BLUE-RAY BIOTECH

EzDrop 1000 Micro-Volume Spectrophotometer

BRED-1000

Operation Manual

Ver. 1.1

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1 Safety Precautions

Before using the **EzDrop 1000** for the first time, please read this entire Operation Manual carefully. To guarantee problem free, safe operation of the **EzDrop 1000**, it is essential to observe the following section.

1.1 Intended Use

This instrument is intended to be used by trained personnel to perform solution analysis. In this manual we assume that the user have knowledge of basic laboratory procedures and spectroscopic analysis.

1.2 General Instrument Safety

⚠ PHYSICAL INJURY HAZARD.

Using the instrument in a manner not specified by Blue-Ray Biotech may result in personal injury or damage to the instrument.

1.2.1 Transportation and Storage

This instrument should be transported and stored in an environment with a temperature of -10 to 60°C, relative humidity 20 to 80%.

1.2.2 Installation and Operation

1. Do not use the device in a potentially explosive environment or with potentially explosive chemicals.
2. Avoid placing the device in direct sunlight.
3. Install the device in a location free of excessive dust.
4. Install the device in a room with a temperature of 15–30°C, relative humidity 20–80%.
5. Choose a flat, stable surface capable of bearing the weight of the device.
6. Make sure the power source conforms to the required power supply specifications.
7. To avoid electric shock, make sure the device is plugged into a grounded electrical outlet.
8. Do not allow water or any foreign objects to enter the various openings of the device.

1.2.3 Cleaning, Decontaminating, and Servicing the Instrument

Before using a cleaning or decontamination method other than those recommended by the manufacturer, verify with the manufacturer that the proposed method will not damage the equipment.

Switch off and unplug the device before cleaning, servicing, or replacing the fuses.

Repairs should be carried out by authorized service personnel only.

1.2.4 Instructions for Removal from Use, Transportation, or Disposal

Do not dispose of this product as unsorted municipal waste. Follow local municipal waste ordinances for proper disposal provisions to reduce the environmental impact of waste electrical and electronic equipment (WEEE).

European Union Customers:

Call your local Blue-Ray Biotech Distributor's Customer Service office for equipment pick-up and recycling.

1.3 Chemical Waste Safety

1.3.1 Chemical Waste Hazard

⚠ **HAZARDOUS WASTE.**

Refer to Material Safety Data Sheets and local regulations for handling and disposal.

2 General Description

The **EzDrop 1000** is a fast micro-volume spectrophotometer that provides accuracy and intuitive operational experience only in 3 seconds. It enables the measuring of samples from 190 to 1000 nm, a broad range which offers flexibility for experiment. With the replaceable sample window, users don't have to worry about residues.

2.1 Features

- Large LCD touch panel enhances visibility and ease-of-operation.
- Robust and modern outlook design.
- Simple and easy-to-use graphical interface.
- Multiple built-in protocol functions.
- Fast measuring time, in 3 seconds.
- Wide measuring range, 190 - 1000 nm.
- Quartz sample window, which protects the optical analysis system.
- A Nano hydrophobic coating layer on the quartz window.
- Replicable sample window avoids contamination.
- Thoughtfully designed assist light.
- Auto measurement.
- To automatically create operating history.
- Cushioning design of detecting arm.

2.2 Product Overview

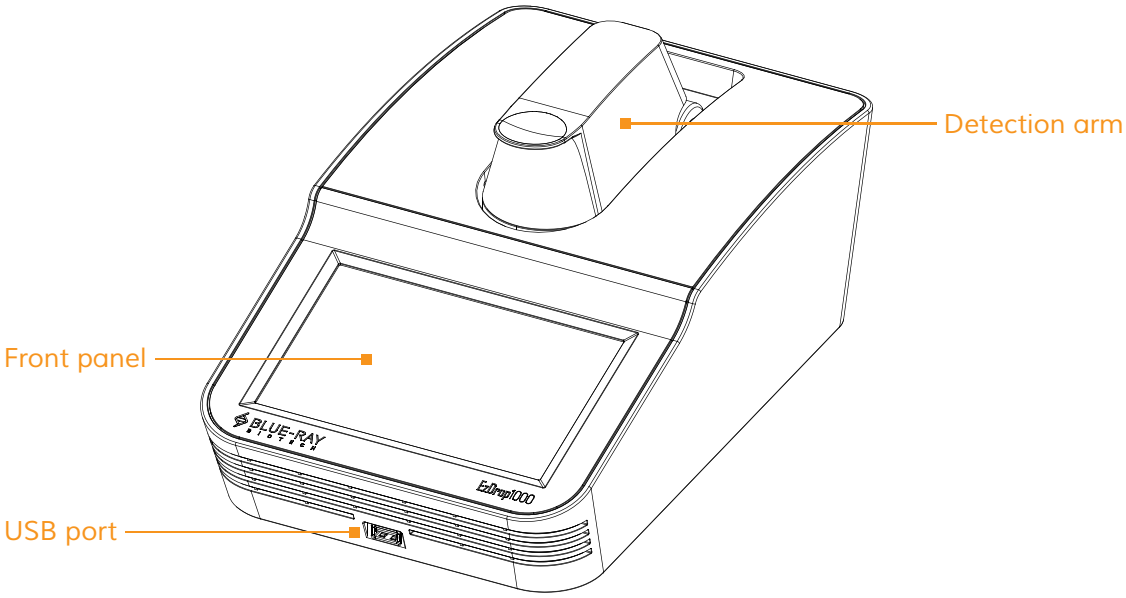


Figure 1. Front view.

Table 1. Detailed description for top view

Name	Function
Front panel	7” high resolution color LCD display with capacitive touch panel. It displays the current status of the system and allows the user to operate the instrument.
USB port	For data output via USB flash drive.
Detection arm	Detection arm with cushioning design to reduce closing impact.

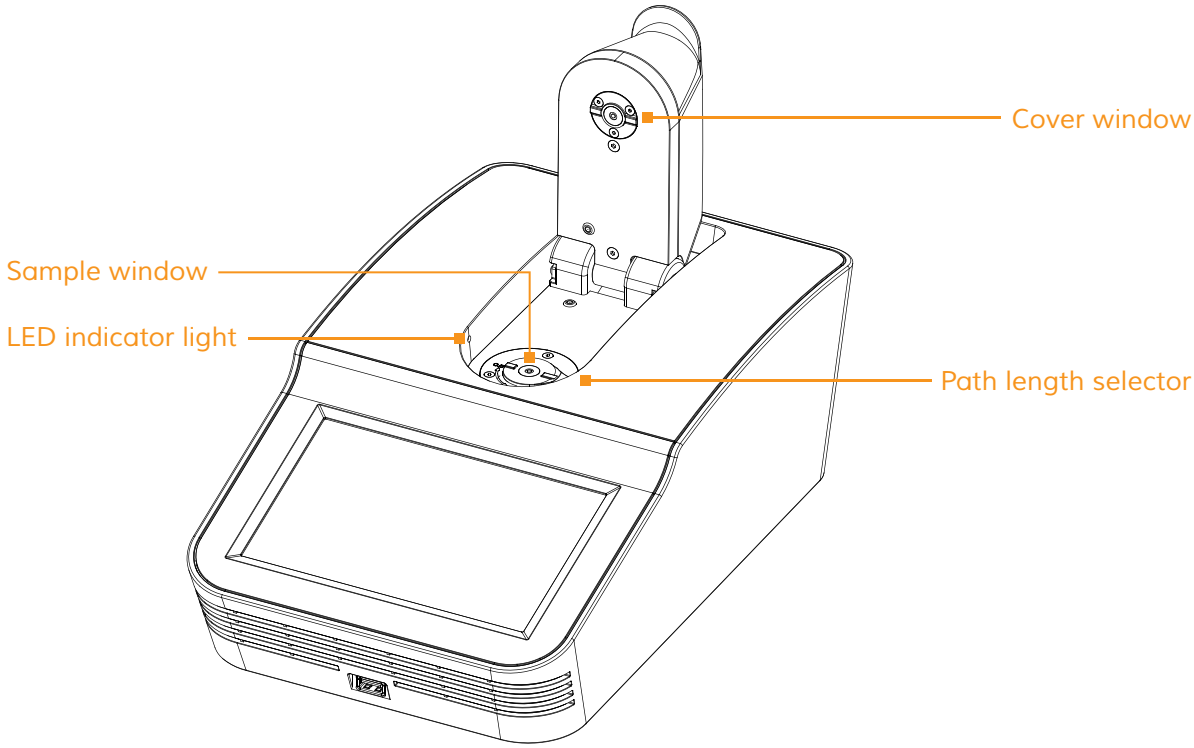


Figure 2. Front view with opened detection arm.

Table 2. Detailed description for top view with opened detection arm

Name	Function
Cover window	Quartz glass with Nano hydrophobic coating layer. It protects optical fibers and also reduces contamination.
Sample window	Quartz glass with Nano hydrophobic coating layer. It has an indicating sample adding design. It reduces the contamination and also protects optical fibers.
Path length selector	Light path of EzDrop can be selected manually by path length selector according to the absorbance (concentration) range difference.
Indicator light	Assisting LED light which makes up for the lack of ambient light, ensuring sample adding quality.

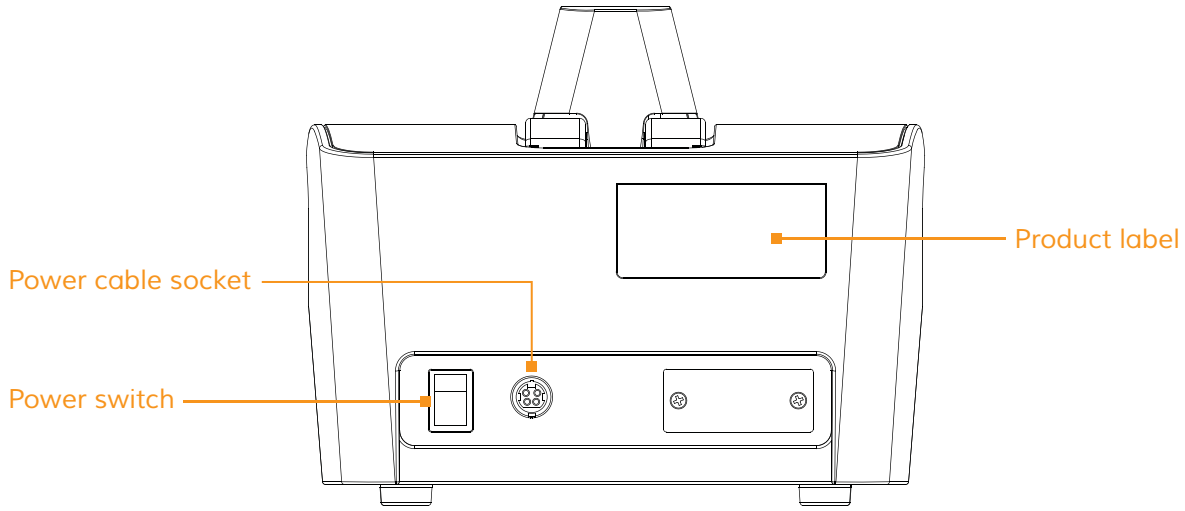


Figure 3. Rear view.

Table 3. Detailed description for rear view

Name	Function
Power cable socket	Power cable socket, connect device to the AC power supply.
Power switch	Power On/Off switch.
Product label	Indicates the model name, serial number, power specification, and other important information.

3 Getting Started

3.1 Unpacking

Once you open the **EzDrop 1000** package, confirm that all of the following items are included:

- EzDrop 1000 x 1
- Quick Operation Guide x 1
- Power Adapter x 1
- Power Cord x 1
- Calibration Report x 1

If any items are missing, damaged, or any incorrect items are included in the package, please contact your local Blue-Ray Biotech distributor or sales representative immediately.

3.2 Initial Operation

Place the device on a steady, flat table. Connect the power cord to the power socket at the rear of the device.

Switch on the device using the power switch at the rear of the device. The LCD display will show the boot screen, start initiation progress, and then the "*EzDrop*" title will be displayed. Please **DO NOT** open the detection arm until system diagnosis is completed. Tap on the "*EzDrop*" title to log into the **Main Screen** and start your operation. Tap on the "*EzDrop*" title again on the **Main Screen** to log out.

Switch off the device when not in use.

Note	The adapter is foolproof, which requires more force to plug in and out.

3.3 Main Screen

On the **Main Screen** there are some information items indicating the status of the **EzDrop 1000**; it also contains 8 main function icons. Please refer to the following Figure 4 and Table 4 for the detailed description.

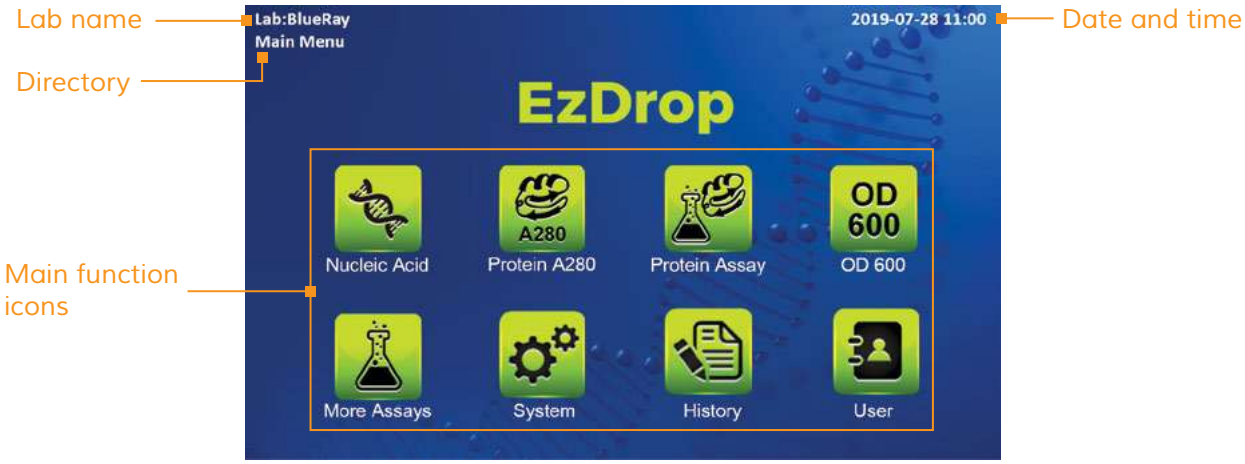


Figure 4. Main Screen overview

Table 4. Main function icons

Icon	Function	Description
	Nucleic Acid	To create and edit nucleic acid protocols.
	Protein A280	To create and edit protein A280 protocols.
	Protein Assay	To create and edit protein standard curve protocols.
	OD 600	To create and edit OD600 protocols.
	More Assays	To create and edit customized protocols.
	System	System setting.
	History	To access stored reports.
	User	User folder management.

3.4 Detection Arm Opening/Closing

To open the arm, hold the detection arm and lift to the end as shown in Figure 5.

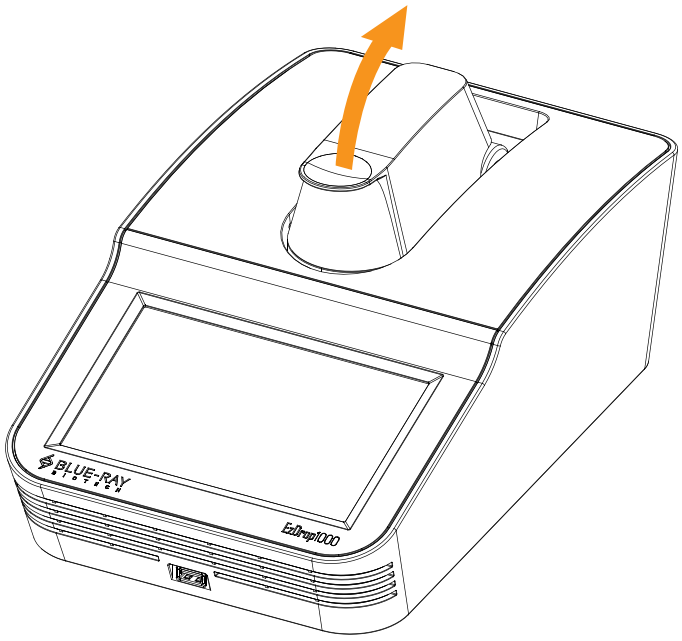


Figure 5. Opening the arm.

To close the detection arm, hold the edge of the arm, and let the detection arm down gently to the correction position as shown in Figure 6. With the cushion design on the detection arm, it reduces impact even when letting the detection arm drop.

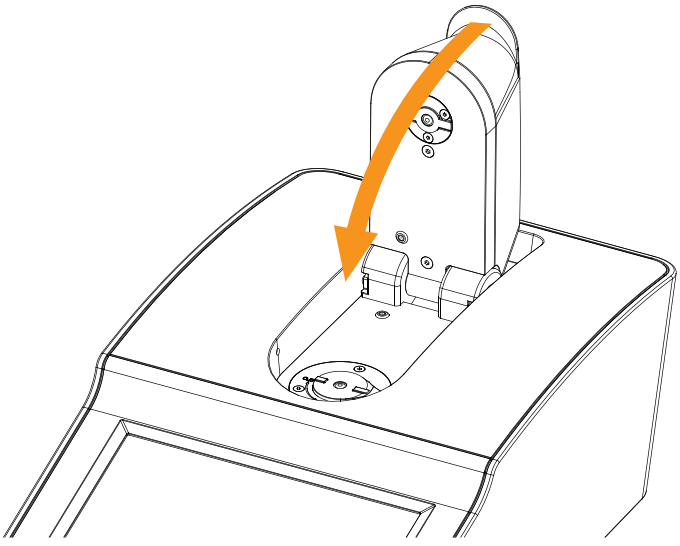


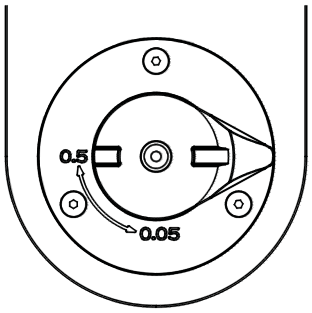
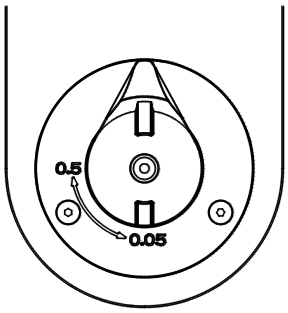
Figure 6. Closing the arm.

3.5 Adjusting the Path Length Selector

The path length of **EzDrop 1000** is not automatically selected but selected by hand. The metal light path selector shown down below in Table 5 is the manual path length selector of **EzDrop 1000**. The measurement range of 0.5 mm path length is 0.04 to 30 Abs, and the range of 0.05 mm is 20 to 400 Abs.

Before starting to examine your samples, check if the light path length selector is in the right position. When the path length selector is in the vertical position to the detection arm (Figure 7), it represents the 0.5 mm path length. In the horizontal position (Figure 8) it represents the 0.05 mm path length. Hold the handle of the light path selector to adjust between 0.5 mm and 0.05 mm path length.

Table 5. Manual path length selector guide

Position	Path length selector	Measuring range
 **Figure 7. 0.5 mm path length.**	0.5 mm path length	From 0.04 to 30 Abs
 **Figure 8. 0.05 mm path length.**	0.05 mm path length	From 20 to 400 Abs

3.6 Basic Operation

3.6.1 Protocol Screen Features

In the protocol application, there are different tab pages (Table 6) and function icons (Table 7).

Table 6. Information tab page

Tab page	Description
Data/Sample Data	The page for the detailed sample information and setting.
Standard	The page only exists in protocols which need to establish a standard curve for measurement; it only presents standard data.
Table	The page of total samples report.
Graph	The page for graph result.
Customized setting	The page only exists in More Assays applications. User can modify protocol customized settings at this page.

Table 7. Function icon

Icon	Function	Description
	Blank	To establish Blank data.
	Auto Run: On	The instruction of Auto Run function is on.
	Auto Run: Off	The instruction of Auto Run function is off.
	Measure	To do sample measurement or to do standard measurement.
	Delete	To delete Sample measurement data. Note: Standard measurement data cannot be deleted but can be overwritten.
	Save Result	To save the report.
	Back	Return to the last page.

3.6.2 Basic measurement operation

1. Choose the correct **Method** type according to experiment.
2. Ensure the surface of the sample window and the cover window are both clean.
3. Adjust the path length selector to appropriate position/light path.
4. Mix the sample gently before adding it to the sample window.
5. Add appropriate solution of at least 1μL and click **Blank** to establish Blank data.
6. Wipe away the blank solution. Add the sample of at least 1μL and click **Measure**.
7. Clean the sample window and cover window with lint-free wipe paper between changing samples and after the experiment is done. Use water, ethanol, or isopropanol if needed.

Note	If the **Auto Run** function is on, the **Measure** will run automatically while closing the detection arm.

4 Application: Nucleic Acid

This application will measure the samples absorbance value at 260 nm, which is the peak of nucleic acid absorbing UV light, to calculate the concentration. The unit is ng/μL. The purity of nucleic acid samples can be estimated by two absorbance ratios, A260/280 and A260/230.

4.1 Overview of Screen Features

The screen of nucleic acid protocol can be separated into 3 parts: information tab bar, information report area, and functions icons.

The information tab bar has 3 tab pages: Data page, Table page, and Graph page. The information areas show different reports on different tab pages.

4.1.1 Data Tab Page

On the data tab page of nucleic acid protocol (Figure 9), the data information parts have the features down below (Table 8).

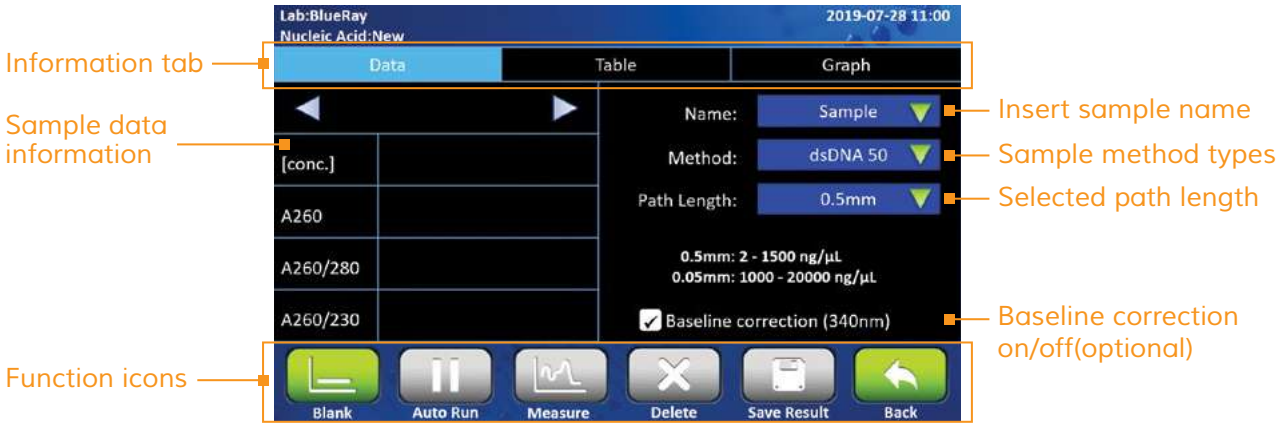


Figure 9. Data tab page.

Table 8. Data tab page information

Features	Description
[conc.]	The concentration is calculated from absorbance at 260 nm, and the unit is ng/μL.
A260	Displays the absorbance at 260 nm, which is normalized to a 10 mm path length equivalent.
A260/280	Displays the ratio of the absorbance at 260 nm and 280 nm. In dsDNA protocol, when the ratio < 1.75, a warning icon ⚠ will pop up. In RNA, a warning pops up when it < 2.0. In ssDNA, a warning pops up when it < 1.75.
A260/230	Displays the ratio of the absorbance at 260 nm and 230 nm.
Name	The sample name can be inserted here. The default is Sample.
Method	Includes sample types like dsDNA, RNA, and ssDNA. The default is dsDNA.
Path Length	The light path chosen by the path length selector will be detected automatically and shown the length here.
Baseline Correction	The wavelength for bichromatic normalization is 340 nm. This is an optional function and the default is on.

4.1.2 Table Tab Page

The table tab page will show all the data results. If the user needs to know more details of one data item, tap the check box column to select the data. The detail will be shown on the **Data** page and the **Graph** page.

Figure 10. Table tab page.

Tap the **Sample** column to change the sample name. The **Blank** also can be renamed, but this is not suggested. You need to measure the **Blank** again if the original blank data has been renamed.

Note	Only one date item can be checked at one time.

4.1.3 Graph Tab Page

The graph of measuring samples can be enlarged or minimized. The axis can be moved by dragging the graph.

Long touch the x, y- axis on graph to turn the modified graph back to default.

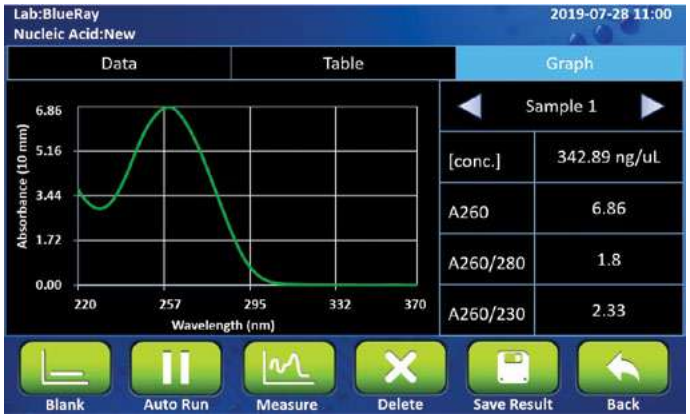


Figure 11. Graph tab page.

4.2 Protocol Operation

1. On the main menu, tap on  to enter protocol section.
2. Ensure the sample window and the cover window on the detection arm are clean.
3. Select the correct **Method** type according to the experiment. The default selection is dsDNA.

4. Open the detection arm and turn the path length selector to the appropriate position. For example, the dsDNA concentration range of 0.5 mm is from 2 to 1500 ng/µL, and 0.05 mm is from 1000 to 20000 ng/µL. All methods' ranges are shown on the **EzDrop 1000** screen.
5. Add appropriate solution of at least 1 µL and tap on  to establish Blank data.
6. Tap on **Name** bar to insert the sample name (optional). The naming system is auto-numbering.
7. Wipe away the blank solution off the sample window and the cover window with lint-free wipes.
8. Add your sample of at least 1 µL and tap on  for sample measurement.
9. Clean the sample window and cover on the detection arm with lint-free wipe paper after the experiment. Use water, ethanol or isopropanol if needed.
10. The **Baseline correction** (340 nm) function is optional, and can be turned on/ off anytime.
11. The default of **Auto Run** function is off  . If **Auto Run** is turned on  , sample measurement will be performed automatically after closing the detection arm.

Note	
	1. In Nucleic Acid, dsDNA, RNA, ssDNA application is offered in this protocol. If you need to test other samples, please use **Factor Method** to customize your protocol settings in **More Assays**. 2. Blank is not allowed to be used for sample naming.

4.3 Calculation

In the nucleic acid protocols, a modified Beer-Lambert equation is used to calculate concentrations with absorbance and factor as follows, with or without baseline correction:

Without background correction:

$c = A260 \times \varepsilon / b$

With background correction

$c = (A260 - A_{Baseline}) \times \varepsilon / b$

c = the nucleic acid concentration in ng/μL

A260 = the absorbance at 260 nm

$A_{Baseline}$ = the absorbance at baseline wavelength

ε = the extinction coefficient factor of nucleic acid in ng*cm/μL

b = the path length in cm

The general extinction coefficient factors used in the calculation of nucleic acid are shown in Table 9.

Table 9. Extinction coefficient factors of nucleic acids

Type	Extinction coefficient factors
dsDNA	50 ng× m/μL
RNA	40 ng×cm/μL
ssDNA	33 ng×cm/μL

5 Application: Protein A280

This application will measure the samples absorbance value at 280 nm, which is the peak of purified protein absorbing UV light, to calculate the concentration. The unit of protein concentration is mg/mL. The purity of homogenous protein can be estimated by absorbance ratios of A260/280.

5.1 Overview of Screen Features

The screen of Protein A280 protocol can be separated into 3 parts: information tab bar, information report area, and functions icons.

The information tab bar has 3 tab pages: Data page, Table page, and Graph page. The information areas show different reports on different tab pages.

5.1.1 Data Tab Page

On the data tab page of nucleic acid protocol (Figure 12), the data information parts have the features below (Table 10).

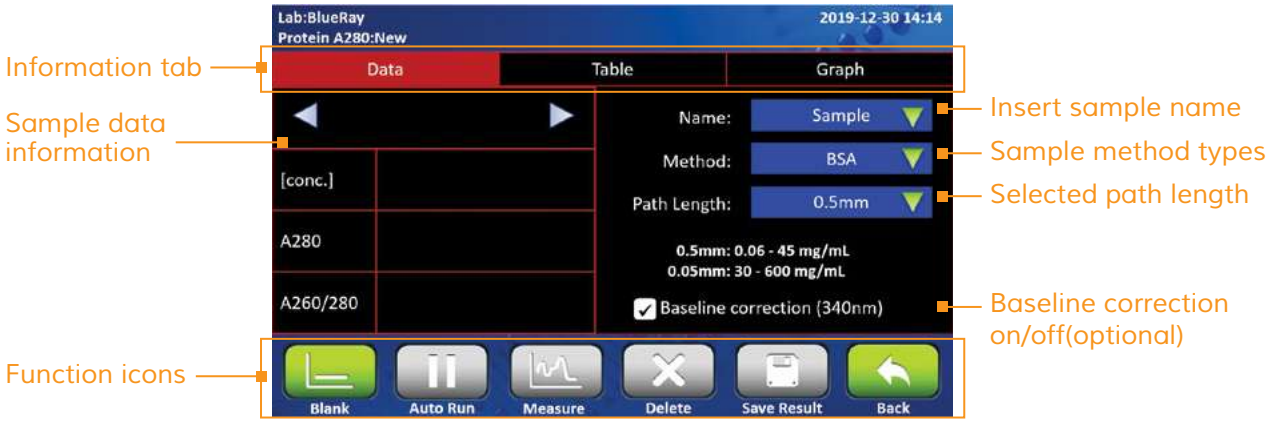


Figure 12. Data tab page.

Table 10. Data tab page information.

Features	Description
[conc.]	The concentration is calculated from absorbance at 280 nm, and the unit is mg/mL.
A280	Display the absorbance at 280 nm, which is normalized to a 10 mm path length equivalent.
A260/280	Displays the ratio of the absorbance at 260 nm and 280 nm. When the ratio of A260/280 > 0.6, a warning icon ⚠ will pop up.
Name	The sample name can be inserted here. The default is **Sample**.
Method	It includes protocol type such as BSA, IgG, Lysosome, 1A = 1 mg/mL, and Customized protein factor. The default is BSA.
Path Length	The light path chosen by the path length selector will be detected automatically and shown which length it is.
Baseline Correction	The wavelength for bichromatic normalization is 340 nm. This is an optional function and the default is on.

5.1.2 Table Tab Page

The table tab page will show all the data results. If the user needs to know more details of one data item, tap the check box column to select the data. The detail will be shown on the **Data** page and the **Graph** page.

Figure 13. Table tab page.

Tap the **Sample** column to change the sample name. The **Blank** can also be renamed, but this is NOT suggested. You need to measure the **Blank** again if the original blank data has been renamed.

Note	Only one date item can be checked at one time.

5.1.3 Graph Tab Page

The graph of measuring samples can be enlarged or minimized. The axis can be moved by dragging the graph.

Long touch the x, y- axis on graph to turn the modified graph back to default.

Figure 14. Graph tab page.

5.2 Protocol Operation

1. On the main menu, tap on 

to enter protocol section.
2. Ensure the sample window and the cover window on the detection arm are clean.
3. Select the correct **Method** type according to the experiment. The default selection is BSA.

4. Open the detection arm and turn the path length selector to the appropriate position. For example, the BSA concentration range of 0.5 mm is from 0.06 to 45 mg/mL, and 0.05 mm is from 30 to 600 mg/mL. All the methods' ranges are shown on the **EzDrop 1000** screen.
5. Add appropriate solution of at least 1 µL and tap on  to establish Blank data.
6. Tap on **Name** bar to insert the sample name (optional). The naming system is auto-numbering.
7. Wipe away the blank solution off the sample window and the cover window with lint-free wipes.
8. Add your sample at of least 1 µL and tap on  for sample measurement.
9. Clean the sample window and cover window on the detection arm with lint-free wipe paper after the experiment. Use water, ethanol or isopropanol if needed.
10. The **Baseline correction** (340 nm) function is optional, and can be turned on/ off anytime.
11. The default of **Auto Run** function is off  . If **Auto Run** is turned on  , sample measurement will be performed automatically after closing the detection arm.

Note	1. In Protein A280, BSA, IgG, Lysosome, 1A = 1 mg/mL, and Customized protein factor application is offered in this protocol. If you need to test other samples, please use Factor Method to customize your protocol setting in More Assays. 2. Blank is not allowed to be used for sample naming. 3. It is suggested to clean the sample window and cover window when exchanging different concentrations of samples.

5.3 Calculation

In the protein A280 protocol, a modified Beer-Lambert equation is used to calculate concentrations with absorbance and factor as follows, with or without baseline correction:

Without background correction:

$c = A280 \times \varepsilon / b$

With background correction

$c = (A280 - A_{Baseline}) \times \varepsilon / b$

c = the purified protein concentration in mg/mL

A280 = the absorbance at 280 nm

$A_{Baseline}$ = the absorbance at baseline wavelength

ε = the extinction coefficient/purified protein factor in g*cm/L

b = the path length in cm

The extinction coefficient factors used in the calculation of purified protein are shown in Table 11.

Table 11. Extinction coefficient factors of purified proteins.

Type	ε (g×cm/L)	Ext. Coeff. (L/g×cm)
BSA	1.50 g×cm/L	0.667 L/g×cm
IgG	0.72 g×cm/L	1.37 L/g×cm
Lysosome	0.38 g×cm/L	0.264 L/g×cm
1 A = 1 mg/mL	1 g×cm/L	1 L/g×cm

6 Application: Protein Assay

This application will measure homogenous protein absorbance value at different wavelengths, according to different protein assay reagents. The unit of this protocol is mg/mL.

6.1 Overview of Screen Features

The screen of protein assay protocol can be separated into 3 parts: information tab bar, information report area, and functions icons.

The information tab bar has 4 tab pages: Sample Data page, Standard page, Table page, and Graph page. The information areas show different reports on different tab pages.

6.1.1 Sample Data Tab Page

On the Sample data tab page of protein assay protocol (Figure 15), the data information parts have the features below (Table12). This page only shows the sample data, and does not show standard data.

Figure 15. Sample Data tab page.

Table 12. Data tab page information.

Features	Description
[conc.]	The concentration is calculated from absorbance at kit-requested wavelength. The unit is mg/mL.
A562/ A595/ A750	Displays the absorbance at kit-requested wavelength. The BCA method uses 562 nm, Bradford method uses 595 nm, and Lowry method uses 750 nm. The absorbance is normalized to 10 mm path length equivalent.
Name	The sample name can be inserted here. The default is Sample.
Method	It includes protein measuring assay such as BCA method, Bradford method, and Modified Lowry method. The default is BCA method.
Path Length	The light path chosen by the path length selector will be detected automatically and shown which length it is. In protein assay protocol, 0.5 mm is the only available path length.
Baseline Correction	The wavelength for bichromatic normalization is different from protein methods. In the BSA method, it is 750 nm; in the Bradford method, it is is 750 nm; and in the Modified Lowry method, it is 405 nm. The default is on. (Optional)

6.1.2 Standard Tab Page

The Standard tab page (Figure 16) is the page to measure standard samples absorbance at specific wavelength and establish standard curve. It only shows the standard data result. The features are shown below (Table 13).

Figure 16. Standard tab page.Table

13. Standard tab page information.

Features	Description
mg/mL	This is the concentration column. The value is inserted by the users.
Abs	The absorbance measured at different wavelength according to the protein method.
Avg. Abs	The average absorbance of the standard repetition. It is calculated automatically.
Curve Type	The standard curve types the user can select: linear, interpolation, and 2nd order polynomial.
Repetition	The repetition frequency of standard numbers. The default value is 1 and the maximum is 3.
Generate Std. Curve	Check the icon to establish the standard curve.

6.1.3 Table Tab Page

The table tab page will show only the sample data result. The standard data is NOT included on this page. If the user needs to know more details of the sample data, tap the check box column to select the sample data. The detail will be shown on the **Sample Data** page and the **Graph** page.

Figure 17. Table tab page.

Tap the **Sample** column to change the sample name. The **Blank** can also be renamed, but this is not suggested. You need to measure the **Blank** again if the original blank data has been renamed.

Note	Only one date item can be checked at one time.

6.1.4 Graph Tab Page

In the protein assay protocol, there are 2 kinds of graph: the standard curve graph and sample absorbance graph.

They can be enlarged or minimized. The axis can be moved by dragging the graph. Long touch the x, y- axis on graph to turn the modified graph back to default.

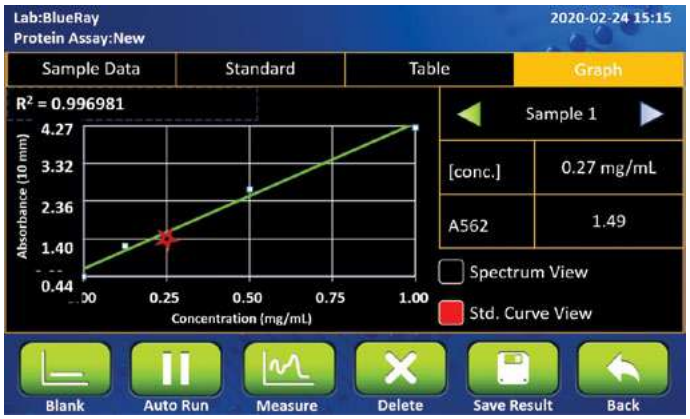


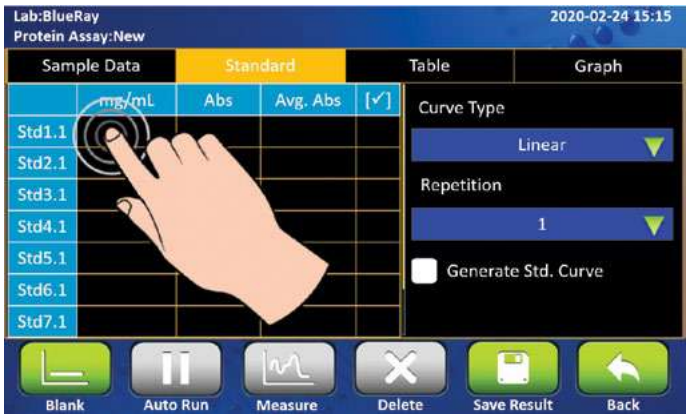
Figure 18. Graph tab page, Standard Curve View.

6.2 Protocol Operation

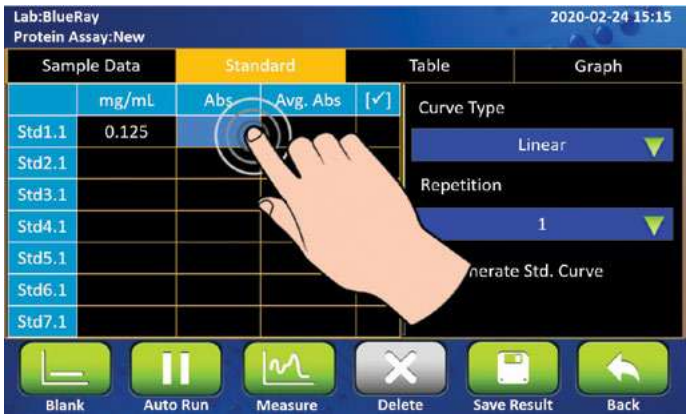
1. On the main menu, select  to enter the protocol.
2. Ensure the sample window and the cover window on the detection arm are clean.
3. Select the correct **Method** according to the protocol.
4. Add the appropriate solution of at least 1 µL and select  to establish Blank data. The screen will automatically jump to the **Standard Curve** tab.
5. Wipe the blank solution off the sample window and the cover window with lint-free wipes.
6. Select the correct **Curve Type** according to your reagent.

Note	a. Linear curve type requires minimum 2 DIFFERENT concentrations to establish standard curve. b. Interpolation curve type requires minimum 2 DIFFERENT concentrations to establish standard curve. c. 2nd order polynominal curve type requires minimum 3 DIFFERENT concentrations to establish standard curve.

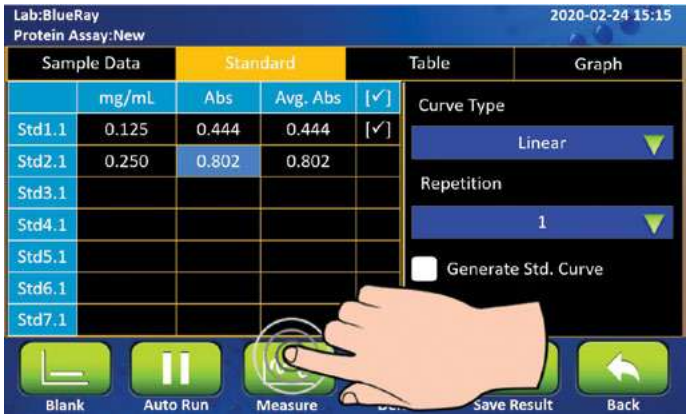
7. Select the repetition frequency you need in the **Repetition** bar.
8. Tap on a cell in the **mg/mL** column to enter the concentration of your standard sample.



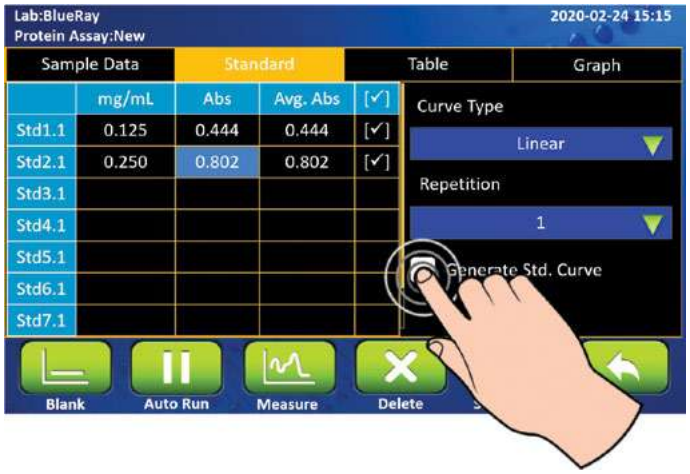
9. Tap on a cell in the **Abs.** column and select  to establish standard data. If the repetition frequency is higher than 1, it will automatically jump to the next cell.



10. If you want to correct the standard absorbance, select  when the indicator is on the cell you want to change.



11. You can uncheck the value if it isn't required to generate the standard curve.
12. After measuring all your standard data, check **Generate Std. Curve** to establish the standard curve.



13. Add your sample of at least 1 µL and select  to enter sample measurement.
14. After the experiment, clean the sample window and cover on the detection arm with lint-free wipes. Use water, ethanol or isopropanol if needed.
15. The correction function is optional, and can be turned on/off anytime.
16. The default of the **Auto Run** function is off  . If **Auto Run** is on  , sample measurement will be performed automatically after closing the detection arm.

Note	1. It is suggested to clean the sample window and cover window when exchanging different concentrations of samples. 2. If the standard curve graph isn't required, you can uncheck **Generate Std. Curve** and continue to insert data.

6.3 Calculation

For protein quantification, the concentration can be calculated by measuring the final absorbance of colorimetric samples and standards.

The BCA method is based on the reduction of Cu^{2+} by alkaline in the protein. This has a peak absorbance at 562 nm and has a baseline correction at 750 nm.

The Bradford method is based on the protein complex with Coomassie blue dye. This measures the absorbance at 595 nm and has a baseline correction at 750 nm.

The Lowry method is based on the protein complex with copper. This has a peak absorbance at 750 nm and has a baseline correction at 405 nm.

Note	1. The detail protocols are described by the assay kits. Please set the protocol according to the kits' instructions. 2. If users need to establish customized standard curve protocols, please refer to Section 8.2.

7 Application: OD 600

This application will measure microbial cell samples absorbance at 600 nm, which can be used for monitoring the samples growth rate. The range of the light path length is shown in the unit of absorbance. The absorbance also can be calculated to concentration with a conversion factor, which is an optional function in this protocol. If the user inserts the conversion factors, the unit of concentration is represented in cells/mL.

7.1 Overview of Screen Features

The screen of OD 600 protocol can be separated into 3 parts: information tab bar, information report area, and functions icons.

The information tab bar has 3 tab pages: Data page, Table page, and Graph page. The information areas show different reports on different tab pages.

7.1.1 Data Tab Page

On the data tab page of OD 600 protocol (Figure 19), the data information parts have the features below (Table 14).

Figure 19. Data tab page.

Table 14. Data tab page information

Features	Description
[conc.]	The concentration is calculated from absorbance at 600 nm, and the unit is cells/mL. This is an optional function.
A600	Displays the absorbance at 600 nm, which is normalized to a 10 mm path length equivalent.
A(Ref.)	Displays the absorbance at self-defined wavelength, which is normalized to a 10 mm path length equivalent.
Name	The sample name can be inserted here. The default is Sample.
Factor	A self-defined conversion factor from A600 to concentration (cells/mL). This is an optional function.
Path Length	The light path chosen by the path length selector will be detected automatically and shown which length it is.
Reference	Self-defined wavelength for bichromatic normalization. This is an optional function and the default is off.

7.1.2 Table Tab Page

The table tab page will show all the data results. If the user needs to know more details of one data item, tap the check box column to select the data. The detail will be shown on the **Data** page and the **Graph** page.

Figure 20. Table tab page.

Tap the **Sample** column to change the sample name. The **Blank** can also be renamed, but this is NOT suggested. You need to measure the **Blank** again if the original blank data has been renamed.

Note	Only one date item can be checked at one time.

7.1.3 Graph Tab Page

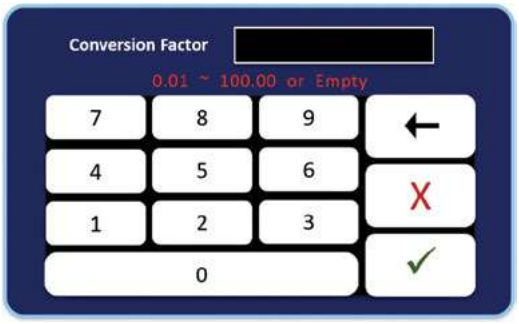
The graph of measuring samples can be enlarged or minimized. The axis can be moved by dragging the graph.

Long touch the x, y- axis on graph to turn the modified graph back to default.

Figure 21. Graph tab page.

7.2 Protocol Operation

1. On the main menu, tap on OD 600 to enter protocol section.
2. Ensure the sample window and the window cover on the detection arm are clean.
3. Insert the **Conversion Factor** to convert from absorbance at 600 nm to cells/mL. This factor is optional, and the default is off.



4. Open the detection arm and turn the path length selector to the appropriate position. The range 0.5 mm is from 0.04 to 30 Abs, and 0.05 mm is from 20 to 400 Abs. All the ranges are shown on the **EzDrop 1000** screen.
5. Add appropriate solution of at least 1 µL and tap on to establish Blank data.
6. Wipe the blank solution off the sample window and the cover window with lint-free wipe paper.
7. Tap on **Name** bar to insert the sample name (optional). The naming system is auto-numbering.
8. Add your sample of at least 1 µL and tap on for sample measurement.
9. Clean the sample window and cover on the detection arm with lint-free wipe paper after the experiment. Use water, ethanol or isopropanol if needed.
10. The **Reference** (self-defined wavelength) function is optional, and can be turned on/off anytime.
11. The default of **Auto Run** function is off . If **Auto Run** is turned on , sample measurement will be performed automatically after closing the detection arm.

Note	1. The conversion factor range is from 0.01 to 100 cells/mL-Abs. 2. Blank is not allowed to be used for sample naming. 3. EzDrop 1000 offers the OD 600 measuring function, but it is suggested to use cuvette photometers OD 600 for more precise data.

7.3 Calculation

The principle of OD 600 is measuring the light scatter of the particles in the sample solution. The absorbance will differ from different spectrophotometer systems.

A modified Beer-Lambert equation is used to calculate the concentration (optional).

$c = A600 \times cf / b$

c = concentration of sample suspension solution in cells/mL

A600 = the absorbance at 600 nm (10 mm equivalent)

cf = the cell number conversion factor, which is represented in the unit of 1×10^8 cells/mL

b = the path length in cm

Note	The cell number conversion factor is an optional function in EzDrop. Users can insert a self-defined number to calculate the concentration if needed.

8 Application: More Assays

In **More Assays, EzDrop 1000** has 3 customized applications for users to establish self-defined protocols.

8.1 Factor Method

In this application, users can measure samples at their selected wavelength. They can also insert self-defined units and the conversion factor (optional). The correction wavelength is also a self-defined function (optional).

8.1.1 Overview

In factor method, the information tab bar has 4 parts: custom setting tab page, data tab page, table tab page and graph tab page.

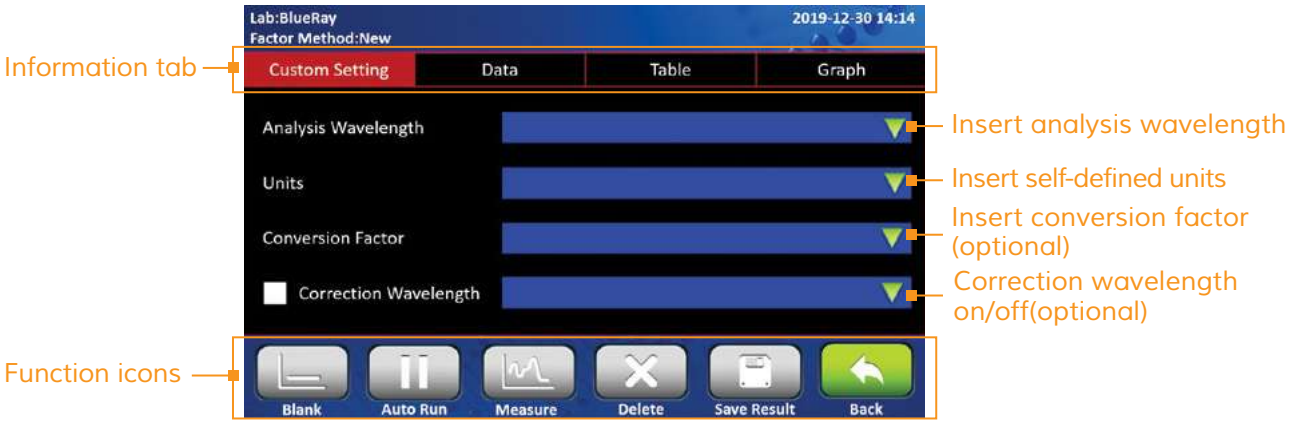


Figure 22. Custom Setting tab page.

On the custom setting tab page (Figure 22), 4 customized options are offered for users (Table 15).

The function icons will be activated after inserting the **Analysis Wavelength, Units, Conversion Factor** (optional) and **Correction Wavelength** (optional) field.

Table 15. Custom Setting tab page information.

Features	Description
Analysis Wavelength	Self-defined wavelength for measuring samples. User has to insert to activate the function icons. (Required)
Units	User can insert their self-defined units. (Required)
Conversion Factor	User can insert their self-defined value according to the relationship between sample absorbance and units. (Optional)
Correction Wavelength	Self-defined wavelength for bichromatic normalization. This is an optional function and the default is off.

Figure 23. Data tab page.

On the data tab page of factor method protocol (Figure 23), the data information parts have the features below (Table 16).

The function icons will be activated after finishing the protocol setting in the **Custom Setting** tab page.

Table 16. Data tab page information.

Features	Description
[conc.]	The concentration is calculated from absorbance at user-defined wavelength. The unit is also user-defined, but only shown on the custom setting page. This is an optional function.
Abs	Displays the absorbance at user-defined wavelength, which is normalized to a 10 mm path length equivalent.
λ(Analysis)	User-defined wavelength decided on the custom setting page.
λ(Corr.)	Self-defined wavelength for bichromatic normalization. This is an optional function and the default is off.
Name	The sample name can be inserted here. The default is Sample.
Path Length	The light path chosen by the path length selector will be detected automatically and show which length it is.

The table tab page will show all the data results. If the user needs to know more details of one data item, tap the check box column to select the data. The details will be shown on the **Data** page and the **Graph** page.

Figure 24. Table tab page.

Tap the **Sample** column to change the sample name. The **Blank** can also be renamed, but this is NOT suggested. You need to measure the **Blank** again if the original blank data has been renamed.

Note	Only one date item can be checked at one time.

The graph of measuring samples (Figure 25) can be enlarged or minimized. The axis can be moved by dragging the graph.

Long press the x- or y- axis on the graph to turn the modified graph back to default.

Figure 25. Graph tab page.

8.1.2 Protocol Operation

1. On the main menu, select  then  to enter protocol.
2. Ensure the sample window and cover window on the detection arm are clean.
3. Insert required **Analysis Wavelength**. (Required)
4. Insert the **Units**. (Required)
5. Insert the **Conversion Factor** if the user needs to convert absorbance to concentration (optional).
6. Insert the **Correction Wavelength** if the user needs bichromatic normalization (optional).
7. Add appropriate solution of at least 1 µL and select  to establish Blank data.
8. Wipe the blank solution off the sample window and the cover window.
9. Add your sample of at least 1 µL and select  to enter sample measurement.
10. After the experiment, clean the sample window and the cover window on the detection arm with lint-free wipes. Use water, ethanol or isopropanol if needed.
11. The correction function is optional, and can be turned on/off anytime.
12. The default of the **Auto Run** function is off  . If **Auto Run** is on  , sample measurement will be performed automatically after closing the detection arm.

Note	1. During the measurement, users can change the conversion factor. This is an optional function. 2. During the measurement, users can change the correction wavelength. This is an optional function.

8.1.3 Calculation

In the **Factor Method** protocol, a modified Beer-Lambert equation is used to calculate concentrations with user-defined measuring absorbance and factor as follows, with or without baseline correction (optional):

Without background correction:

$c = A \times \varepsilon / b$

With background correction

$c = (A - A_{Baseline}) \times \varepsilon / b$

c = the purified protein concentration in the user-defined factor

$A_{user\text{-}defined}$ = the user-defined absorbance

$A_{Baseline}$ = the user-defined absorbance at baseline wavelength

ε = the user-defined extinction coefficient factor

b = the path length in cm

8.2 Std. Curve Method

In this application, users can use self-defined wavelength to establish a standard curve for sample measuring. The correction wavelength is also a self-defined function (optional).

8.2.1 Overview

In std. curve method, the information tab bar has 5 parts: custom setting tab page, sample data tab page, standard tab page, table tab page and graph tab page.

The Custom Setting tab page has 3 user-defined options: analysis wavelength, units and correction wavelength (Figure 26, Table 17). The function icons will be activated after inserting the **Analysis Wavelength**, **Units**, and **Correction Wavelength** (optional) field.

Figure 26. Custom Setting tab page.

Table 17. Custom Setting tab page information.

Features	Description
Analysis Wavelength	Self-defined wavelength for measuring samples. User has to insert to activate the function icons. (Required)
Units	User can insert their self-defined units. (Required)
Correction Wavelength	Self-defined wavelength for bichromatic normalization. This is an optional function and the default is off.

On the **Sample Data** tab page of std. curve method protocol (Figure 27), the data information parts have the features below (Table 18).

The function icons will be activated after finishing the protocol setting on the **Custom Setting** tab page.

Figure 27. Sample Data tab page.

Table 18. Sample data tab page information.

Features	Description
[conc.]	The concentration is calculated from absorbance at user-defined wavelength. The unit is also user-defined, but only shown on the custom setting page. This is an optional function.
Abs	Displays the absorbance at user-defined wavelength, which is normalized to a 10 mm path length equivalent.
λ(Analysis)	User-defined wavelength decided on the custom setting page.
λ(Corr.)	Self-defined wavelength for bichromatic normalization. This is an optional function and the default is off.
Name	The sample name can be inserted here. The default is Sample.
Path Length	The light path chosen by the path length selector will be detected automatically and show which length it is.

The Standard tab page (Figure 28) is the page to measure standard samples absorbance at specific wavelength and establish the standard curve. It only shows the standard data result. The features are shown below (Table 19).

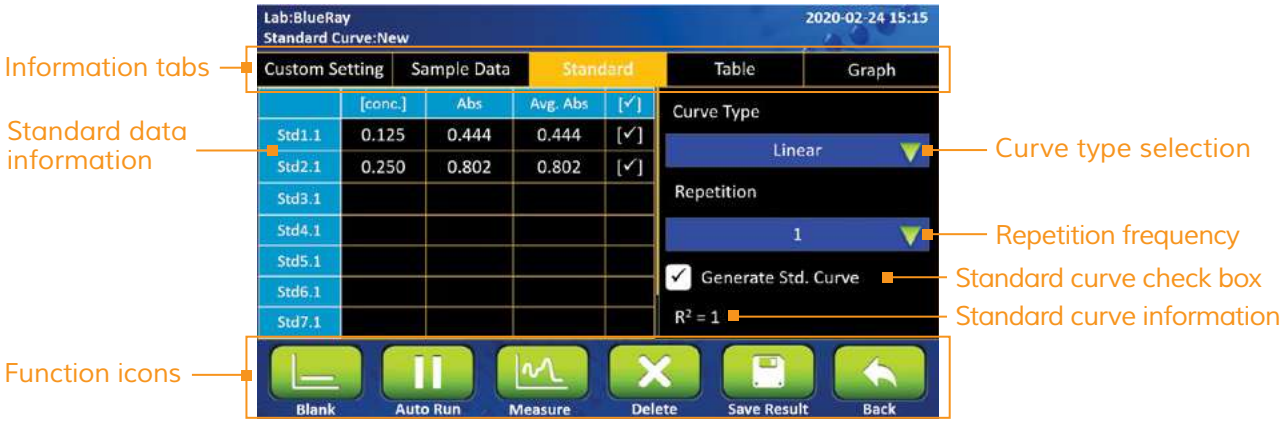


Figure 28. Standard tab page.

Table 19. Standard tab page information.

Features	Description
[conc.]	This is the concentration column. The unit is based on the self-defined value on the **Custom Setting** page. The value is inserted by the users.
Abs	The absorbance measured at different wavelength according to the protein method.
Avg. Abs	The average absorbance of the standard repetition. It is calculated automatically.
Curve Type	The standard curve types the user can select: linear, interpolation, and 2nd order polynomial.
Repetition	The repetition frequency of standard numbers. The default value is 1 and the maximum is 3.
Generate Std. Curve	Check the icon to establish the standard curve.

The table tab page (Figure 29) will show all the data results. If the user needs to know more details of one data item, tap the check box column to select the data. The detail will be shown on the **Data** page and the **Graph** page.

Figure 29. Table tab page.

Tap the **Sample** column to change the sample name. The **Blank** can also be renamed, but this is NOT suggested. You need to measure the **Blank** again if the original blank data has been renamed.

Note	Only one date item can be checked at one time.

In the std. curve method protocol, there are 2 kinds of graph: the standard curve graph and sample absorbance graph (Figure 30).

They can be enlarged or minimized. The axis can be moved by dragging the graph. Long press the x- or y- axis on the graph to turn the modified graph back to default.

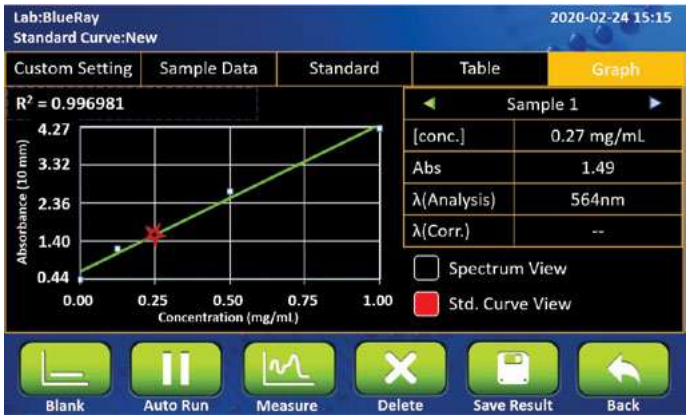


Figure 30. Table tab page.

8.2.2 Protocol Operation

1. On the main menu, select  then  to enter protocol.
2. Ensure the sample window and the cover window on the detection arm are clean.
3. Insert **Analysis Wavelength**. (Required)
4. Insert the **Units**. (Required)
5. Insert the **Correction Wavelength** if the user needs bichromatic normalization (optional).
6. Add the appropriate solution of at least 1 μL and select  to establish Blank data. The screen will automatically jump to the **Standard Curve** tab.
7. Wipe the blank solution off the sample window and the cover window.
8. Select the correct **Curve Type** according to your solution dye.

Note	1. Linear curve type requires minimum 2 DIFFERENT concentrations to establish standard curve. 2. Interpolation curve type requires minimum 2 DIFFERENT concentrations to establish standard curve. 3. 2nd order polynominal curve type requires minimum 3 DIFFERENT concentrations to establish standard curve.

9. Select the repetition frequency you need in the **Repetition** bar.
10. Tap on a cell in the **[conc.]** column to enter the concentration of your standard sample.
11. Tap on a cell in the **Abs.** column and select  to establish standard data. If the repetition frequency is higher than 1, it will automatically jump to the next cell.
12. If you want to correct the standard absorbance, select  when the indicator is on the cell you want to change.
13. You can uncheck the value if it isn't required to generate the standard curve.
14. After measuring all your standard data, check **Generate Std. Curve** to establish the standard curve.

Note	If the standard curve graph isn't required, you can uncheck **Generate Std. Curve** and continue to insert data.

15. Add your sample of at least 1 μL and select  to enter sample measurement.

16. After the experiment, clean the sample window and the cover window on the detection arm with lint-free wipes. Use water, ethanol or isopropanol if needed.
17. The correction function is optional, and can be turned on/off anytime.
18. The default of the **Auto Run** function is off  . If **Auto Run** is on  , sample measurement will be performed automatically after closing the detection arm.

8.2.3 Calculation

In the protocol of **Std. Curve Method**, the concentration is calculated by the absorbance values measuring in user-defined wavelength and the established standard curve. The standard curve can be in types of linear, interpolation, or 2nd order polynomial.

Note	The detail protocols are described by the assay design. Please set the protocol according to Chapter 6: Protein Assay on page 21.

8.3 UV-Vis Method

In this application, there is no concentration conversion function for the sample's absorbance. Only absorbance measurement for samples is offered.

8.3.1 Overview

The information tab bar has 4 parts: custom setting tab page, data tab page, table tab page and graph tab page.

Figure 31. Custom Setting tab page.

In the **Custom Setting** page (Figure 31), there are 8 self-defined wavelength field in this protocol. The setting range is from 190nm to 1000nm. At least 1 user-defined wavelength is required to activate the function icons.

Figure 32. Date tab page.

On the **Data** tab page of UV-Vis Method protocol (Figure 32), the data information parts have the features below (Table 20).

The function icons will be activated after finishing the protocol setting on the **Custom Setting** tab page.

Table 20. Sample data tab page information.

Features	Description
A---	These columns will automatically turn to the user-defined wave-length after finishing the protocol setting on the **Custom Setting** tab page. After measuring samples, it will show the absorbance of the samples in user-defined wavelength.
Name	The sample name can be inserted here. The default is Sample.
Path Length	The light path chosen by the path length selector will be detected automatically and show which length it is.

The table tab page (Figure 33) will show all the data results. If the user needs to know more details of one data item, tap the check box column to select the data. The detail will be shown on the **Data** page and the **Graph** page.

Figure 33. Table tab page.

Tap the **Sample** column to change the sample name. The **Blank** can also be renamed, but this is NOT suggested. You need to measure the **Blank** again if the original blank data has been renamed.

Note	Only one date item can be checked at one time.

Figure 34. Table tab page.

The graph (Figure 34) of measuring samples can be enlarged or minimized. The axis can be moved by dragging the graph.

Long press the x- or y- axis on the graph to turn the modified graph back to default.

8.3.2 Protocol Operation

1. On the main menu, select  then  to enter protocol.
2. Ensure the sample window and cover window on the detection arm are clean.
3. Insert required **Analysis Wavelength**. **EzDrop 1000** affords a maximum of 8 wavelengths.
4. Add appropriate solution of at least 1 µL and select  to establish Blank data.
5. Wipe the blank solution off the sample window and the cover window.
6. Add your sample of at least 1 µL and select  to enter sample measurement.
7. After the experiment, clean the sample window and the cover window on the detection arm with lint-free wipes. Use water, ethanol or isopropanol if needed.
8. The correction function is optional, and can be turned on/off anytime.
9. The default of the **Auto Run** function is off  . If **Auto Run** is on  , sample measurement will be performed automatically after closing the detection arm.

9 System Setting

Tap on the **System** icon on the **Main Screen** to enter the **System** setup section as shown in Figure 35 below. Here you can adjust several parameters for the **EzDrop 1000**.

Figure 35. System overview.

9.1 Date & Time

Users can change the date and time setting of the **EzDrop 1000** from here.

9.2 Beep Sound

Users can turn **ON** or **OFF** the system buzzer from here.

9.3 Brightness

Users can adjust the brightness of the display panel according to your environment's lighting condition.

9.4 Indicator Light

Users can turn **ON** or **OFF** the LED auxiliary light beside the detection arm from here.

9.5 Storage

This function shows the information of total and remaining storage space in the **EzDrop 1000**.

9.6 Self-test

Users can do a system self-test of the **EzDrop 1000**.

9.7 About

Users can check the basic information of **EzDrop 1000** with this icon, including the System Version, Initialization Date, and Calibration Date. The link to the operation manual is also here.

9.8 Admin

The default Administrator password is "**0000**". The Administrator of this unit has rights to delete any **User folder** and any **Reports** inside a **User folder**. Users can change the Administrator password and the Lab Name from here.

9.9 Service

Only authorized service personnel have the password to enter Service Mode and perform necessary maintenance and repairs.

10 History Information

Tap on the **History** icon on the main screen to enter the History list information screen. A sample screen is shown in Figure 36 below.

Figure 36. History list overview.

All stored reports are shown in the history list. If all the reports can't be shown on one page, you can slide up or down on the screen to check the rest of the reports.

The lock symbol on the right corner of the user column indicates that the report is saved in a password protected user folder. If the report in the user folder has been deleted, the record will still be shown in history list.

The function icons on the lower part of the screen allow users to duplicate the report setting to a new protocol or view the report.

10.1 Duplicating Report Setting

Select the saved report with the protocol setting you want to duplicate. Tap on the **New Protocol** icon to duplicate the report setting. The new protocol will have the same setting as the original report, but can still do setting modification.

10.2 Viewing a Report

To view the detail of a report, tap on the report record to select and highlight it. You can then tap for the second time or tap on the **View** icon to open it. If the report is from a password protected user folder, you'll be requested to input the password. Input the password and tap on to confirm ✓ the password or tap on X to abort the operation. If the password is entered correctly, the report will then open. If the password is entered incorrectly, a warning message box will pop up indicating the wrong password was input. Tap on ✓ to return to the password input screen and input the correct password.

11 User Folder Management

Tap on the **User** icon on the main screen to enter the **User folder** management screen. A sample screen is shown in Figure 37 below.

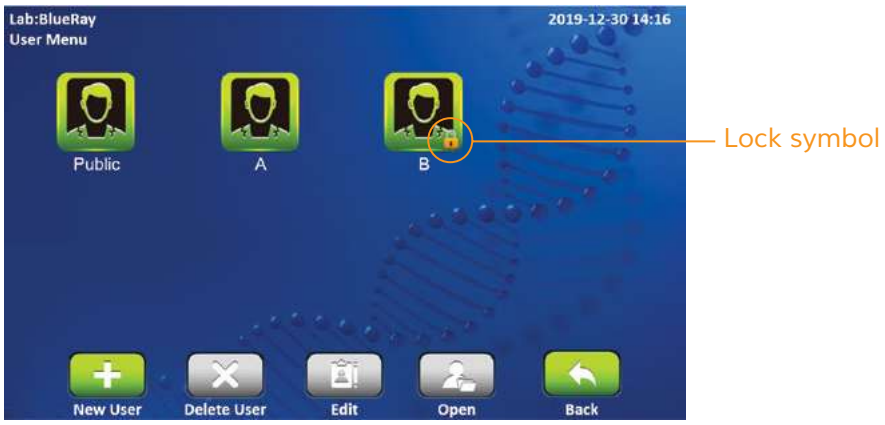


Figure 37. User folder overview.

All Protocols are stored inside the user folders. There are 8 user folders displayed on one page. If there are more than 8 user folders registered in the system, you can drag up or down on the screen to see the other pages.

The lock symbol on the lower right corner of the folder icon indicates that the folder is password protected.

Users can utilize the function icons on the lower part of the screen to open, create, edit and delete the user folders. The **Back** icon is used to return to the Upper page.

11.1 Creating a New User Folder

On the **User folder** screen, tap on the icon "**New User**" to create a new User folder. Input the folder name and password (optional). Tap the user icon (8 different icons are available) to change the icon for the new folder.

11.2 Viewing a User Folder

To view the contents in a **User folder**, tap on the folder icon to select and highlight it. You can then tap for the second time or tap on the **Open** icon to open it. If the folder is password protected, you'll be requested to input the password. Input the password and tap on **OK** to confirm the password or tap on **CANCEL** to abort the operation. If the password is entered correctly, the folder will then be opened. If the password is entered incorrectly, a warning message box will pop up indicating the wrong password was input. Tap on to return to the password input screen and input the correct password.

11.3 Editing a User Folder

To edit the properties of a **User folder**, tap on the folder icon to select and highlight the folder, then tap on the **Edit** icon to edit it. You can change the folder name and password (optional) or change the icon you want to use for the folder. Tap on **OK** to store and finish editing.

11.4 Deleting a User Folder

To delete a **User folder**, tap on the folder icon to select and highlight the folder, then tap on the **Delete** icon to delete it. You are required to enter the password if the folder is password protected. The screen will prompt "Are you sure you want to delete user folder?" Tap on to confirm the deletion. Tap on to abort the deletion.

Note	User folders which contain any reports cannot be deleted. You should delete all the reports in them first.

11.5 Using a USB Flash Drive as a User Folder

To use a **USB flash drive** as a **User Folder** to keep your reports, please insert your USB flash drive into the front USB port and the wait 5 - 10 seconds, and the icon will pop up. (The icon loading time depends on the specification of the flash drive. It is recommended to format your flash drive in the FAT or FAT32 file system prior to using it with the **EzDrop 1000**). You can also use the USB flash drive to transfer the reports between the **EzDrop 1000** and your computer.

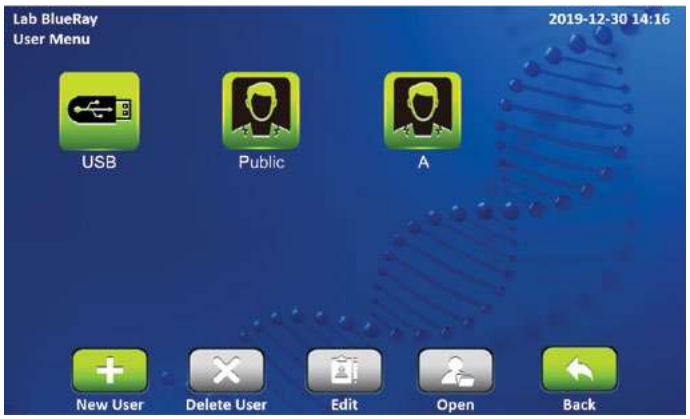


Figure 38. User folder overview.

12 Maintenance

12.1 Cleaning the Unit

Please avoid liquid spilling onto or into the unit. Liquid may damage EzDrop internal components. In addition, periodically wipe it clean of dust and other residue that comes with normal operation of the unit. Use a soft, lint-free cloth and deionized water.

12.2 Cleaning the Quartz Glass

Please add deionized water on the sample window, lower the detection arm, and wipe with lint-free wipes. 70% ethanol or isopropanol can also be used on the surface to clean both the sample window and the cover window.

It is better to clean the quartz glass every time before starting and after finishing experiments. It is also possible to clean the quartz glass when exchanging different concentrations of samples.

Note	1. Use only a dry, soft, lint-free cloth to clean the front screen. 2. Do not use a spray bottle to apply water or any other solutions onto any surface of the instrument as the liquid may damage internal components. 3. Do not use Hydrofluoric Acid (HF) as the fluoride ion will dissolve the coating on the surface. 4. Do not use an acid solution on the path length selector as it will damage the metal part and affect the path length.

12.3 Annual Maintenance

For the best performance, it is suggested to do annual maintenance on the **EzDrop 1000**. It includes light-path confirmation and Nano-coating layer recoating. Please contact your local Blue-Ray Biotech distributor for the service.

12.4 Replacement

When the surface of quartz glass has been damaged or contaminated, please contact your local Blue-Ray Biotech distributor for exchange service.

13 Troubleshooting

Problem	Cause	Action
The display is off even when the power is switched on	Power is not reaching the system.	Check power source voltage.
	Power cord is not plugged into the socket properly.	Reconnect the power cord.
	Faulty Power adaptor.	Return the unit for service.
Can't reach sample accuracy	The solutions are not homogenous and well-mixed prior to sampling.	Ensure all solutions are homogenous and well-mixed prior to sampling.
	Sample has air bubbles.	Remove air bubbles from sample.
	There are scratches on the surface of quartz glass.	Return the unit for service.
	Quartz glass surface is contaminated.	Clean the quartz glass above and below with a suitable solution.
	Pulsed Xenon flash lamp problem.	Return the unit for service.
	Optics module problem.	Return the unit for service.
	Optical fiber problem.	Return the unit for service.
	Mechanism alignment problem.	Return the unit for service.
Detection time is too long	Faulty electronic module.	Return the unit for service.
	Faulty optics module.	Return the unit for service.

Problem	Cause	Action
Path length selector does not work	Faulty path length selector mechanism.	Return the unit for service.
	Path length selector sensor problem.	Return the unit for service.
No beep sound when tapping icons	Sound may currently be set to off.	Check Beeper setting in System Mode.
	Faulty touch panel.	Return the unit for service.
The display goes off	Faulty backlight.	Return the unit for service.
	Faulty LCD panel.	Return the unit for service.
Display is too dark or bright	Display brightness is not adjusted properly.	Adjust Display Brightness Potentiometer.
Detection arm will not close	Foreign object between detection arm and the area inside the detection arm.	Remove the foreign object or matter.
	Faulty detection arm mechanism.	Return the unit for service.
Error message appears	Refer to list of error messages in Section 13.1 below.	Check the nature of the error and take the suggested actions.

13.1 Error Messages

Message	Cause	Action
Er01 ERR_NO_SDCARD	Did not receive SD card signal in 1 second continuously.	Return the unit for service.
Er02 ERR_SELFTEST_NG	Automatically detected numerical anomalies. Insufficient light source intensity or excessive noise.	Return the unit for service.
Er03 ERR_METER_NO_ ANSWER	Optics module problem.	Reboot the unit.
Er04 ERR_METER_CALIBRATE	Optics module problem.	Reboot the unit.
Er05 ERR_UART_NO_ANSWER	Electronic module Board problem.	Reboot the unit.
Er06 ERR_UART_WRONG_ ANSWER	Electronic module Board problem.	Reboot the unit.
Er07 ERR_UART_WRONG_ COMMAND	Electronic module Board problem.	Reboot the unit.
Er08 ERR_UART_TRANSMIT_ OVERFLOW	Electronic module Board problem.	Reboot the unit.

If the same error message appears after rebooting the unit, please return the unit for service.

Appendix A: Technical Specifications

Optics Information	
Sample Volume	1 µL minimum volume
Sample Number	1
Pathlength	0.5 mm / 0.05 mm
Light Source	Pulsed Xenon flash lamp
Detector Type	2048 element CMOS
Wavelength Range	190 - 1000 nm
Bandwidth	1.3 nm
Wavelength Accuracy	1.0 nm
Spectral Resolution	1.5 nm (FWHM at Hg 253.7 nm)
Absorbance Precision (raw)	0.0015 A (0.5 mm)
Absorbance Precision	0.03 A (1 cm equivalent)
Absorbance Accuracy	3.0% at 0.75 A at 300 nm
Absorbance Range (1 cm equivalent)	0 (0.04) - 400 A
Detection Range	dsDNA: 2 - 20000 ng/µL
	BSA: 0.06 - 600 mg/mL
Sample Surface Material of Construction (Lower and Upper)	Stainless steel and quartz window with hydrophobic treatment
Measurement Time	< 3 sec
Software	
Operating System	Custom Linux based OS
Registered User Folder No.	> 500 sets
User Folder Password Protection	Yes
General	
Display	7” color LCD with capacitive touch panel
Data Port	1 USB Type-A front port for USB flash drive
Footprint Dimensions (W x D x H)	206 x 333 x 166 mm
Weight	3.5 kg (7.8 lb)
Glove Compatibility	All common lab gloves
Internal Storage	32 GB flash memory
Power Adapter	Input: AC 100-240 V, 50/60 Hz; Output: DC 24 V, 2.08 A
Certifications	CE, RoHS

Specifications are subject to change without prior notice.

Appendix B: CE Declaration

CE

BLUE-RAY BIOTECH CORP.

4F., No. 31, Sec. 2, Chang-An E. Rd.,
Zhong-Shan Dist., Taipei City 10456,
Taiwan (R.O.C.)

Declaration of Conformity
Product Name: Micro-Volume Spectrophotometer
Model Names: EzDrop 1000
All models comply with the following European standards:

EMC: EN 61326 (Group 1, Class A)

Safety: EN 61010-1 and EN 61010-2-101

To the best of my knowledge and belief, these units conform to these standards.

Name: **Jimmy Kuo**
Position: Quality Assurance Manager
Issue Date: 2020.07.13

Appendix C: Order Information

Cat. No.	Description
BRED-1000	EzDrop 1000 Micro-Volume Spectrophotometer

BLUE-RAY
BIOTECH

www.blue-raybio.com

Blue-Ray Biotech Corp.

4F., No. 31, Sec. 2, Chang-An E. Rd., Zhong-Shan Dist.,
Taipei City 10456, Taiwan (R.O.C.)

P/N: 401-EDBR01-11