performance, and safety features of the instrument.



The instrument is a normal indoor instrument which conforms to class I of the GB 4793.1 standard.



This instrument is designed for use in a laboratory environment. The device must be operated by skilled laboratory personnel with appropriate training.



To prevent injury or voiding the warranty, the operator should not attempt to repair the instrument without explicit guidance from Accuris Instruments. If service is required, please contact Accuris Instruments or your local distributor for repair.



Before powering on, confirm that the voltage used meets the electrical requirements of the instrument as stated on the rating plate. If the electric cord is damaged, replace it with the same type of cord. Hold the socket firmly before pulling the plug from an outlet. Do not pull the electric cord.



The instrument should be installed in an environment of standard room temperature, low dust, low humidity, and away from direct sunlight, electromagnetic interference, and heat sources. Do not block the vents on the instrument.



Always power off the instrument when you are finished using it. Unplug the power cord and cover the instrument with a cloth or plastic sheet to prevent excessive dust from entering the housing. Pull the connector plug from the electrical outlet immediately and contact the vendor in the event of:

- Liquid entering the housing.
- Abnormal operation: such as any abnormal sound or smell.
- The instrument is dropped or there is any damage to the housing.
- Any malfunction.

3. Maintenance

The instrument should be kept in a dry environment away from electromagnetic interference.

4. Transportation and storage requirements

Ambient temperature: 10°C ~ 35°C Relative humidity: ≤ 80% Atmosphere pressure range: 500 ~ 1060hpa Place in a well-ventilated room, away from corrosive gas.

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Chapter 1 Introduction

The SmartReader[™] Multimode is a multi-detection instrument capable of performing absorbance, fluorescence, and luminescence-based readings. Equipped with a 10-inch color touch screen, programming and operation is performed on-board. The built-in software allows for multiple algorithmic analyses of standard curves, qualitative & quantitative measurements, kinetics, spectroscopy, etc. An optional security software (FDA 21 CFR Part 11) is available for this instrument that allows for remote programming/operation via a PC.

1.1 Key Features

- The instrument has a 10-inch color touch screen with built-in processing to allow for on-board programming/operation. No PC connection is required.
- The instrument has plate shaking capabilities (linear & orbital) and an integrated incubator for accurate and uniform temperature control up to 45°C.
- > The instrument is equipped to perform the following detection methods:
 - Absorbance (ABS)
 - Fluorescence Intensity (FI)
 - Fluorescence Resonance Energy Transfer (FRET)
 - Luminescence
- Depending on the detection method, the instrument selects the measurement wavelength by using either filters or a monochromator.
 - ABS measurements utilize a monochromator.
 - FI / FRET measurements utilize filters.
 - Most luminescence-based measurements do not require wavelength selection; however, a luminescence filter in included to eliminate background noise during measurements.
- > The following accessories are available for this instrument:
 - Automatic Injection Module (up to two) for automatic reagent addition.
 - SmartDrop[™] Accessory Plate for microvolume analyses of nucleic acids and proteins.
 - 21 CFR Part 11 compliant PC software

Chapter 2 Specifications

2.1 Required Installation Environment

Environmental temperature: $10 - 40^{\circ}$ C Relative humidity: $\leq 80 \%$ Input voltage: AC 100 - 240 V, 50 - 60 Hz, 2A

2.2 Specifications

Name	SmartReader™ Multi-Mode (MR9620)				
Measurement	Absorbance, Fluorescence (FI, FRETF),				
Technologies	Luminescence (Glow, Flash)				
Absorbance					
Plate Formats	6, 12, 24, 48, 96 & 384-well microplates				
Light Source	Xenon Flash Lamp				
Wavelength Range	200 – 1000 nm (1 nm steps)				
Wavelength Accuracy	±2 nm				
Wavelength Repeatability (SD)	0.2 nm				
Bandwidth (FWHM)	< 2.5 nm				
Measuring Range	0 - 4.0 OD				
Resolution	0.0001 OD				
Accuracy @ 450nm	$\begin{array}{c} \pm (1.0 \% + 0.003) @ (0.0 - 2.0] \\ \pm 2.0 \% @ (2.0 - 3.0] \end{array}$				
Repeatability @ 450nm	CV <1.0% or SD <0.003 Fast mode (0.0 - 3.0] CV <0.5% or SD <0.003 Precise mode (0.0 - 3.0]				
Stability @ 450nm	< 0.005 Abs (0.0 - 2.0 Abs] < 2% (2.0 - 3.0 Abs]				
Linearity @ 450nm	R ² ≥ 0.999 [0.0 - 3.0 Abs]				
Stray Light	0.1 % @ 220 nm				
Reading Time	96 well: Fast mode: < 15 s; Precise Mode < 28 s				
Fluorescence					
Plate Formats	6, 12, 24, 48, 96 & 384-well microplates				
Reading Mode	Top reading				
Excitation Light Source	Xenon Flash Lamp				
Detector	PMT				
Wavelength Range	Excitation: 200 - 1000 nm Emission: 270 - 850 nm				
Filter EX / EM	Included: 470/525 nm, 523/564 nm, 624/692 nm				
Detection Limit	≤ 1 pM				
Linear Dynamic Range	6 logs				

Luminescence				
Plate Formats	6, 12, 24, 48, 96 & 384-well microplates			
Detector	PMT			
Detection Limit	100 amol / well			
Linear Dynamic Range	6 logs			
Crosstalk	≤ 0.005%			
Shaking & Incubation				
Shaking Mode	Linear (4.3 Hz, 7.0 Hz, & 13.5 Hz) Orbital (180 RPM, 240 RPM, & 300 RPM) Double Orbital (90 RPM, 120 RPM, & 150 RPM)			
Shaking Frequency	Low, medium, high			
Incubation Temperature	RT+ 4°C – 45°C			
Temperature Uniformity	± 0.5°C @ 37°C			
Firmware				
Display	10-inch LCD display			
Operation	Touch screen; mouse			
Data Capacity	10GB			
Automatic Injection Mod	ule (AIM)			
Plate Formats 96-well microplates				
Capacity	Up to two			
Dispensing Volume	5 – 1000 μL, 1 μL increment			
Liquid Injection Speed	125-500 μL / s			
Accuracy	± 1 μL @ 5 - 50μL ± 2 % @ 51 - 1000μL			
Waste Liquid Collection	50 mL			
General Specifications				
Communication Ports	2 USB A type ports 1 USB B type port 1 Ethernet port 1 RS232 interface (AIM connection)			
Size(W×D×H) cm	42.0 × 55.0 × 38.6 cm / 16.5 x 21.7 x 15.2 in.			
Power Supply	AC 100 to 240 V, 50 to 60 Hz			
Power	100-240 V, 2 A			
Weight	33 kg / 72.8 lbs.			

Chapter 3 Instrument Overview

3.1 Structure

Front

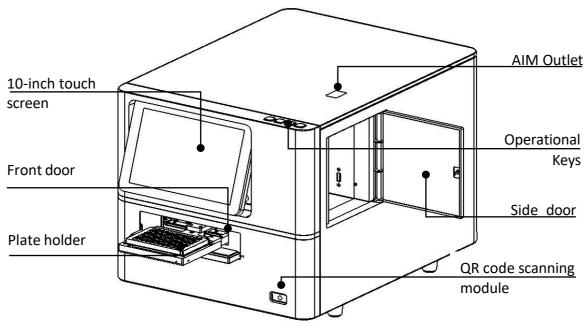


Figure 3.1.01 Front View

Side Door

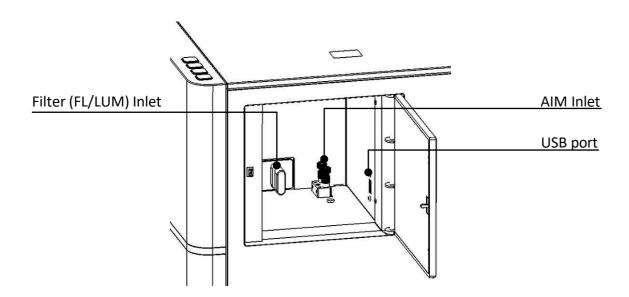


Figure 3.1.02 Side Door View

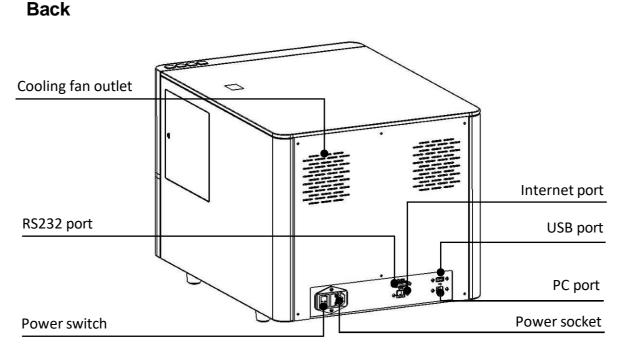


Figure 3.1.03 Back View

Figure 3.1.04; Prior to inserting the filter cartridge, the QR code (found on the filter cartridge) must be scanned by the QR code scanning module. The filter cartridge should enter smoothly if inserted in the correct orientation.

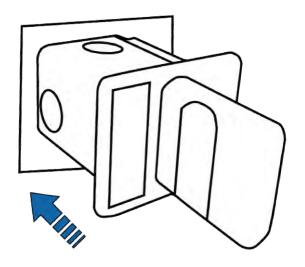


Figure 3.1.04 Filter Cartridge Insertion

Chapter 4 Instrument Setup

4.1 Preparation Before Use

IMPORTANT: This instrument weighs 33 kg (72.8 lbs.) and requires two persons to lift.

Remove the instrument from the shipping box. Place the instrument on a flat surface. Open the side door; press the button on the head of the locking pin and pull up to release the pin.

Note: The locking pin ensures that the microplate motor stays secure during transport. Please pull out the locking pin before use.

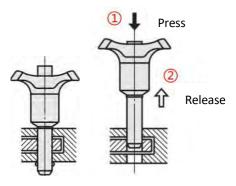
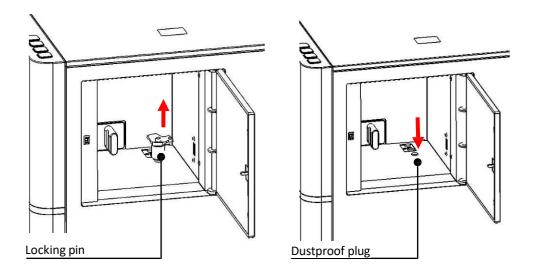
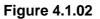


Figure 4.1.01





Chapter 5 Programming & Operation

5.1 Instrument Startup

Power the instrument on. Upon start-up, the instrument will perform an automatic calibration and self-check (Fig. 5.1.01).



Figure 5.1.01 Self Check Upon Startup

After calibration/self-check, the login screen will be displayed (Fig. 5.1.02).

Admin	
Password login Scan code login	
Admin	
login	
Remember Password	

Figure 5.1.02 Login Interface

	Administrator account: can view & edit user	Initial
Admin	permissions, generate system-wide logs, & add/delete	password:
	users.	"0000"
User	Can only perform operative functions.	

Note: Please store the set Admin password in a safe place. Contact Accuris Instruments if the admin password has been lost.

Select "Account" to enter the Account-Admin interface (**Fig. 5.1.03**). To make user-specific password changes, enter the "Password" tab (**Fig. 5.1.04**).

)			Accou	int - Admin				
Password	No.	Group 🗸	Name	Create Time	Creator			
Manage	01	User	A1	2022/01/12/ 17:09	Admin	0	P	创
	02	User	A2	2022/01/12/ 17:08	Admin	0	P	创
								1000
	Total Us	er:2					1	Add

Figure 5.01.03 Account-Admin Interface

		Accou	ınt - Admin				
No	Group 😒	Name	Create Time	Creator			
01	User	A1	2022/01/12/ 17:09	Admin	0	P	世
02	User	A2	2022/01/12/ 17:08	Admin	0	P	団
		Chang	e Password				
	Pleas	e input again		-			
			1				
	Canc	el	ок				
Total Us	er : 2						Add

Figure 5.1.04 Change Account Password

After entering the user-specific password, the Main Menu Interface is displayed (**Fig. 5.1.05**)

988	Admin		01/13/202	22 14:29 🕜 Help
•		Protocols	My Favorites	Recent
9		20220112_192643	3 01/12/20	22 19:27 >
Quick Start	All Results			
	8			
Standard Curve	Share			
-				
Settings	SmartDrop [™] Plate			More

Figure 5.1.05 Main Menu Interface

Table 5 - 2 Main	Menu Interface	Operations

Name	Function
Quick Start	Select to create a new protocol.
All results	Select to view a list of all previously saved protocol results.
Standard curve	Select to view the standard curve library
Share	Select to view a list of executed protocols, standard curves, etc., for transfer (USB, FTP, etc.)
Settings	Select to enter the settings interface
SmartDrop™ Accessory Plate	Select to enter the SmartDrop Accessory Plate Interface. This interface allows for microvolume analyses of Nucleic Acids & Proteins using the SmartDrop Accessory Plate (not included).
Protocol Select to view a list of protocols saved to this shortcut.	
My favorites	Select to view a list of favorite protocols.
Recent Select to view a list of the most recent protocols created/ru	

5.2 Quick Start Interface

Select "Quick Start" on the main interface to enter the Quick Start interface. Users can select protocol parameters according to experimental requirements (**Fig. 5.2.01**).

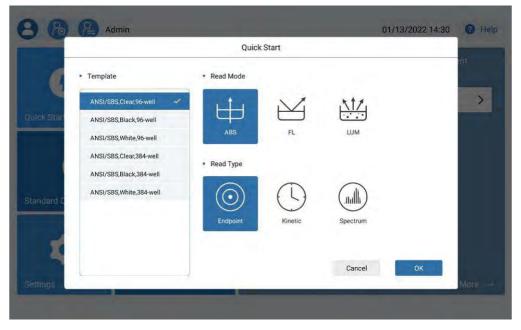


Figure 5.2.01 Quick Start Interface

There are three read modes: ABS, FL, LUM. The ABS mode has three reading types: EndPoint, Kinetic, & Spectrum. FL & LUM only have two read types: EndPoint and Kinetic. The Endpoint method only takes one reading at the end of a protocol, whereas the Kinetic method performs readings during selected intervals, with a minimum of two reads and a maximum of 99. The Spectrum method performs readings within the designated wavelength range.

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

Table 5 - 3 Functions Available For ABS, FL, & LUM Readings

The instrument can accept 6, 12, 24, 48, 96, & 384 well microplates. Table 5 - 4 lists the types of compatible 96 & 384-well microplates for use with the instrument.

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

After selecting protocol parameters, select "OK" to enter the main protocol interface (**Fig. 5.2.02**). It consists of title bar, main display area, menu bar and settings bar.



Figure 5.2.02 Main Protocol Interface

5.2.01 Title Bar

The title bar can be used to return to the previous page, perform protocol operations, name, and modify files (**Fig 5.21.01**).

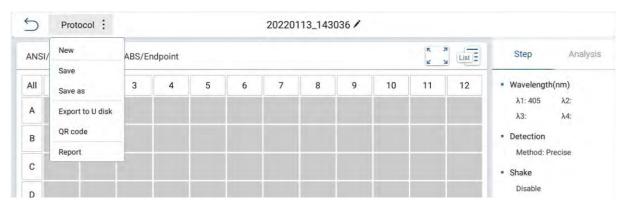


Figure 5.21.01 Title Bar

Name	Functions
5	Return to the main menu. Click and a prompt box will pop up asking the user 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.
/	Name/Rename the current file. Click to display the input box to modify the current name.
Protocol	Click to display operation options, including New, Save, Save as, Export to U disk, scan QR code.
New	Click and the selection box (Fig. 5.21.02) will be displayed.
Save	Save the current file/results.
Save as	Save the protocol under a different name.
Export to U disk	Export file to a USB drive (USB drive must be inserted into instrument prior to performing this operation).
QR code	Generate a QR code for the data on the left of the standard curve.

Click the "/", and the input box for modifying the protocol name will pop up, (**Fig. 5.21.02**). The red text indicates that the new protocol name has already been used once before.

Protocol Na	ime
20220113_143036	
Protocol name repeated!	

Figure 5.21.02 Create a New Protocol

5.2.02 Main Display Area

The default plate layout is set to a 96-well microplate format, 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. Select "All" above row label "A" to select all the wells of the plate.

In the Settings Bar, users can view Kinetic or Spectrum analyses. According to the set reading type (Endpoint, Kinetic, Spectrum), the contents of the main display area vary. **Fig. 5.22.01** shows the results of an executed Endpoint protocol.

ANS	SI/SBS,C	lear,96-we	ell ABS/E	indpoint					[Log	List	Step Analysis
All	1	2	3	4	5	6	7	8	9	10	11	12	Raw Data
A	Blk 0.0442	Std 001 0.1940	Ctrl 001 0.2270	Un 001 0.2660	Pos 0.2980	Neg 0.3182							
в	Blk 0.0456	Std 002 0.2020	Ctrl 002 0.2378	Un 002 0.2624	Pos 0.2939	Neg 0.3251							
с	Blk 0.0469	Std 003 0.1928	Ctrl 003 0.2266	Un 003 0.2660	Pos 0.2920	Neg 0.3228							
D	Blk 0.0480	Std 004 0.1962	Ctrl 004 0.2349	Un 004 0.2560	Pos 0.2892	Neg 0.3193							
E	Blk 0.0448	Std 005 0.2022	Ctrl 005 0.2369	Un 005 0.2606	Pos 0.2906	Neg 0.3224							
F	Blk 0.0507	Std 006 0.1961	Ctrl 006 0.2321	Un 006 0.2623	Pos 0.2927	Neg 0.3189							
G	Blk 0.0472	Std 007 0.1965	Ctrl 007 0.2327	Un 007 0.2652	Pos 0.2892	Neg 0.3228							
н	Blk 0.0487	Std 008 0.1944	Ctrl 008 0.2310	Un 008 0.2609	Pos 0.2853	Neg 0.3258							
λ1:	405								0.0442	0.32	58	01	Data Source Raw Data

Figure 5.22.01 Endpoint Protocol Results

After the protocol is finished, the heat diagram is shown (Fig. 5.22.02).

Note: Only Endpoint protocols have heat diagrams.

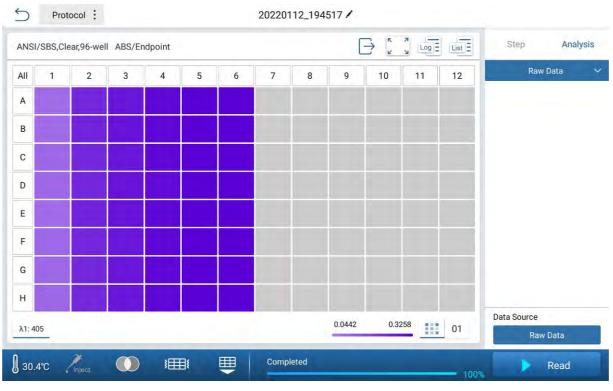


Figure 5.22.02 Heat Diagram Interface (Endpoint)

Fig. 5.22.03 shows the interface when a Kinetic protocol has finished.

ANS	SI/SBS,CI	ear,96-we	II ABS/K	inetic		_				N K	Log	List E	Step Anal	1515
All	1	2	3	4	5	6	7	8	9	10	11	12	Raw Data	1
A	BHA	Un 009 1:1.0000	Un 017 1:1 0000	Un 025 1:1-0000	Un 033 1:1.0000	Un 041 1:1.0000								
в	BIK	Un 010 1:1.0000	Un 018 1:1.0000	Un 026 1:1.0000	0n-034 1:1.0000	Nn 042 1:1:0000								
с	Bik	Un 011 2.1.0000	Un 019 7:1.0000	Un 027 1/1.0000	Un 035 1\1 0000	Un 943 1:1.0000								
D	Blk	Un 912 1:1.0000	U/1020 1:1.0000	Un 028 1.1.0000	Un 036 1.1.0000	Un 044 1.1.0000								
E	Bik	UN 913 1:1.0000	Un 021 1:1.0000	UN 029 1:1.0000	Un 037 1:1.0000	Un 045 1:1.0000								
F	Bik	Un 014 1:1.0000	Un 922 1:1.0009	Un 930 1:1.0080	Un 038 1:1.0000	Un 045 1:1 0000								
G	BUK	Un 915 1:1.0000	Un 023 1:1.0000	Un 031 1:1.0000	Un 839 1.1.0000	Up-047 1:1.0000								
н	Blk	Un 016 1:1.0000	Un 924 7:1.0000	Un 032 1:1.0000	Un 040 1:1.0000	Nn 048 1:1.0000								
λ1:	405										_		Data Source	

Figure 5.22.03 Kinetic Protocol Results

5.2.03 Settings Bar

In the Settings Bar, the "Step" tab can be used to view the selected wavelengths, detection methods, reading intervals, shaking levels, etc. To adjust these settings, see **Chapter 5.3.1**.

	Step	Analysis					
•	Wavelength	n(nm)					
	λ1: 405	λ2:					
	λ3:	λ4:					
•	Detection						
	Method: P	recise					
	Reading Tir	mes					
	Detection : No. of readings						
	Number: 5						
	Interval: 00:00:05						
	Shake						
	Disable						
	Wait Time a	at start					
	Disable						
•	Area Select	ion					
	Step Para.	Layout					

Figure 5.23.01 Settings Bar

5.2.04 Menu Bar

The lower area of the display is the menu bar (**Fig. 5.24.01**). It includes operations for incubation, injectors, filters, shaking, plate in/out, & commencing a plate reading.

🜡 31.6°C	Inject	1		Info:Please set parameters.	0%	Read
			Figu	re 5.24.01 Menu Bar		

Table 5 - 4 Legend: Menu Bar Operations

Name	Definition
₿ 31.6℃	Select to adjust the incubation settings
Inject	Select to adjust the Automatic Injection Module settings
	Select to pop up the filter settings box (FL/LUM mode only)
3	Select to perform quick temporal shaking (1 second)
	Select to insert/retrieve the plate holder.
🕨 Read	Select to start a plate read.

Incubation Settings:

Select 131.6° to enter the incubation parameters interface (**Fig. 5.24.2**). Incubation can be toggled on/off, and the temperature can be adjusted from a range of 15° C – 45° C. Once the incubation settings have been adjusted, select "OK" to save your adjusted setting, or select "Cancel" to return to the main protocol interface.

	Incubator
Incubator	
Temperature	20.0 ℃ +
Cancel	ок

Figure 5.24.02 Incubator Settings Interface

Name	Function
Incubator	On or off, off by default
Temperature	Input the target temperature, ranging from RT+4°C to 45°C;
OK	Click to save the current setting
Cancel	Return button

Table 5 - 5 Legend:	Incubation Settings
---------------------	---------------------

Automatic Injection Module (AIM) Settings: If the instrument does not have an automatic injection module (optional), the icon will be unavailable. When the icon is highlighted in white, select to view and/or adjust the Injection Module parameters (Fig. 5.24.03 and Fig. 5.24.04).

	Inje	ctor		
 Wash 	V Injector 1	V Injector 2	Start Wa	sh
• Mode	Prime Mar	ual		
Injector 1	Start Prime	Reverse	1	
Injector 2	Start Prime	Reverse	Ľ.	
			Cancel	ОК

Figure 5.24.03 AIM Settings - Prime Mode

 Wash 	Injector 1	~	Injector 2	Start Wash
* Mode	Prime	Manual		
Injector 1	300		Start	Reverse
Injector 2	300		Stårt	Reverse

Figure 5.24.04 AIM Settings - Manual Mode

Table 5 - 6 Legend: Automatic Injection Module Operations

Name	Function
Wash	Select the injector(s) to be used in the current protocol.
Mode	Select the injector mode. The default setting is set to Prime. In Prime mode, the wash volume of is fixed. Select "Manual" to manually prime the AIM tubing.
Start Wash	Select to start reagent injection.
Start	Select to aspirate reagents from their reservoir to the corresponding injector.
Reverse	Select to move residual reagent in the tubing back into the reagent reservoir.

Filter Settings: (Fluorescence/Luminescence Only):

Select " \bigcirc " to enter the filter parameters interface. (**Fig. 5.24.05**) The interface will display the excitation / emission λ for the currently installed filter. To add a new filter, select "Replace"; the QR code scanner, found at the bottom right corner of the front of the instrument, will turn on. Scan the QR code located on the new filter to incorporate it into the system.

		Filter			
Excitation:	485				
Emission:	535		-	Replace	
Cancel				ОК	

Figure 5.24.05 Filter Settings 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;

Table 5 - 7 Legend: Filter Settings

5.3 Step Settings Interface

5.3.1 Step Settings Interface: Absorbance

The step settings interface for both Endpoint and Kinetic modes for absorbance are identical (**Fig 5.31.01**). Users can select up to 4 wavelengths to utilize in the readings. To input any wavelength from 200-1000 nm, select the value of the current wavelength to adjust it. λ 1 defaults to 405nm, λ 2 to 450nm, λ 3 to 492nm, and λ 4 to 630nm. Detection can be set to Precise (96 well: <26 seconds), or Fast (96 well: <15 seconds). The default detection mode is set to precise.



Figure 5.31.01 Step Settings Interface (Endpoint / Kinetic): Absorbance

The step settings interface for the Spectrum mode is shown in **Fig 5.31.02**. Enter the starting wavelength and the ending wavelength (200 – 1000nm) to define the range of readings. The default starting value is set to 200nm, and the default ending value is set to 300nm. The "Step" input box allows for specifying measurement intervals (default step value is set to 10). For example: A spectrum reading range from 200nm – 400nm with a step value of 10 will conduct measurements at 200nm, 210nm, 220nm... 400nm.

ANSI/SBS,Clear,96-well	ABS/Spectrum			
Wavelength	Start	200		
	End	300	Start	End
	Step	10		
Detection	Precise		Fast	

Figure 5.31.02 Step Settings Interface (Spectrum): Absorbance

5.3.2 Step Settings Interface: Fluorescence

The general step settings interface for both Endpoint and Kinetic modes for fluorescence are identical (**Fig 5.32.01**).

ANSI/SBS,Clear,96-well	FL/Endpoint			
 Wavelength 	Ex: 485			
	Em: 535			
Detection	Precise	Normal	Fast	
Number	20			
PMT Gain	Automatic	~		
Settle Time	150 ms			
Integration Time	40 µs			

Figure 5.32.01 Step Settings Interface (Endpoint / Kinetic): Fluorescence

Name	Function
Wavelength	Select to display the current excitation wavelength (EX) and emission wavelength (EM) of the instrument.
Detection	Select to adjust reading speeds. Select precise, normal, or fast. If precise detection is selected, the "Number" input box will appear. The "Number" indicates the # of measurements made under precise mode.
PMT Gain	Optional Automatic/Low/Medium Low/Medium High/High, default automatic. By default, when a plate read is initiated, the reader performs an automatic check to determine the optimum PMT gain setting for the wells to be measured.
Settle Time	Settle time can be entered, default 150ms, range 5-999ms.
Integration Time	Integration time can be entered, default 40us, range 5-1000us.

Table 5 - 8 Legend: Step Settings (Endpoint/Kinetic): Fluorescence

PMT Gain: Low signal intensities require higher gains, whereas intense signals require lower gains. By default, PMT Gain is set to "Automatic".

Integration Time: The period of time from when the lamp flashes to excite the sample to when the detector finishes gaining the signal.

Settle Time: The period of time prior to AIM reagent addition.

5.3.3 Step Settings Interface: Luminescence

The general step settings interface of Endpoint and Kinetic modes for luminescence are identical (**Fig. 5.33.01**).

ANSI/SBS,Clear,96-well	LUM/Endpoint	Step
Detection		Injector
- Detection		General
PMT Gain	Automatic 🗸	Shake
Settle Time	150 ms	Advanced
Delay 1	20 ms	Area Selection
Integration Time 1	400 ms	
Delay 2	20 ms	
Integration Time 2	400 ms	

Figure 5.33.01 General Step Settings Interface (Endpoint / Kinetic LUM)

Delay 1 / Delay 2: The period of time from after the AIM has performed reagent addition to when measurement begins.

The automatic injection module (AIM) is limited to fluorescence and luminescence-based readings. In this interface (**Fig. 5.33.02**), users can select either/both AIM's and adjust their respective dispense volume (5-500 μ L) & speed (5-500 μ L/s) (**Fig. 5.33.02** & **Fig. 5.33.03**). The default dispense volume is set to 100 μ L, and the default speed value is set to 200 μ L/s.

		Injector
Injector	No reagent Reagent 1 Reagent 2 Both	
	Horeagent Reagent Louis	General
Volume	100 µL	Shake
		Advanced
Speed	200 µL/s	Area Selection

Figure 5.33.02 AIM Reagent 1 Selected

ANSI/SBS,Clear,96-well	Step	
njector		Injector
jector	No reagent Reagent 1 Reagent 2 Both	General
Volume 1	100 µL	Shake
		Advanced
Speed 1	200 µL/s	Area Selection
Volume 2	100 µL	
Speed 2	200 µL/s	

Figure 5.33.03 Both AIM Reagents Selected

5.3.4 Kinetic Read Settings

When a kinetic reading type is selected, enter the step settings interface, and select "Reading Times". The settings are divided into total time and number of readings, as shown in **Fig. 5.34.01** and **Fig. 5.34.02**. Users can input the total time required for a kinetic assay and input the frequency of readings, or simply input the number of readings required and the frequency of readings. **Table 5-9** lists the parameters that can be set.

ANSI/SBS,Clear,96-well A	BS/Kinetic	
Detection	Total Time	No. of readings
Total Time (hh:mm:ss)	00 : 00 :	25
Interval (hh:mm:ss)	00 : 00 :	05
Read		
Reading 1	Reading 2	Reading 3
Interval		
4	Total Time	

Figure 5.34.01 Kinetic Mode - Total Time Setting

ANSI/SBS,Clear,96-well	ABS/Kinetic	
Detection	Total Time	No. of readings
Number	5	
Interval (hh:mm:ss)	00 : 00 :	05
Read Reading 1	Reading 2	Reading 3
Interval	Total Time : Numbers×Interva	

Figure 5.34.02 Kinetic Mode - No. of readings Setting

Name	Function							
Total Time/No. of readings	The total time / intervals under which kinetic readings will be performed; The maximum time is 99:59:59							
Number	The number of readings to be performed; The maximum number is 99							
Interval	The frequency at which individual readings are performed; The maximum time is 99:59:59;							

Table 5 - 9 Legend: Kinetic Read Settings

5.3.5 Shake Settings Interface

Under any reading mode (ABS, FL, or LUM), select "Shake" in the step settings interface to enter the shake settings interface (**Fig. 5.35.01**).

ANSI/SBS,Clear,96-well	ABS/Kinetic		
Shake			
Speed	Low Me	dium High	
Туре	Linear	Orbital	Double Orbital
Mode	First	Each	
Duration (hh:mm:ss)	00 : 00	: 25	



	rabie e regenarenane eettinge
Name	Default settings
Shake	Toggle switch to enable shaking; The default value is off;
Speed	"Low", "Medium", & "High" shaking speed can be selected; The default value is set to "Low".
Туре	"Linear", "Orbital", & "Double Orbital" shaking type can be selected; The default value is set to linear.
Mode	Select when readings occur; select "First" to shake only once when the protocol begins. Select "Each" to shake prior to every plate reading (kinetic mode only); The default value is set to "First".
Duration	Select the duration of shaking of up to 23:59:59; The default value is set to 00:00:25.
From	Select the set shaking parameters to operate based on the entire plate, or by each individual well (luminescence mode only); The default value is set to plate.

Table 5 - 10 Legend: Shake Settings

5.3.6 Advanced Settings Interface

Select "Advanced" in the general step settings interface to enter the advanced settings interface. Users can adjust settings for "Wait Time at start": the time after a protocol has begun prior to reading the inserted plate (**Fig. 5.36.01**).



Figure 5.36.01 Advanced Settings Interface

5.3.7 Plate Layout Interface

Select the "Layout" button found at the bottom of the Settings Bar on the main display area (**Fig. 5.37.01**).



Figure 5.37.01 Plate Layout Interface

Sample types include blank, standard, quality control, unknown, negative, positive and clear.

Name	Function	lcon
Blank	By default, the blank corresponds to a group name and number. The "Blank Subtraction" in can be used to calculate the average of all blank samples, and then subtract the average blank value from a selected group of unknowns, standards, etc.	Blank
Standard	To generate a standard curve, standard samples must be included in the plate layout. Standards can be inputted as single samples, or in replicates. The concentration of the standard must be set in advance.	Standard
Control	The Control button allows the user to input quality control samples. Quality control samples can be run in replicates.	Control
Unknown	The Unknown button allows the user to input sample types of unknown concentrations. Unknowns can be	Unknown

Table 5 - 11 Legend: Available Sample Types in Pla	te Lavout Interface
	to Eugoat intoriado

	inputted as single samples, or in replicates, with an optional dilution factor setting.	
Negative	Negative control samples are used for the correlation of unknown samples to the standard curve.	Negative
Positive	Positive control samples are used for the correlation of unknown samples to the standard curve.	Positive
Clear	The Clear button allows the user to unassign any sample type on the plate layout. When a new protocol is created, the default setting for all wells is set to Clear.	Clear

5.4 Analysis Interface

Select the "Analysis" button found at the top of the settings bar to enter the analysis interface (Fig. 5.4.01). The main display area includes the operation bar and the display area.

ANS	si/SBS,C	lear,96-we	ell ABS/E	ndpoint					Ľ	2 4	Log	List	Step Analysis
All	1	2	3	4	5	6	7	8	9	10	11	12	Raw Data
A	Blk 0.0442	Std 001 0.1940	Ctrl 001 0.2270	Un 001 0.2660	Pos 0.2980	Neg 0.3182							Analysis Area
в	Blk 0.0456	Std 002 0.2020	Ctrl 002 0.2378	Un 002 0.2624	Pos 0.2939	Neg 0.3251							Allalysis Alea
с	Blk 0.0469	Std 003 0.1928	Ctrl 003 0.2266	Un 003 0.2660	Pos 0.2920	Neg 0.3228							
D	Blk 0.0480	Std 004 0.1962	Ctrl 004 0.2349	Un 004 0.2560	Pos 0.2892	Neg 0.3193							
E	Blk 0.0448	Std 005 0.2022	Ctrl 005 0.2369	Un 005 0.2606	Pos 0.2906	Neg 0.3224							
F	Blk 0.0507	Std 006 0.1961	Ctrl 006 0.2321	Un 006 0.2623	Pos 0.2927	Neg 0.3189							
G	Blk 0.0472	Std 007 0.1965	Ctri 007 0.2327	Un 007 0.2652	Pos 0.2892	Neg 0.3228							
н	Blk 0.0487	Std 008 0.1944	Ctrl 008 0.2310	Un 008 0.2609	Pos 0.2853	Neg 0.3258							
λ1:	405								0.0442	0.32	58	01	Data Source Raw Data

Figure 5.4.01 Analysis Interface

Table 5 - 11 Legend: Data Analysis Interface							
Name	Function						
Raw Data	Click to display the algorithm that can be selected;						
Data Source	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 own corresponding algorithm processes, and the algorithmic parameters cannot be deleted.

Users can execute the existing calculation method in the data analysis area to view the corresponding data/content in the main display area and the settings bar. For example, if the standard curve calculation method in the analysis interface is selected, the standard curve interface will be displayed, and the parameter settings of the standard curve will be displayed in the settings bar.

5.4.1 Endpoint Analysis

Endpoint calculations include blank subtraction, basic calculation, standard curve, quality control, classification.

Name	Restriction condition
Blank Subtraction	Blank samples must be set to perform blank subtractions.
Standard Curve	The standard samples must be set in both the plate layout and in the set concentrations.
Quality Control	Quality control sample must be set up in the plate layout to analyze QC.
Classification	Negative and positive control samples must be set.

Table 5 - 13 Algorithm: Endpoint Calculations	
---	--

Name	Algorithm
Blank Subtraction	 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 Select data as A. Select one of the operators +, -, *, / between A and B. Select data as B. Get the calculation result.
Standard Curve	 Linear The read values of the standard samples are linearly fitted by the least square method. Linear (through the point of origin) The read values of the standard samples are linearly fitted by the least square method and must pass through the point of origin. Logistic (4PL) Uses 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 connected from point to point directly. 6. Cubic Spline Multiple linear system of equations. 7. Logit/log
	- The core is the least square method.
Classification	 Select data source (concentration or absorbance). Input values K₁, K₂,K₃. The critical value is calculated according to the formula K₁*NC+K₂*PC+K₃ (where NC is the average value of negative sample reading, PC is the average value of positive sample reading). Input values K₄. According to the weak positive formula: ±K₄%* critical value, to calculate the range of weak positive. According to the positive formula: > critical value, to calculate the positive range.
Quality Control	 Select data source (concentration or absorbance). 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.

5.4.2 Kinetic Analysis

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

Table 5 - 14 Restrictions: Kinetic Analysis	
Name	Restriction condition
Blank Subtraction	Blank samples must be set to perform blank subtractions.
Kinetic Analysis	Kinetic readings must be performed prior to analysis.

Table 5 - 15 Algorithm: Kinetic Calculations

Name	Algorithm
Blank Subtraction	 The read value of all blank wells in the sample group are averaged. Subtract this average value from all samples within the group.
Basic Calculation	 Data calculations: Select data as A. Select one of the operators +, -, *, / between A and B. Select data as B. Get the calculation result.
Kinetic	1. Average, SD, and CV
Analysis	 Select the 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 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 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, select a single reading.
6. Select Reading Range
- Set reading range and take the kinetic read data of each
wavelength.
7. Maximum (Peak)
- The maximum value of each curve

5.4.3 Spectrum Analysis

Table 5 - 16 Restrictions: Spectrum Analysis

Name	Restriction condition
Blank Subtraction	Blank samples must be set to perform blank subtractions.
Spectral Analysis	Spectrum readings must be performed prior to spectral analysis. Must be in spectrum running mode

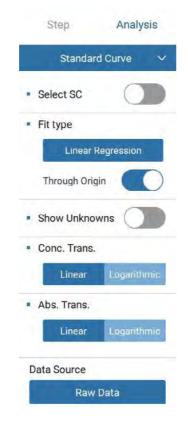
Table 5 - 17 Legend: Spectrum Calculations

Name	Algorithm
Blank Subtraction	 The readings of all blank well sin 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.
	1. Spectral Maximum (select spectrum range)
	- Select spectrum range.
	- Select threshold.
	- Find out the absorption peak with the maximum
	wavelength, which is greater than threshold.
	2. Spectral Normalization(select spectrum range)
	- Set the spectral range, take the maximum absorption peak
	as the number 1, and the remaining values are converted
Spectral	into percentages based on this baseline.
Analysis	3. Ratio within Spectrum
	- Set two wavelength values, $\lambda 1$ and $\lambda 2$, which can be
	selected in the spectral range. Take the value of $\lambda 1/\lambda 2$.
	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.

5.4.4 Standard Curve Analysis

Fig. 5.44.01; Standard curve parameters can be adjusted in the "Analysis" tab of the settings bar.



1	Table 5 - 18 Legend: Standard Curve Settings						
Name	Function						
Fit type	Select to designate a standard curve fitting (Fig. 5.7.01)						
Show	Select to display values of unknown samples on the						
Unknowns	standard curve.						
Through	Select to view the generated standard curve as it passes						
origin	through the point of origin.						
Conc.	Transfer the concentration of the readings to a linear or						
Trans.	logarithmic display.						
Abs. Trans.	Transfer the absorbance of readings to a linear or logarithmic display.						

Figure 5.44.01 Standard Curve Settings

Fig. 5.44.02 shows the interface for selecting a standard curve type. On this page, users can select the type of standard curve fits : linear regression, 4PL, quadratic polynomial, cubic polynomial, quartic polynomial, point to point, cubic spline, and logit/log.

Selec	t Data
Linear Regression	
4PL	
Quadratic Polynor	mial
Cubic Polynomial	
Quartic Polynomia	al
Point to Point	
CubicSpline	
Logit/Log	
Cancel	ок

Figure 5.44.02 Standard Curve Settings: Fit Type

Tak	ble 5 - 19 Standard Curve Operations
Name	Function
	Select to save the generated standard curve to the library or to generate a QR code.
Saved to SC	Select to save the generated standard curve to the standard curve library
QR code	Select to save & view the generated standard curve as a QR code
Log	Select to view the running log

10 Standard Curva Operations

List	Select to view the list of sample types in the current plate layout, along with values for measuring absorbance & concentrations for each wavelength measured.
A1: 610 A2: 665 A3: 430 A4: 280	Select the wavelength used to perform the standard curve analysis

5.4.5 Kinetic Reading Analysis

For Kinetic readings, the following calculation parameters can be set/adjusted: average, integral, baseline subtraction, select single reading, select reading range, maximum rate, maximum (peak), & average rate.

NS	SI/SBS,C	Step Analys					
AII.	1	2	3	4	5	Select Data	Kinetic
Ą	Blk 0.0443	Un 009 0.1190	Un 017 0.1546	Un 025 0.1819	Un 033 U 0:2044 0	Select Data	• Cal. Type
	Blk	Un 010	Un 018	Un 026	Un 034 U	Average / SD /CV%	Average / SD /CV%
В	0.2237	0.2400				Integral	
c	Blk 0.2104	Un 011 0.2090	Un 019 0.2101	Un 027 0.2134	Un 035 U 0.2180 0	Baseline Subtraction	Select readings From
	Blk	Un 012	Un 020	Un 028	Un 036 U	Select Single Reading	
D	0.2235	0.2312	0.2328	0.2329	0.2320 0	Select Reading Range	Το
E	Blk 0.2164	Un 013 0.2157	Un 021 0.2164	Un 029 0.2179	Un 037 U 0.2204 0	Maximum Rate	
F	Blk 0.2238	Un 014 0.2288	Un 022 0.2298	Un 030 0.2297	Un 038 U	Maximum(Peak)	
	Blk	Un 015	Un 023	Un 031	Un 039 U		
G	0.2191	0.2184	0.2187		0.2214 0	Average Rate	
н	Bik 0.2237	Un 016 0.2274	Un 024 0.2281	Un 032 0.2280	Un 040 U	Cancel	
	0.2257	0.2274	0.2201	0.2260	0.2274		Data Source
1:	405						Raw Data

Figure 5.45.01 Kinetic Analysis: Data Source

5.4.6 Spectral Reading Analysis

For spectral readings, the following calculation parameters can be set/adjusted: spectral maximum, spectral normalization, ratio within spectrum, select wavelength range, and select single wavelength (**Fig. 5.46.01**).

ANSI/SBS,Clear,96-well ABS/Spectrum											List)	Step Analysis		
All	1	2	3	4	5	6	7	8	9	10	11	12	Spect	ral
A													Cal. Type	
в		Blk					Se	lect Data	a				Spectral Ma	aximum
						Spe	ctral Maxir	num					 Select wavel 	ength
C						Spe	ctral Norm	alization					Start	400
D						Ratio within Spectrum					End	500		
E						Select Wavelength Range					- Threshold	T		
F						Sele	ect Single V	Vavelength	n					
G							Cancel		ОК					
н														
													Data Source	
													Raw D	

Figure 5.46.01 Spectral Analysis: Data Source

5.4.7 Multi-Wavelength Analysis

When basic calculation is selected, the following calculations can be set/adjusted: A+B, A-B, A*B, A/B (**Fig. 5.47.01**).

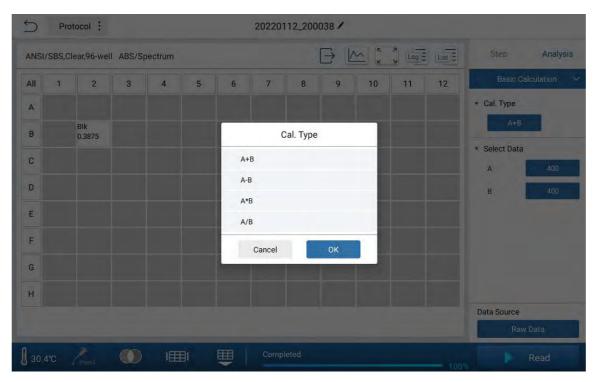


Figure 5.47.01 Multi-Wavelength Calculation Types

Fig. 5.47.02 shows the interface for selecting basic calculation data. The raw data and all calculated steps are displayed on the left, and all calculation options are displayed on the right.

ANSI/SBS,	Step Analysi					
All 1	2	3	4	5	Select Data 11 12	Basic Calculation
A					400	 Cal. Type
в	Blk 0.3875				401 🗸	A+B
с					402	Select Data
					403	A 400
D					404	B 400
E					405	
F					406	
G					407	
н					Cancel	
						Data Source

Figure 5.47.02 Multi-Wavelength Calculations: Select Data

5.4.8 Quality Control Analysis

After reading a plate, quality control calculations can be carried out in the "Analysis" tab found in the settings bar (**Fig. 5.48.01**).

NSI/	SBS,Cle	ar,96-well AB	S/Endpoint			List E	Step	Analysi
	No.	Sample	Input	Value	Result		Quality	Control
/	1	Ctrl 001	Target:1.0 SD:0.5	Coefficient:0.500 Upper:2.000 Lower:0.000	Passed	⑪	Input	
/	2	Ctrl 002	Target:1.0 SD:0.5	Coefficient:0.500 Upper:2.000 Lower:0.000	Passed	一	Target	1.0
/	3	Ctrl 003	Target:1.0 SD:0.5	Coefficient:0.500 Upper:2.000 Lower:0.000	Passed	创	SD	0.5
/	4	Ctrl 004	Target:1.0 SD:0.5	Coefficient:0.500 Upper:2.000 Lower:0.000	Passed	⑪		< Add Rule
1	5	Ctrl 005	Target:1.0 SD:0.5	Coefficient:0.500 Upper:2.000 Lower:0.000	Passed	⑪		
1	6	Ctrl 006	Target:1.0 SD:0.5	Coefficient:0.500 Upper:2.000 Lower:0.000	Passed	団		
1	7	Ctrl 007	Target:1.0 SD:0.5	Coefficient:0.500 Upper:2.000 Lower:0.000	Passed	⑪		
/	8	Ctrl 008	Target:1.0 SD:0.5	Coefficient:0.500 Upper:2.000 Lower:0.000	Passed	団		
1: 40	5						Data Source	/ Data

Figure 5.48.01 Quality Control Calculation Settings

I apro	e 5 - 20 Legend. Quality Control Calculation Settings
Name	Function
Target	Target Value; Default = 1.000, range 0-999999, up to three decimal places;
SD	Standard Deviation; Default = 0.500, range 0-999999, up to three decimal places;
Add Rule	Select to add a rule. After a reading has been performed with the set rule(s), the instrument will determine whether each individual sample measurement conforms to the previously set rules.

Table 5 - 20 Legend: Quality	y Control Calculation Settings
Table 5 - 20 Legena. Quant	y control calculation octaings

5.4.9 Classification Analysis

Select "Classification" from the drop-down menu on the "Analysis" tab to view the "Classification Calculation Settings" (**Fig. 5.49.01**).



Figure 5.49.01 Classification Calculation Settings

	Table 5 - 21 Legend: Classification Calculation Settings
Name	Function
Data Type	The value can be absorbance or concentration
K1	Click to enter K1 values, default 1, range 0-999999, Up to three decimal places.
K2	Click to enter K2 values, default 0, range 0-999999, Up to three decimal places.
Кз	Click to enter K3 values, default 0, range 0-999999, Up to three decimal places.
K4	Click to enter K4 values, default 1, range 0-999999, Up to three decimal places.
Positive	Select the positive judgment sign.

In the main display area, the type will be displayed in the upper right corner of each data well in the display area. The positive icon is "##", the weak positive icon is" ##", and the negative icon is "=", as shown in **Figure 5.49.01**.

5.5 SmartDrop[™] Accessory Plate

The SmartDrop Plate is an optional accessory available for the SmartReader MultiMode. If the user has purchased the SmartDrop Accessory Plate, this function can be used for microvolume readings. Click the "SmartDrop Accessory Plate" button on the main menu interface to view the reading types available: users can select "Nucleic Acid", "Protein", or "UV-VIS" (**Fig. 5.80.01**).

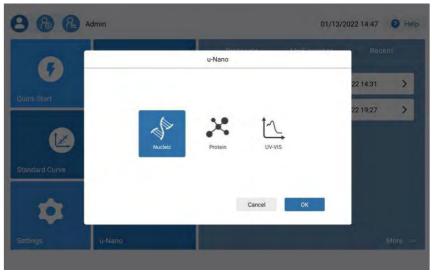


Fig. 5.5.01 Main Menu Interface: SmartDrop Accessory Plate

5.5.1 Nucleic Acid Interface

Select Nucleic Acid and click "OK" to enter the Nucleic Acid Interface. The main display area of the interface is shown in **Fig. 5.51.01** and **Fig. 5.51.02**. The plate layout can be found on the left of the display: rows (A-H) & columns (3-4).

S	> Nucl	eic	Туре	IsDNA 5	Ó.G	λ(nm):	280,260,280		C	Keywords	Q
All	3	4	Well	230	260	280	260/280	260/230	Conc.	Protocols	Status
A	Bik -0.033 -0.009 -0.008	Bik 0.033 0.009 0.008	A3	-0.033	-0.009	-0.008	1.079	0.283	-0.474	20220110_14	
в	Un 003 16 286 37 908 20 292	Lin 004 T.6.365 38,079 20.358	A4	0.033	0.009	0.008	1.079	0.283	0.474	20220110_1	
D			B3	16.286	37.908	20.292	1.868	2.327	1895.443	01/10/2022 141	55:54
С	UN 005 8.265 19.162 10.293	Un 005 8,272 19,223 10,360	B4	16.365	38.029	20.358	1.868	2.323	1901.483		
D	Un 007 4.230 4.876 5.325	Un 008 47260 0.028 5.349	C3	8.283	19.102	10.293	1.855	2.305	955.126		
E	Un 009 2 189 5 072 2 752	Un 010 2 218 5 116 2.773	C4	8.272	19.223	10.360	1.855	2.323	961.160		
2	UT 011		D3	4.230	9.876	5.325	1.854	2.334	493.803		
F	1.002 2.570 1.344 Un 013	Un 012 1.105 2.614 1.364	D4	4.260	9.928	5.349	1.856	2.330	496.428		
G	0.576 1.321 0.718	Un 014 0.618 1.351 0.734	E3	2.189	5.072	2.752	1.843	2.317	253.645		
н	UN 015 0 278 0 534 0 345	0.0016 0.301 0.663 0.366	E4	2.218	5.116	2,773	1.844	2.306	255.814	Total : 2	1/1 >
-	Blank	Un	known	den			1	340 Basel	ine	E B	靣

Figure 5.51.01 Main Menu Interface: Nucleic Acids (Fixed Wavelengths)

S	Nucle	ic	Туре	dsDNA	50.0	λ(nm):	220-350		MC	Keyword	s (2
All	3	4	Well	230	260	280	260/280	260/230	Conc.	Protocols		Status
4	Blk	Blk	A3	-0.033	-0.012	-0.008	1.461	0.386	-0.642		0_145939	8
в	Up 103	Ur 004	A4	0.033	0.012	0.008	1.461	0.386	0.642	2022011	0_132111	
	Up/005	Ur 7006	B3	16.626	38.966	22.059	1.766	2.343	1948.313	01/10/202	2 14:55:54	EU
С	1	1	B4	16.683	39.048	22.075	1.768	2.340	1952.445			
D	Uy 007	07.008	C3	8.208	19.215	10.723	1,791	2.340	960.791			
E	UP COS	Up 010	C4	8.164	19.265	10.956	1.758	2.359	963.279			
	Uprall	Urn12	D3	4.114	9.840	5.608	1.754	2.391	492.000			
F	L	- L	D4	4.124	9.864	5.562	1.773	2.391	493.247			
G	Up 013	Up 014	E3	2.070	5.027	2.816	1.785	2.428	251.382			
н	Up 15	Ur 016	E4	2.092	5.072	2.908	1.744	2.423	253.646	Total : 2	3 1/1	>
	Blank	Unk	nown	Steat			[340 Basel	ine 🕥	E	\rightarrow	同

Figure 5.51.02 Main Menu Interface: Nucleic Acids (Spectral)

	Table 5 - 22 Legend: Nucleic Acid Interface Operations
Name	Function
Ċ	Exit the Nucleic Acid Interface. A prompt will appear to ask if the current file should be saved prior to exiting. Select "Yes" to save the currently open file prior to exiting. Select "No" to exit the interface without saving the currently open file.
Protocol	Displays a selection box that allows the user to create a new protocol, save/save as the current protocol, export to a USB drive, export the protocol to a USB drive as a QR code, or export a report to a USB drive.
/	Modify the currently set protocol name.
Upload	Upload the current protocol to the FTP. If the FTP upload feature is not enabled in the instrument settings, the button will not be available.
Туре	Select the type of nucleic acid for measurement, including dsDNA, ssDNA, RNA, Others; The extinction 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 extinction coefficient from a range of 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 available in spectrum mode)
C	Click to refresh the current interface data;

Table 5 - 22 Legend: Nucleic Acid Interface Operations

	0
Name	Function
Blank	Assign a blank to a well for measurement.
Unknown	Assign an unknown sample to a well for measurement.
Clear	Clear/Erase the currently set well .
Baseline	Can set whether to perform a baseline-correction from a range of 220-350nm.
Well	Display a list of the set wells.

When reading the spectrum of nucleic acids, select the well and click the curve icon (Marchived (Marchived)) to display the spectral curve (Fig. 5.51.03).

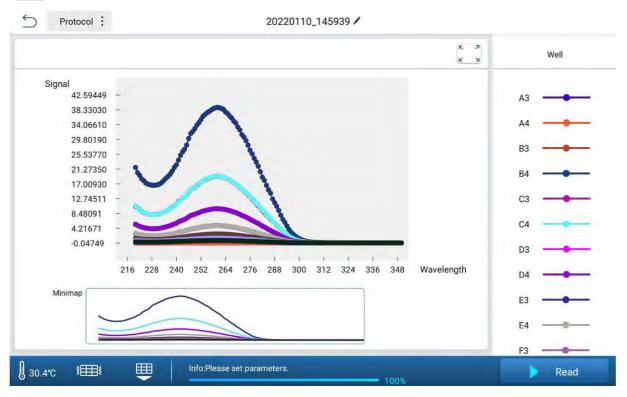


Figure 5.51.03 Nucleic Acid Spectral Curve Interface

Table 5	- 24 Legend: Nucleic Acid Menu Bar Settings
Name	Function
€ 27.5℃	In the SmartDrop Accessory Plate mode, the volume is small, so Incubation parameters are set off to safeguard against evaporation.
3000	Select to perform a temporal shake.
	Select to insert/retrieve the plate holder into/from the instrument.
Read	Select to start a reading.

.

On the right of the nucleic acid interface is a list of all nucleic acid wells which include data for relevant wells. The executed icon is displayed next to the data, as shown in **Fig. 5.51.04**.



Figure 5.51.04 SmartDrop Accessory Plate Files Interface

Table 5 - 25 Legend: Files Settings

Name	Function			
Keywords Q	Input-based search.			
	Select the protocol for further operation.			
20220110_145939 01/10/2022 14:59:52	View File name and creation date.			
	Shows whether the protocol has been executed. The icon with a check mark indicates a protocol has been executed and data has been generated.			
Total : 16	Display the total number of saved protocols on the instrument.			
< 1/2 >	Previous page, current page / total pages, next page			
F	Import files into the instrument via USB. The imported files must be found in the directory as follows: The folder name of Proteins is Protein, and the folder name of UV-VIS is UV (Fig. 5.51.05).			
\ominus	Export the current protocol to a USB drive (Fig. 5.51.06).			



Delete a protocol. A system confirmation will be required to ensure protocol deletion.

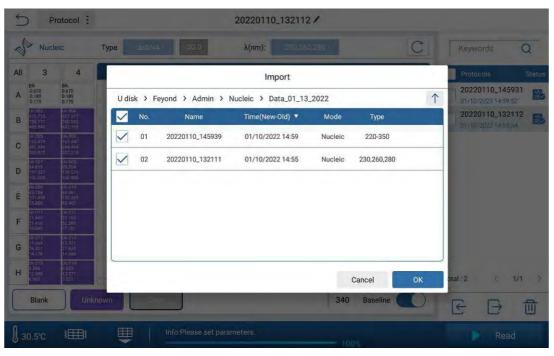


Figure 5.51.05 Protocol Import via USB

S	Nucle	ic	Туре	DNA SI),D	λ(nm):			MC	Keywords	Q
All I	3	4	Well	230	260	280	260/280	260/230	Conc	Protocals	Statu
A Bik	inner	Bik	A3	-0.033	-0.012	-0.008	1.461	0.386	-0.642	20220110_14593	
Ur.	003	Up 204	A4	0.032	0.012	0.009	1.461	A99 0	0.642	20220110_13211	
B 7	L		B3	16.6		Expor	t		1948.313	D1/10/2022 14:55:54	
C P		UP-006	B4	16.6					1952.445		
D 🖤	807	UY 008	C3	8.20 Na	me Data_0	01_13_2022		-	960,791		
E UT	009	Upero	C4	8.10					963.279		
Úr.	Q11	Up 012	D3	4.1					492.000		
FV	1	"L	D4	4.11	Cancel			Ж	493.247		
G		U/2/014	E3	2.070	5.027	2.816	1.785	2.428	251.382		
+	015	Upore	E4	2.092	5.072	2.908	1.744	2.423	253.646	Total:2 < 1/	n s
Bla	ank	Unka	nwor					340 Baseli	ne	EB	団

Figure 5.51.06 Protocol Export via USB

5.5.2 Proteins Interface

Select "Protein" and click "OK" to enter the Protein Interface. Users can select to read in multi-wavelength mode (260 & 280nm only; **Fig. 5.52.01**), or spectrum mode (220-350nm, 1nm step; **Fig 5.52.02**).

2							C	Keywords Q
All	3	4	Well	260	280	260/280	Conc.	Protocols Status
A	Bik -0.010 -0.050	Bik 0.010 0.050	A3	-0.010	-0.050	0.211	-0.076	03
в	Un 003 25.039 21.711	Un 004 25:035 23.460	A4	0.010	0.050	0.211	0.076	04
	Un 605		B3	25.039	21.711	1.153	32.405	01/11/2022 12:50:20
С	18.387 20.620	Un 006 18.471 22.708	B4	25.035	23.460	1.067	35.016	01/10/2022 15:13:51
D	Un 007 13.615 16.792	Un 008 13,577 16,232	C3	18.387	20.620	0.891	30.777	02
E	Un 009 6.828 10.319	Un 010 6.788 8.866	C4	18.471	22.708	0.813	33.892	
	Un 011 3.404 5.782	Un 012 3.413 5.131	D3	13.615	16.792	0.810	25.063	
F		-	D4	13.577	16.232	0.836	24.227	
G	Un 013 1.647 4.563	Un 014 1.641 3.168	E3	6.828	10.319	0.661	15.401	
н	Un 015 0.452 0.642	Un 016 0.443 0.152	E4	6.788	8.866	0.765	13.233	Total : 4 < 1/1 >
-	Blank	Unk				340	Baseline	

Figure 5.52.01 Main Menu Interface : Proteins (Fixed Wavelengths)

•	Prote	ui.	Type BSA	6.7	λ(nm):	220-350	MC	Keywords	Q
All	3	4	Well	260	280	260/280	Conc.	Protocols	Status
A	Bik	Bik	A3	-0.014	-0.006	2.130	-0.010	03	2
в	On 003	on 004	A4	0.014	0.006	2.130	0.010	04	
в	Cn 005	3n 006	B3	24.669	39.699	0.621	59.253	01/11/2022 12:50:20	
С	hous	01000	B4	24.521	39.485	0.621	58.933	01/10/2022 15:13:51	
D	Cn 007	3n 008	C3	18.140	30.217	0.600	45.101	02 01/10/2022:15:10:43	*
E	tin 009	an 010	C4	18.178	30.326	0.599	45.263		
	Un 011	Vn 012	D3	13.415	21.035	0.637	31.395		
F	1	L	D4	13.329	20.889	0.638	31.178		
G	Un 013	Un 014	E3	6.709	10.734	0.625	16.020		
н	Un 015	Un 016	E4	6.669	10.691	0.623	15.958	Total: 4 < 1	/1 >
-	Blank	Unk				340	Baseline	€ D	创

Figure 5. 52.02 Main Menu Interface : Proteins (Spectral)

Protein sample types include: A280, BSA, IgG, Lysozyme, & others. The coefficient of A280 is set to 10.0, BSA is 6.7, IgG is 13.7, Lysozyme is 26.4, and the default value of Others is 25.0. The coefficient can be manually adjusted from a range of 0.01-99.99.

÷) Р	rotocol :			20220113_	145701 /			
2	C Prote	ein	Туре А280	10.0	λ(nm):	260,280	C	Keywords	Q
All	3	4	Well	260	280	260/280	Conc.	Protocols	Status
А	Bik	Bik		-				03	7 👪
в	Un 003	Un 004			Тур	e		04	EV.
С	Un 005	Un 006			A280	~		01	. 66
D	Un 007	Un 008			BSA			02	3
E	Un 009	Un 010	1		Lysozyme				
F	Un 011	Un 012			Others				
G	Un 013	Un 014			Cancel	ок			
н	Un 015	Un 016						Total:4 ¢ 1	1/1 >
C	Blank	Uni	nown			340	Baseline	E D	创
83		3	U I						

Figure 5.52.03 Protein Sample Types

5.5.3 UV-Vis Interface

Select UV-Vis and click "OK" to enter the UV-Vis Interface (**Fig. 5.53.01**). λ (nm): Set the starting wavelength, ending wavelength, and step. The default starting value is set to 200, and the default ending value is set to 350. The step value can be 1/5/10. The default value is set to 1. Baseline-correction can be toggled on/off, with the option to adjust the wavelength.

2	UV-VIS	λ(nm): Start 200 I	End 350 Step 1 5 10	M C	Keywords Q
All	3	The second se		Abs,	Protocols Status
A	BUK E	A3	200	-0.039	UV_vis
в	VI 003	A3	210	-0.035	0.0 110 5055 1055000
D	Im 005	A3	220	-0.026	
С	1003	A3	230	-0.015	
D	007 X	A3	240	-0.025	
E	94n 009 V	H 010 A3	250	-0.027	
	Nn 011 1	A3	260	-0.016	
F	1	A3	270	-0.012	
G	Un 013	A3	280	-0.018	
н	Un 015 L	In 016 A3	290	-0.008	Total:1 < 1/1 >
	Blank	Unknown		340 Baseline	

Figure 5.53.01 Main Menu Interface : UV-Vis

5.5.6 Data & Report Exporting

After the results have been processed, both the processed data and raw data can be exported in the Report interface. Click the "Protocol" button in the upper left corner, and then select "Report" to enter the "Data Export Interface" (**Fig. 5.56.01**).

ANSI/SBS,Clear,96-well ABS/Endpoint						Export		Log List	Step Analysi	
All	1	2	3	4		Information		11 12	Raw Data	
A.	Blk 0.0442	Std 001 0,1940	Ctrl 001 0.2270	Un 001 0.2660	Pos 0.29	General information	~			
в	Blk 0.0456	Std 002 0.2020	Ctrl 002 0.2378	Un 002 0.2624	Pos 0.29	Instrument information Protocol parameters	× ×			
с	Blk 0.0469	Std 003 0.1928	Ctrl 003 0.2266	Ün 003 0.2660	Pos 0.29	Layout	~			
D	Blk 0.0480	Std 004 0.1962	Ctrl 004 0.2349	Un 004 0.2560	Pos 0.28	Raw Data	\checkmark			
E	Blk 0.0448	Std 005 0.2022	Ctrl 005 0.2369	Un 005 0.2606	Pos 0.29	Result				
F	Blk 0.0507	Std 006 0.1961	Ctrl 006 0.2321	Ün 006 0.2623	Pos 0.29	Blank Subtraction Basic Calculation	~			
G	Blk 0.0472	Std 007 0.1965	Ctrl 007 0.2327	Un 007 0.2652	Pos 0.28	Standard Curve	~			
н	Blk 0.0487	Std 008 0.1944	Ctrl 008 0.2310	Un 008 0.2609	Pos 0.28	Type XLS CS	SV			
λ1:	405					Cancel	Export	111 O1	Data Source Raw Data	

Figure. 5.56.01 Data Export Interface

Users can select which data to be included in the exported report by clicking on the checkmark " $\sqrt{}$ " box. A $\sqrt{}$ indicates the respective data will be included in the exported report.

In the File Type row, users can select the report to be exported as the following file types:

- XLS
- CSV

Select "Export" to export the data to a USB drive.

Chapter 6 Troubleshooting

No.	Error	Analysis	Troubleshooting
1	The Microplate Reader does not power on	Power supply failure	Check the power plug .Check the voltage Contact Accuris Instruments
2	"Communication timeout" during self-check	Instrument Error	Restart the instrument and try again; if the problem persists, please contact Accuris Instruments.
3	"E913, E923, E933, E943" during self check	Insufficient light intensity	Contact Accuris Instruments.
4	"E912, E922, E932, E942" during self check	Light intensity is too strong	Contact Accuris Instruments.
5	"E911, E921, E931, E941" during self-check	Excessive dark current	Contact Accuris Instruments.
6	"E612, E622, E632, E642" during self-check	Detection module failure	Contact Accuris Instruments.
7	"E402, E403, E415, E425, E435, E445" during self check	Motor failure	Contact Accuris Instruments.
8	"E011~E056" during self check	Incubation Error	Contact Accuris Instruments.
9	Test results are greatly deviated, or are all zero	Xenon lamp damage	Restart the instrument and try again; if problem persists, contact Accuris Instruments.
10	Microplate holder unable to be inserted/retrieved	Physical obstruction present	Check whether obstacles are around the plate holder or whether the plate cover is elevated.
11	Crashing sound during operation	Microplate not inserted correctly. Microplate lid may have fallen off	Check microplate positioning If noise still there when performing a measurement without a plate, restart the instrument If the self-check is normal but the noise still persists, contact Accuris Instruments.
12	Test results unstable	Light path Error	Check if the plate is placed correctly, and if liquid spilled out. Check whether the plate holder is operating correctly. Restart the instrument. If the self-check is normal but the problem still persists, contact Accuris Instruments.
13	Instrument stops running during detection	Communication Error	Press "stop" and restart the measurement.