# **Operation Manual**

V1.2

# Nano-500 Micro-Spectrophotometer





Hangzhou Allsheng Instruments Co.,Ltd.

# Foreword

Thank you for purchasing a Micro-Spectrophotometer. This manual provided as operational and easy troubleshooting guide. Please read this instruction carefully before operation and save for future reference.

# **Opening Check**

Please check the instrument and Appendix with the packing list when you first open the package. If there is anything don't match, please contact with the vendor.

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File No.:AS169SM

File version No.:1st version, 2018 Dec.

# **Safety Warnings and Guidelines**

#### 1 Warning

To assure the safe operation, please read carefully this manual before operating.

#### 2 Safety Tips

The operation, maintenance and repair of the instrument should comply with the basic guidelines and the remarked warning below. If you don't comply with them, it will have effect on the scheduled using life of the instrument and the protection provided.



This product is indoor instrument.



Users are not allowed to open or repair the instruments, which will lead injury and loss of warranty,



Power off when you finish your work. Pull off the connector plug when there's long time no use of the instrument and cover it with a cloth or plastic paper to prevent from dust. Pull the connector plug from the jack at once in the following case, and contact the vendor:



- 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;
- The function has obviously changed.

#### 3 The maintenance of instrument

The pedestal should be cleaned by the cloth stained with pure water.

If there are smutches on the instrument, clean them with cloth stained with alcohol.

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# **Chapter 1 Introduction**

The Nano-500 is a spectrophotometer that measures 0.5µL-2µL samples with high accuracy and reproducibility. Sample pedestals apply surface tension to make the sample column, so that hold samples in the pedestal. During measurement, the light goes through the sample column; In addition, the Nano-500 has the capability to measure highly concentrated samples without dilution (100X higher concentration than the samples measured by a standard cuvette)

# **Chapter 2 Specifications**

# 1. The normal operating condition

Ambient temperature:5°C ~ 35°C

The relative humidity:≤70%

Power Supply:DC24V 2A

# 2. The basic parameters and performance

Model		Nano-500				
Minimum S	ample Size	0.5µL-2µL (2µL recommended)				
Path Length	า	0.05 , 0.2mm or 1mm				
Light Sourc	e / Life	Xenon flash lamp / >10 <sup>9</sup> flashes				
Detector Ty	'ne	2048—element linear silicon CCD array				
Wavelength	n Range	200—800nm				
Wavelength	n Accuracy	±1 nm				
Spectral Re	solution	≤3nm(FWHM@Hg 253.7nm)				
Absorbance Precision		0.003Abs(1mm path length)				
Absorbance	e Accuracy	±1%(7.332Abs, at 260nm wavelength)				
	Dener	0.04—300(at 260 wavelength, 10mm				
	e Range	equivalent)				
Detection		2ng/ul_dsDNA~15.000ng/ul_dsDNA				
Concentration Range						
Detection Time		<6seconds				
OD600 Ab	s range	0~4.000 Abs				
Ab	s stability	[0,3)≤0.5% [3,4)≤2%				

Abs repeatability	[0,3)≤0.5% [3,4)≤2%				
Abs Precision	[0,2)≤0.005A;[2,3)≤1%;[3,4)≤2%				
Linearity	<i>R</i> <sup>2</sup> ≥0.995				
Repeatability	≤1.5%				
Stability	≤1.5%				
input	DC24V 2A				
	25W				
on	208×320×186 mm(W×D×H)				
	3.6 kg				
	Abs repeatability Abs Precision Linearity Repeatability Stability input				

# 3. Models

According to the fluorescence detection wavelength, the 4 models of Nano-500 as below:

Model	Light source	Excitation wavelength	Emission wavelength
Nano-500U	UV LED	365±20nm	420-480nm (60nm)
Nano-500B	Blue LED	460±20nm	525–570nm (45nm)
Nano-500G	Green LED	525±20nm	575–640nm (65nm)
Nano-500R	Red LED	625±20nm	670–725nm (55nm)

Nano-500B is the standard equipped which excitation wavelength is 460nm.

# **Chapter 3 Preparations**

# 1. Structure description





## Notes: Make sure the power supply with ground wire.

# 2. Sample size requirements

Although sample size is not critical, it is essential that the complete liquid column can be formed between the upper measurement pedestal and lower measurement pedestal to make sure the precision of the measurement.

It is best to use a precision pipettor (0-2 $\mu$ L) with precision tips to assure the precision of the sampling. If users are unsure about sample characteristics or pipettor accuracy, a 2 $\mu$ L sample is recommended.

### 3. Basic use for the pedestal

3.1 With the upper pedestal open, pipette the sample (2µL) onto the lower pedestal.





Fig 3.2 Dropping liquid

3.2 Lower the sampling arm, the sample column is automatically drawn

between the upper and lower measurement pedestals. Then the measurement initiates.



Fig 3.3 Liquid column

3.3 When the measurement is complete, open the upper pedestal and wipe the sample from both the upper and lower pedestals using a soft laboratory wipe. Simple wiping prevents sample carryover in the pedestals.



Fig 3.4 Wipe the sample

Notes: After each measurement, clean the pedestals for 3 times with clean pure water.

### 4. OD600 measurement

Nano-500 is with measurement of OD600. Lift the upper pedestal, enter into OD600 interface from the touch screen. Make "blank" according to experiments, blank for air, cuvette, or buffer in cuvette. Then add 2~3mL sample into the cuvette, put the cuvette into the slot and start to measure. (As picture below)



Fig 3.5 OD600 and Fluorometer

Notes: The Light path direction is showed as the arrow as above picture, please pay attention to the cuvette position when loading.

# 5. Fluorometer

Nano-500 has the fluorescence detection function, the default equipment is 460nm excitation wavelength which emission wavelength is 525nm. See the fluorescence detection part in chapter 4 for detailed operation.

# **Chapter 4 Operation**

# 1. Instrument self-testing

Instrument will start self-test once powered on.



Fig 4.1 POST

2. Main interface



Fig 4.2 Main interface

## 3. Nucleic acids measurement

#### 3.1. Introduction

Users can measure the concentration of nucleic acid by using the instrument. If want to measure nucleic acids, select Nucleic Acid mode in the "main menu"

The following "Beer – Lambert" equation is used to calculate the nucleic acids concentration:

$$C = \frac{A * \varepsilon}{b}$$

C=DNA concentration, unit: ng/µL

A=AU absorbance

 $\epsilon$ =extinction coefficient, unit :ng-cm/µL

b=Path Length, unit: cm

Normally DNA extinction coefficient:

dsDNA:50ng-cm/µL

ssDNA:33ng-cm/µL

RNA:40ng-cm/µL

When selecting pedestal mode, the Micro-spectrophotometer can measure high

concentration nucleic acid sample without dilution from 1.0mm to 0.05mm short path length.

The absorbance value of nucleic acid measurement is consistency of

the reading value under 1cm path length.

Nano-500 can accurately measure double-stranded Nucleic Acid samples up to 15000ng/µL without dilution, it can choose path length automatically.

#### 3.2. Nucleic Acids measurement

Click "Nucleic acid" to enter into the interface as below :



Fig 4.3 Initial interface of Nucleic Acids detection

Fig 4.3, there are three options of Nucleic Acids, Report, Help for different functions.

#### 1) Interface Fig 4.3, only the light blue area is clickable.

① <sup>ID : 180717\_125723</sup>: The sample batch No., default value is the current time, users can also edit ID by self. One ID can include as many as 1000 detection results.

2 <sup>DNA-50</sup> <sup>50</sup> : Click to choose Nucleic Acids type, DNA-50 for dsDNA,

RNA-40 for RNA, ssDNA-33 for ssDNA, when you choose "others" and type in the Nucleic Acids factor the instrument will calculate as you set.

Blank
 Blank the buffer, this step is essential before measurement.
 Blank absorbance value is during 0.004-0.03 Abs. The validity of blank
 control is 30 min and after 30 min, the system will automatically remind
 you to make blank detection, If the blank calibration failed, there is a icon
 showed on the top right corner, click it to view the detailed warning

information.

(4) Baseline at 340nm : You can choose or cancel the baseline calibration, the default baseline calibration wavelength is 340nm. User can also input wavelength according to requirement. Any experiment, the baseline is automatically set as the absorbance value of the chose wavelength, all results should minus this value.

Notes: If you don't calibrate the baseline, the light spectrum will deviate, and lead to unprecise result.

(5) Auto Blank C: Click the right icon to select the automatic blank detection, when it is turned on, it will do the blank detection automatically the fist time close the rotating arm. When it is turned off the icon will be Auto Blank

Note: The automatic blank only takes effect when there is no blank data of the current detection. If you want to do reblank then

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#### need to click the right button "Blank".

<sup>(6)</sup> Auto Sample <sup>(1)</sup>: Click the right icon to select automatic detection, when it is turned on, it will do the detection automatically once the rotating

arm is closed. When it is turned off the icon will be Auto Sample

Note: The automatic detection only takes effect when there is blank data of the current detection. If no blank data, need to do blank first.

<sup>Data</sup>: Click it to switch to check the history data list as Fig 4.5, and then click <sup>Graph</sup> to switch to check the curve.

#### 2) Operation steps

① Set the batch NO. and Nucleic Acids type;

2 Clean the upper and lower pedestals with dust proof paper, input the 2µL buffer solution to make blank;

③ Clean the buffer solution on the ower pedestals with dust proof paper;

(4) Measure sample with volume of  $2\mu$ L. Click "Measure" and then enter the interface as Fig 4.4;

Note: The sample must be the new adding before your measurement.

5 After measurement, pedestals must be cleaned before next measurement.

🚁 Nucleic acid	E Report	<ol> <li>Help</li> </ol>
ID: 181212_143323 DNA-	50 <b>v</b> 50 Ex. Picture	Blank
Con.: <b>295.47</b> ng/µL	Data wavelength: 260nm Absorb:5.909	Sample
A260 : <b>5.909</b> A280 : <b>3.278</b>	5.0	Print
A230 : 3.583	2.0	Spectrum Data
A260/A230 : <b>2.3</b>	1.0 0.0 270 232 244 256 268 280 292 304 316 328	Enlarge Curve
Auto Blank 🚺 Auto Samp	e Losob Baseline at 340nm	Back
Path>>Nucleic acid>>Nucleic acid	<b>b</b> 2018-12-12 14:3	4:23

Fig 4.4 Result of Nucleic Acids measurement

🚁 Nucleic acid		💼 Report		<b>(</b> )	Help
ID: 181212_143323 DNA-	50 🔻	50	Ex. Pic	ture	Blank
Con.: <b>293.888</b> ng/µL	Graph	wavelength	260nm Absor	rb: <b>5.877</b>	Sample
A260 : <b>5.877</b>	No.	A260/A280	A260/A230	C(ng/µL)	Sample
A280 : 3.259	1	1.8	2.3	295.47	Print
A230 : <b>3.601</b>	2	1.8	2.3	295.067	Spectrum Data
A260/A280 : 1.8	3	1.8	2.3	293.885	Enlarge Curve
AL00/AL00. 2.3	4	1.8	2.3	293.888	
Auto Blank 🚺 Auto Samp	le 🚺	✓	Baseline at 340	Dnm	Back
Path>>Nucleic acid>>Nucleic acid			<b>b</b> 2018-1:	2-12 14:35:45	-

Fig 4.5 Data list

#### 3) The detection result data will display as Fig 4.4.

Concentration: Nucleic acid concentration.

A260: The absorbance of 10mm wavelength under 260nm.

A280: The absorbance of 10mm wavelength under 280nm.

A230: The absorbance of 10mm wavelength under 230nm.

**A260/A280:** The ratio of absorbance 260nm,280nm can be used to judge the purity of DNA or RNA. Pure DNA ratio can reach around 1.8, Pure RNA ratio can reach about 2.0. If the ratio value is lower, it means the sample contains some protein, phenol or other contaminants.

**A260/A230:**The ratio of absorbance 260nm,230nm, usually is in the range of 1.8-2.2, If the ratio value is lower, it means the sample contains some contaminants.

4) Click it to input the wavelength and then the absorbance accordingly will be displayed as Fig 4.6.



Fig 4.6 Nucleic Acids detection curve

#### 5) The function of buttons:



printer.

(4) Spectrum Data : Click it to save the full wavelength detection data, if not, only the data of Fig 4.5 will be saved.

(5) Enlarge Curve : Click it to amplify the Fig 4.6 interface, you can move the red coordinate line to change the wavelength and view the absorbance accordingly.

6 Back : Click it back to the main interface.

#### 3.3. Nucleic acids detection report

	luclei	c acio	đ		Ê	Repor	t		(	Help	)
ID		No.	A260	A280	A230	A260/A280	A260/A230	C(ng/µL)	Time		Print
180826_130420		1	4.047	2.292	1.81	1.77	2.24	202.359	2018-08-26 13:08:23	- i	Spectrum Data
180823_103935	✓	2	4.138	2.349	1.85	1.76	2.24	206.929	2018-08-26 13:12:16	-	Evenet Date
180822_171728											Export Data
180822_132814											Delete Data
180822_100402											Delete file
hub											Export File
180821_103226											
Path>>Nucleic a	acid>>	Repor	t				G	2018-08-	26 13:12:56		

Fig 4.7 Report interface

Click "Report" to check results, choose one ID No. You can read all the results of this ID.

As Fig 4.7, select results by clicking the file name, or can select one or all of the results as showed on Fig 4.7, users also can operate by buttons on the right:

1 Print : Click it to print the data as Fig 4.5 with the equipped

#### printer.



Fig 4.8 Nucleic acid full wavelength detection data.

③ Export Data : Export the result to U disk (Insert the U disk into the USB port at back of instrument).

Delete Data : Delete the selected results.

Delete file : Delete all the files by click "File Name" and click

"Delete file".

(4

(5)

6 Export File : Click it to export files to the U disk.

# 3.4. Nucleic acids Help Center

We are sorry to inform you the "Help" has not been finished yet.

#### 4. Protein A280

#### 4.1. Introduction

Proteins, unlike nucleic acids, can exhibit considerable diversity. Protein A280 method is applicable to purified proteins (includes Trp, Tyr residues or Cys-Cys disulfide) exhibiting absorbance at 280nm. It does not require generation of a standard curve. The software calculates the protein concentration directly after measure the absorbance value.

The Protein A280 displays UV spectrum, measures the protein's absorbance at 280nm and calculate the concentration (mg/ml). Like the Nucleic Acids mode, it displays and records 10mm equivalent data.

The Spectrophotometer will accurately measure protein samples up to 90mg/ml BSA) without dilution. When the optical intensity (after measurement sample extinction) is lower than 200(under 10mm path length), software will inform the customer to choose shorter path length to make sure the precision of the measurement. Unique screen is shown as below.

The hydrophobic between the water molecules is the main factor of surface tension. In general, the presence solute of liquids ((including protein, DNA, RNA, salt ion, detergent molecule) can significantly reduce surface tension. Although, for most samples, a 1µL sample size is enough, a 2µL sample size is recommended for protein measurements that the

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liquid column be formed.

#### 4.2. Protein A280 measurement

Click "Protein A280" enter the interface Fig 4.9.



Fig 4.9 Protein detection interface

As Fig 4.9, there are three options at the top of the screen, Protein

A280, Report, Help.

#### 1) Interface Fig 4.9, only the light blue area is clickable.

(1) <sup>ID : 180826\_131326</sup> : The sample batch No., default value is the current time, users can also edit ID by themselves. One ID can include as many as 1000 detection results.

2 10.0 : Click to choose Nucleic Acids type, when you choose "others" and type in the Nucleic Acids factor the instrument will calculate as you set.

3 Blank : Blank the buffer, this step is essential before

measurement. Blank absorbance value is during 0.004-0.03 Abs. The validity of blank control is 30 min and after 30 min, the system will automatically remind you to make blank detection. If the blank calibration failed, there is a icon *i* showed on the top right corner, click it to view the detailed warning information.

(4) Baseline at 340nm : You can choose or cancel the baseline calibration, the default baseline calibration wavelength is 340nm. User can also input wavelength according to requirement. Any experiment, the baseline is automatically set as the absorbance value of the chose wavelength, all results should minus this value.

Notes: If you don't calibrate the baseline, the light spectrum will deviate, and lead to unprecise result.

(5) Auto Blank C: Click the right icon to select the automatic blank detection, when it is turned on, it will do the blank detection automatically the fist time close the rotating arm. When it is turned off the icon will be Auto Blank

Note: The automatic blank only takes effect when there is no blank data of the current detection. If you want to do reblank then need to click the right button "Blank".

<sup>(6)</sup>Auto Sample <sup>(1)</sup>: Click the right icon to select automatic detection, when it is turned on, it will do the detection automatically once the rotating

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arm is closed. When it is turned off the icon will be Auto Sample

Note: The automatic detection only takes effect when there is blank data of the current detection. If no blank data, need to do blank first.

<sup>Data</sup>: Click it to switch to check the history data list and then click
 Graph to switch to check the curve.

#### 2) Operation steps

① Set the batch NO. and Nucleic Acids type;

2 Clean the upper and lower pedestals with dust proof paper, input

the 2µL buffer solution to make blank;

③ Clean the buffer solution on the ower pedestals with dust proof paper;

(4) Measure sample with volume of  $2\mu$ L. Click "Measure" and then enter the interface as Fig 4.10;

Note: The sample must be the new adding before your measurement.

Protein A280	E Report	() Help
ID: 181212_143636 A280	T 10.0 Ex. Picture	Blank
Con.: <b>3.288</b> mg/mL	Data wavelength: 280nm Absorb: 3.288	3 Sample
A280 : <b>3.288</b> A260 : <b>5.926</b>	5.0	Print
A260/A280 : <b>1.8</b>	3.0	Spectrum Data
	1.0	Enlarge Curve
Auto Blank 🕥 Auto Samp	220 232 244 256 268 280 292 304 316 328 Aboob Baseline at 340nm	Back
Path>>A280>>A280	© 2018-12-12 14	:38:28

Fig 4.10 Result of Protein measurement

5 After measurement, pedestals must be cleaned before next measurement.

#### 3) The detection result data can be displayed as Fig 4.11.

Con.:	3.288	mg/mL
	A280 : 3.288	
	A260 : 5.926	
A26	0/A280:1.8	

Fig 4.11 Protein measurement data

Notes: The mass extinction coefficient can be any value if user choose other types, instrument will calculate the concentration according to the mass extinction coefficient.

Con.: Protein concentration;

A260: The absorbance of 10mm wavelength under 260nm;

A280: The absorbance of 10mm wavelength under 280nm;

A260/A280: Ratio absorbance of 260nm and 280nm.

4) Click it to input the wavelength and then the absorbance of it will

be displayed as Fig 4.12.



#### 4.3. Protein A280 detection report

	Proteir	1 A280		Ê	Report		<b>(</b> ) H	elp
ID		No.	A260	A280	A260/A280	C(mg/mL)	Time	Print
190326_092040		1	-0.066	-0.039	0.00	-0.039	2018-12-12 13:45:02	Spectrum Data
181212_143636		2	22.15	13.092	1.69	13.092	2018-12-12 13:48:04	
181212_133929		3	4.791	3.011	1.59	3.011	2018-12-12 13:48:54	Export Data
								Delete Data
								Delete file
								Export File
Path>>A280>>	Report					<b>b</b> 2018-12	-12 14:39:00	1

Fig 4.13 Protein detection report interface

# Notes: The interface is the same as Nucleic Acids detection report, please refer to 3.3. Nucleic Acids detection report.

Click Spectrum Data to enter the interface Fig 4.14 and move the red coordinate line to change the wavelength and view the absorbance of it.



Fig 4.14 Protein full wavelength detection data

# 4.4. Help

We are sorry to inform you the "Help" has not been finished yet.

# 5. Colorimetry

#### 5.1. Introduction

The BCA, Lowry and Bradford are colorimetry detection methods for testing impure protein concentrations.

It is commonly used to detect low concentration and light-absorbing impurities in the ultraviolet regions proteins. A standard curve must be constructed when detecting protein concentrations by colorimetry method. So we combine these three protein test methods into the colorimetry method.

BCA Method: The protein restore the bivalent copper ion to cuprous ion, the latter combined with BCA in the alkaline solution to create a purplish red complex. The chelate created by Cu-BCA has the maximum light absorption at 562nm which is standardized by the light coefficient at 750nm.

Lowry Method: The protein reacts with basic cupper sulfate to create which restore phosphomolybdate the cop-protein complex, and phosphotungstate in the phenol reagent to create а blue compound(molybdenum blue-tungsten blue), which can be detected at 750nm.

Bradford Method: The Coomasie Bright Blue G-250 is reddish-brown in acidic solutions and turns blue after combined with protein. The chroma is proportional to protein concentration, which belongs to dye binding method. The protein-dye complex can be detected at 595nm and standardized at 750nm.

The Nano-500 colorimetry detection mode can be used to detect most of colormetry detection kits in the worldwide markets.

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# 5.2. Colorimetry

Colorimetry	ណា 🕬	Curve	💼 Report	6	Help
ID: 181212_143957	BCA-562	▼ Curve	qwe 🔻	Ex. Picture	Blank
Con.: <b>0.000</b> g	g/mL	Data waveleng	gth: 000nm Abso	orb:0.000	
A562:0.000	0.8				
	0.6				
	0.4 —				
	0.2				
Auto Blank 🚺 A	Auto Sample (	Absorb	44 580 616 652 6	88 724 760 796	Back
Path>>Colorimetry>>Colo	primetry		<b>b</b> 2018-1	2-12 14:40:02	1

A standard curve is required every time before measurement.

Fig 4.15 Colorimetry detection interface

: Click to select the colorimetry type.

-

curve qwe : Curve of the colorimetry type.

#### Measurement steps:

V

BCA-562

① Choose colorimetry type, and curve type.

② Use buffer to make blank.

③ Clean the pedestals by dust-free paper, and input the sample

#### name .

(4) Measure sample with volume of  $2\mu$ L.

# 5.3. Curve

A standard curve is required by colorimetry, and 5 standard samples concentration are needed, the concentration range of standard points should cover all standby sample concentration.

Introduction for Colorimetry interface:

Click "Curve" on the top to build a standard curve before colorimetry assay.



Fig 4.16 Colorimetry detection curve interface

Steps to build up curve:

Click • New Curve , Input curve name, and click "Sure", then you
 will come to standard sample table for curve , see Fig 4.17:

🔐 Co	lorimetry	â	🖞 Curve		I R	leport	(	Help
BCA-562	V	Curve b	ca 🔻	⊡ N	lew Curve	🗓 Del	ete Curve	Blank
Sample name	g/mL 🔻	Absorb	Absorb one	Absorb two	Absorb	Absorb four	Absorb five	
Sample1	0.000	0.000	0.000	0.000	0.000	0.000	0.000	
Sample2	0.000	0.000	0.000	0.000	0.000	0.000	0.000	
Sample3	0.000	0.000	0.000	0.000	0.000	0.000	0.000	
Sample4	0.000	0.000	0.000	0.000	0.000	0.000	0.000	Unspilely Guille
Sample5	0.000	0.000	0.000	0.000	0.000	0.000	0.000	Import Curve
Sample6	0.000	0.000	0.000	0.000	0.000	0.000	0.000	Export Curve
Sample7	ი იიი	0 000	0 000	0 000	0 000	0.000	0.000	
🗄 Save	concern	Ť.	Delete conc	ern	Import	concern		
Path>>Colori	metry>>St	d. Curve			G	2018-08-26	13:38:19	

Fig 4.17 Curve interface to input concentration value

2 Click g/ml to choose unit for sample, click concentration area, it shows samples can be random, the added sample should keep consistent with the selected concentration value.

(3) Then select a standard sample as Fig 4.17 and then click "Blank" and "Sample" in turn to measure the absorbance of standard sample.

Each standard sample can be measured by 5 times, and the average value can be used to build the standard curve. You can delete the standard sample values ( long press sample2, the option window appears), you also can delete some single value among the 5 measurements( long press the one you want to delete, the option window appears).

4 After measuring all samples, click Save Curve to save curve.

Notes: If user plans to leave the interface before building curve complete, the system will appear a dialog window to ask you save curve. You only can find the standard curve at the measurement interface after you save it.



#### Function for buttons:

concentration value.

(5) Delete concern : Click it to delete the current concentration value.

6 Click it to import concern

# 5.4. Colorimetry report

🔐 Color	rimetry	สส์	Curve	💼 Repo	ort 🤅	) Help
ID	Ň	o. A56:	2 C(g/mL)	Curve Name	Time	BCA-562 🔻
181212_141525	<b>V</b> 1	-0.01	6 0.000	qwe	2018-12-12 14:15:52	Print
						Export Data
						Delete Data
						Delete file
						Export File
Path>>Colorime	etry>Report			<b>G</b> 201	8-12-12 14:41:05	1

Fig 4.19 Colorimetry detection report interface

It is similar as the Nucleic Acids detection interface, so here only introduce the differences.

BCA-562 Click it to choose the colorimetry type and the detection data will be displayed.

# 5.5. Colorimetry help

We are sorry to inform you the "Help" has not been finished yet.

# 6. Fluorometer

#### 6.1. Introduction

Click "Fluorometer" button in the main interface and enter the Fluorometer interface as Fig 4.20 below. Click the "Fluorescence" button to test the sample fluorescence directly, there is no curve creation and sample concentration analyses in this test. Click "dsDNA", "Protein" or "Oligo" button to create standard curve, calibrate curve or test samples etc. Click "Kinetics" button to start the kinetic measurement and create the kinetics curve.



Fig 4.20 Fluorometer interface

#### 6.2. Fluorescence

Click "Fluorescence" button in the Fluorometer interface and enter the interface as Fig 4.21 below.

Fluorescence		Report	<li>Help</li>
ID: 181212_144148			Measure
Fluorescence : 5855	No.	Fluorescence	
	1	5861	Print
	2	5855	
			Back
Excitation 460nm Emission 5	25-570nm		
Path>>Fluoroemter>>Fluorescence		<b>L</b> 2018-12-12 14	1:41:58

Fig 4.21 Fluorescence test interface

#### 6.2.1. Fluorescence measurement

(1) Button introduction:



wavelength.

### (2) Operation steps:

①Set the sample ID.

2)Put the cuvette holder into the fluorescence test groove.

3Add 200ul sample into the PCR tube, put the tube into cuvette

holder.

④Click "Measure" button to measure the sample and the result

will be showed in the left of interface.

#### 6.2.2. Fluorescence Report



Fig 4.22 Report

The same as the Nucleic acid report.

#### 6.2.3. Colorimetry help

We are sorry to inform you the "Help" has not been finished yet.

#### 6.3 dsDNA、RNA、Protein

Note: As the software function of dsDNA, RAN and Protein are the same, this manual only introduces the software function of dsDNA. Click "dsDNA" button in the Fluorometer interface to enter the interface as Fig 4.23 below.

🗬 dsDNA	🞢 Curve	💼 Report	<li>Help</li>
ID: 180826_171333	Curve: 2018 🔻	Vol : 10 μL	Measure
Original con.: 245.3	ng/µL		
Sample con.: 12.265	ng/µL		Print
Fluorescence : 11996.	D		
Excitation 460nm Emis	sion 525-570nm		Васк
Path>>Fluoroemter>>dsDI	NA	2018-08-26 17:13	:50

Fig 4.23 dsDNA measure interface

#### 6.3.1. dsDNA

(5)

#### (1) Interface introduction

(1) $10 \times 180826_{171333}$ : Set the test ID, the default is current time.
2 <sup>Curve: 2018</sup> Click to choose the standard curve, or the
sample can not be measured.
$3^{\text{Vol:}}$ <sup>10</sup> <sup>µL</sup> : Click to input the original volume of sample.
(4) Measure : Click it to measure sample and the result will be
showed in the right of interface.

#### Note: The sample can not be measured without standard curve.

Print : Print current measure result.

<sup>(6)</sup>Measure result showed as Fig 4.24 below.



Fig 4.24 Result of dsDNA test

Original con.: The original sample concentration.

Sample con.: The PCR tube sample concentration.

Fluorescence: The Fluorescence value of the measurement.

#### (2) Operation steps

1)Add the sample into the PCR tube and dilute the total volume to

200µl, put the tube into the cuvette holder.

②Set the test ID, standard curve and sample original volume.

③Click Measure button to test and the result will be showed in the left of interface.

# Note: The default sample test volume is 200µl, make sure the correct volume before the measurement.

#### 6.3.2. Curve

You need to create the standard curve before the measurement, a simple standard curve can be made with two points, in order to make sure the accuracy of the result, a hypodispersion five points standard curve is

#### necessary.

🧬 ds	DNA	ñ	Curve		🗐 R		(	i) Help
Curve 20	18 🔻			H New	Curve	🗊 Delete (	Curve	Measure
NO.	ng/µL 🔻	Fluo. mean	Fluo. one	Fluo. two	Fluo. three	Fluo. four	Fluo. five	
Sample1	0.000	7407.33	7414.0	7400.0	7408.0	0.000	0.000	Save Curve
Sample2	25.0	14463.3	14478.0	14468.0	14444.0	0.000	0.000	Display Curve
Sample3	50.0	24764.0	24797.0	24746.0	24749.0	0.000	0.000	Import Curve
Sample4	100.0	43970.3	44019.0	43968.0	43924.0	0.000	0.000	import curve
Sample5	200.0	75511.3	75619.0	75491.0	75424.0	0.000	0.000	Export Curve
Sample6	300.0	105529.	105670.	105518.	105400.	0.000	0.000	Calibration Curve
Sample7	400.0	143063.	143243.	143056.	142890	0.000	0.000	
📩 Save	concern	0	Delete conc	ern				
Path>>Fluoro	pemter>>Cu	irve			G	2018-08-26	17:12:29	-

Click "Curve" enter the standard curve interface as Fig 4.25 below.

Fig 4.25 Fluorescence standard curve

#### (1) Interface introduction

The main layout of the interface is the same as the standard curve interface of the colorimetry, Here are several different layouts.

①There is no "Blank" button, click "Measure" to test the sample directly.

②Calibration Curve: Calibrate the created standard curve to eliminate the drift error of the device.

#### (2) Operation introduction

New Curve:

Click <sup>⊡</sup> New Curve

to input the ID and choose the type of

#### curve.

📌 ds	DNA	â	Curve				G	) Help
Curve	٧			🕂 New	Curve	🗊 Delete (	Curve	Measure
NO.	ng/µL 🔻	Fluo: mean	Fluo. one	Fluo. two	Fluo. three	Fluo, four	Fluo. five	
Sample1	0.000			New Cu	rve		000	
Sample2	0.000	Curve Type	first or	der 💿 d	uadratic	cubic	000	
Sample3	0.000		0				000	Import Curve
Sample4	0.000	Please	input file na	ame			000	Import ourve
Sample5	0.000		Cancel		s	ure	000	Export Curve
Sample6	0.000	0.000	0.000	0.000	0.000	0.000	0.000	Calibration Curve
Sample7	0.000 e concern	0.000	n nnn Delete conc	0.000 ern	0.000	0.000	0.000	
Path>>Fluor	oemter>>Cu	irve			C	2018-09-28	13:09:01	

#### Fig 4.26 choose the type of curve

🧬 ds	DNA	âĭ	Curve		🗐 R		0	Help
Curve 12	3 🔻			🕂 New	Curve	🗊 Delete (	Curve	Measure
NO.	ng/µL 🔻	Fluo. mean	Fluo. one	Fluo. two	Fluo. three	Fluo. four	Fluo. five	
Sample1	0.000	0.000	0.000	0.000	0.000	0.000	0.000	
Sample2	0.000	0.000	0.000	0.000	0.000	0.000	0.000	
Sample3	0.000	0.000	0.000	0.000	0.000	0.000	0.000	Import Curvo
Sample4	0.000	0.000	0.000	0.000	0.000	0.000	0.000	Import Curve
Sample5	0.000	0.000	0.000	0.000	0.000	0.000	0.000	Export Curve
Sample6	0.000	0.000	0.000	0.000	0.000	0.000	0.000	Calibration Curve
Sample7	0.000	0.000	0.000	0.000	0.000	0.000	0.000	
🛃 Save	concern	<b>Ö</b> (	Delete conc	ern	Import of	concern		
Path>>Fluor	pemter>>Cu	urve			G	2009-09-01	08:04:19	

#### Fig 4.27 New Curve

②Click ng/µL to set the units of standard sample and input the concentration of it in sample1 0.000 . Make sure the set concentration is the same as standard sample. There is no requirement of the orders when set the concentrations.

③In the interface as Fig 4.27, when a standard sample is chosen, the bottom colour will be changed blue, then click "Measure" to test the fluorescence of it. Each standard sample can be tested 5 times and the average value is the standard curve sample point. Hold the area of the name of standard sample to delete the standard sample, click the fluorescence value to delete the tested value.

4 Click Save Curve to save the created standard curve.

#### Calibration curve:

Click Calibration Curve enter the calibration curve interface as Fig
 4.26 below, the calibration point range is 1-3.

	🧬 ds	DNA	ណ៍	Curve		Re Re		0	Help
	Curve:	2018							Measure
		ng/µL	Fluo. mean	Fluo. one	Fluo. two	Fluo. three	Fluo. four	Fluo. five	
S	ample1	0.000	0.000	0.000	0.000	0.000	0.000	0.000	
S	ample2	0.000	0.000	0.000	0.000	0.000	0.000	0.000	
S	ample3	0.000	0.000	0.000	0.000	0.000	0.000	0.000	
									Cancel
Pat	h>>Fluor	oemter>>C	urve			•	2018-08-26	17:13:06	

Fig 4.28 Calibration curve interface

2 Input the concentration of the calibration sample into the box

Sample1 0.000 . There is no requirement of the orders when set the concentrations.

③Click "Measure" to test the fluorescence of current standard

sample.

④ Click "Calibrate" to complete the calibration.

#### 6.3.3. Report

📌 dsDl	NA	-	វវវិ	Curve	Í	Report		٩	Help
ID		No.	Curve	Original	Vol	Fluorescence	Time		Print
181212_144923		1	123456	0.0 ng/µL	10.0 µL	5849	2018-12-12 14:49:29		Export Data
		2	123456	0.0 ng/µL	10.0 µL	6632	2018-12-12 14:49:42		
		3	123456	0.0 ng/µL	10.0 µL	8762	2018-12-12		Delete Data
		4	123456	2581.53 ng/µL	10.0 µL	8740	2018-12-12 14:50:05		Delete file
	~	5	123456	2578.78 ng/µL	10.0 µL	8738	2018-12-12 14:50:10		Export File
		6	123456	2580.15 ng/µL	10.0 µL	8739	2018-12-12 14:50:16		
		7	123456	2548.57 ng/µL	10.0 µL	8716	2018-12-12		
Path>>Fluoroe	mter>>	Report				<b>b</b> 2018-12	-12 15:04:13		



The same as the Nucleic acid report.

#### 6.3.4. Colorimetry help

We are sorry to inform you the "Help" has not been finished yet.

#### 6.4. Kinetics

In the Fluorometer interface, click "Kinetics" enter the interface Fig

4.28 below.

	Kinetics	🗈 Report 🗿 H	lelp
ID : 180826_	140800 Total :	00:00:10 Interval : 00:00:05 Ex. Picture	Measure
Cycle	Fluorescence	8,000.0	
1	7364	7,000.0	Print
2	7349	5,000.0	Enlarge Curve
		4,000.0	
		3,000.0	
		2,000.0	
		1,000.0	
		0.0 Fluorescence	Back
Excitation 460n	m Emission 525	-570nm	
Path>>Fluoroer	mter>>Kinetics	► 2018-08-26 14:08:28	-

Fig 4.30 Kinetics interface

#### 6.4.1. Kinetics test

(1) Interface introduction

①<sup>ID: 180826\_140800</sup>: Set the test ID, the default is current time.

(2) Total: 00:00:10 : Set the total time, the "00:00:00" correspond to "Hour: Minute :Second".

(3) Interval : 00:00:05 : Set the interval between two tests, the "00:00:00" correspond to "Hour: Minute :Second".

(4) Measure : Click it start the measurement and enter the interface as Fig4.29 below, click "Stop" button to stop the current measurement.

Kinetics	Report	(i) Help
ID : 180826_140846 Total : 0	0 00 55 Interval : 00 00 05	Ex. Picture
Cycle Fluorescence		Interstite Interstite
	Important Note	
	Unknown sample detecting, please waiting(1/11)	
	Stop	
	0.2	
	0.0 E Fluomscence	Back
Excitation 460nm Emission 525-	-570nm	
Path>>Fluoroemter>>Kinetics	<b>G</b> 2018-0	8-26 14:08:51

Fig 4.31 Kinetics test interface



: Click to print test result.

6 Enlarge Curve : Click it to check the amplified curve after

measurement

⑦ Ex. Picture : Click it to export the curve as picture format to the U

disk.

(2) Operation steps

①Set the test ID, total time and interval time.

2)Put the sample into the cuvette holder and close the lid.

③Click the "Measure" to start the measurement.

④Test times and fluorescence value will be showed in the left and

the curve will be made in the middle of the interface.

#### Note: 1. The maximum test time is 99, if set more than 99

times, the device can only test 99 times.

2. Click "Stop" in the testing, it will stop when the next

test complete and it can not continue again.

# 6.4.2. Kinetics test report

🧭 Kinel	tics		🚺 Report		()	Help
ID	Cycle	Fluorescence	Excitation	Emission	Time	Print
181212_142344	1	5834	460nm	525-570nm	2018-12-12 14:23:57	Export Data
	2	5831	460nm	525-570nm	2018-12-12 14:23:57	
						Delete file
						Export File
Path>>Fluoroemter	>>Report			<b>b</b> 2018-1	2-12 15:06:39	1

Fig 4.32 Kinetics test report

The same as the Nucleic acid report.

#### 6.4.3. Colorimetry help

We are sorry to inform you the "Help" has not been finished yet.

# 7. Uv-Vis Full-spectrum Scanning

# 7.1 Introduction

UV-VIS module allows the Spectrophotometer to function as a conventional spectrophotometer. Sample absorbance is displayed on the screen from 200nm to 800nm.

Samples with high absorbance (up to 300A equivalent at 10mm path) can be measured directly.

#### 7.2 Uv-Vis measurement

Uv-Vis measurement interface as Fig 4.33:



Fig 4.33 Uv-Vis detection interface

It is similar as the Nucleic Acids detection interface, here only introduce

the differences.



click it to enter the interface Fig 4.34. It shows the 200-800 wavelength light intensity of blank sample.



Fig 4.34 Blank light intensity

2 You can input the wavelength as Fig 4.35 before the detection and

the absorbance will be showed after the detection.

No.	Wave	Absorb
1	230	0.000
2	260	0.000
3	492	0.000
4	630	0.000
5	000	0.000

Fig 4.35 Check the absorbance of wavelength

③ After blank detection, click Sample and then Sample data will be available. Click it enter the interface as Fig 4.36. It shows the light

intensity of 200-800 wavelength.



Fig 4.36 The sample light intensity

#### **Operation steps:**

① Set the batch NO. and Nucleic Acids type;

② Clean the upper and lower pedestals with dust proof paper, add

2µL buffer solution to make blank;

③ Clean the buffer solution on the pedestals with dust proof paper;

(4) Measure sample with volume of 2µL and click "Measure" to detect the sample;

Note: The sample must be the new adding before your measurement.

<sup>(5)</sup> After measurement, pedestals must be cleaned before next measurement.

# 7.3. Uv-Vis Report

<b>※</b>	Jv-Vis				Î Re	port		()	Help
ID		No.	W1	W2	W3	W4	W5	Time	Print
190403_151546	✓	1	0/0.0	0/0.0	0/0.0	0/0.0	0/0.0	2018-12-12 14:25:56	Spectrum Data
190403_145607									
190326_085027									Export Data
181212_142517									Delete Data
									Delete file
									Export File
Path>>Uv-Vis>>	>Repor	t					<b>b</b> 2018-	12-12 15:08:06	10

Fig 4.37 Uv-Vis detection report

It is similar as the Nucleic Acids detection, here only introduce the difference.



Fig 4.38 Uv-Vis optical wavelength data

# 7.4. Uv-Vis Help

We are sorry to inform you the "Help" has not been finished yet.

## 8. OD600

#### 8.1. Introduction

OD600 mean a solution absorbance value at under wavelength of 600nm.

An important application is to measure bacterial density, which tests the culture solution concentration by the bacterial ABS.

### 8.2. OD600 measurement

li i	Report		<b>і</b> н	elp
Dark current	000	intensity	000	Blank
No.		OD600		Samula
				Back
		<b>b</b> 2018-12-	12 15:08:29	-
	Dark current	Report Dark current 000 No.	Report         Dark current       000       intensity         No.       OD600	Image: Report     Dark current     000     No.     OD600     Image: No.     OD600     Image: No.     OD600

Fig 4.39 OD600 detection interface

#### **Operation steps:**

- ① Set the batch NO. and Nucleic Acids type;
- ② Blank before each measurement. Users can make blank without

anything, blank with empty cuvette, or buffer in cuvette.

- ③ Add 2ml~3ml sample into the cuvette after blank.
- ④ Click Measure, the OD600 value will show at the left.

### 8.3. OD600 Report

🍇 c	D600		💼 Repo	rt	<li>Help</li>
ID		No.	OD600	Time	Print
bmm!	✓	1	0.000	2019-03-26 08:55:23	Export Data
190403_100208		2	0.000	2019-03-26 08:55:40	Delete Data
		3	0.000	2019-03-26 08:55:51	Delete Data
		4	6.497	2019-03-26 08:56:03	Delete file
		5	6.497	2019-03-26 08:56:07	Export File
		6	5.594	2019-03-26 08:56:13	
		7	0.001	2019-03-26	
Path>>0D600>>	Report			2018-12-12 15:0	8:47

Fig 4.40 OD600 detection report interface

# 8.4. OD600 Help

We are sorry to inform you the "Help" has not been finished yet.

# 9. System

SystemImage

Click "System" on the main interface, as Fig 4.41:

Fig 4.41 System setting

# 9.1. Time setting

Click "Time" to start setting, as Fig 4.42.

Automatic date & time Use network-provided time	
Automatic time zone	
Use network-provided time zone	
Set date	
August 26, 2018	
Set time	
14:53	
Select time zone	
GMT+00:00 GMT+00:00	
	NEXT

Fig 4.42 Time setting interface

①"Automatic date & time": It needs to connect the internet to calibrate time automatically, it is unavailable at present.

2 "Automatic time zone": It needs to connect the internet to calibrate time zone automatically, it is unavailable at present.

③"Set date": Click it enter the date setting interface as Fig 4.43 below.





④ "Set time": Click it enter the time setting interface as Fig 4.44

below.





⑤"Select time zone": Click it enter the time zone setting interface as

Fig 4.45 below.

Д	GMT+06:30	
U	Krasnovarsk	
1	GMT+07:00	
A		
U	Bangkok	
1	GMT+07:00	
s		
A	Jakarta	
	GMT+07:00	
s	Shanghai	
0	GMT+08:00	
	Hona Kona	
S	GMT+08:00	
G		
l	Irkutsk	
L	GMT+08:00	



6 "Use 24-hour format": Set the 24-hour format as Fig 4.46 below.

Automatic time zone	
Use network-provided time zone	
Set date	
August 10, 2018	
Set time	
08:56	
Select time zone	
GMT+08:00 China Standard Time	
Jse 24-hour format	
13:00	
	NEXT

Fig 4.46 Use 24-hour format

# 9.2. Language setting

Click the "Language" icon, set language at the dialog window. As Fig 4.47.

	Syster	n	111
6	Salaat Lang		
Time	中文 English	© ()	
	Sure		
Brightness	Upgrade	Repair	Back
Path >>Main Menu		<b>b</b> 2018-08-26 14:55:26	

Fig 4.47 Language setting

# 9.3. Print

Click "Print" icon, set the print mode on the dialog window. As Fig 4.48.

	System		111
Time	Print Setting		
Time	Manual Print	$\odot$	
	Automatic Print	$\bigcirc$	
	Sure	_	
Mar 1	C.		
Brightness	Upgrade	Repair	_
			Back
Path >>Main Menu		<b>()</b> 2018-08-26 14:55:41	

Fig 4.48 Print setting

# 9.4. Brightness

	Sys	stem		111
6	Bright	tness		
Time	Cancel	Sure		
		×		
Brightness	Upgrade	Repair		Back
Path >>Main Menu		<b>C</b> 2018-08-	-26 14:56:05	

Fig 4.49 Brightness setting

Click "Brightness" icon, slide to set the brightness to a suitable one. As Fig 4.49.

# 9.5. Upgrading

Put the upgrading software on the root directory of mobile hard disk drive and insert it into the instrument, then click "upgrade" icon to install the software.

# 9.6. Maintenance

This part is for production and maintenance , which is not allowed to enter into.

# **Chapter 5 Trouble and shootings**

No.	Fault phenomenon	Cause analysis	Shootings
1	Instrument can not turn on.	No power supply, Switch defective, Power adapter defective.	Check the power supply, Replace the switch, Contact the vendor.
2	Measurement result not precise	Liquid column unformed, Pedestal contaminated, others.	Add sample again, make sure the liquid column formed well, Clean the pedestals, Contact supplier or manufacturer.
3	OD600 module failure	Poor connection between cable and board.	Contact supplier or manufacturer.
4	Insufficient light intensity error	Analysis module defective, optical fiber broken.	Contact supplier or manufacturer.
5	Touch screen hops	Power supply without grounding.	Provide effective grounding power supply.
6	Communication timeout	Analysis module communication failure.	Restart instrument, or contact supplier or manufacturer.

Memo



Memo



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