spex® sampleprep

Operating Manual

Spex NanoSNAP™

Nano Spectrophotometer for Nucleic Acids and Proteins Measurement

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1.0 Safety Precautions

Before using the Spex NanoSNAP microvolume spectrophotometer for the first time, please read this entire Operating Manual carefully. To guarantee problem-free, safe operation of the Spex NanoSNAP, 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 Spex 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 °C to 60 °C, relative humidity 20% to 80%.

1.2.2 Installation and Operation

1. Indoor use only
2. Do not use the device in a potentially explosive environment or with potentially explosive chemicals or combustible substances.
3. Maximum altitude 2000 m
4. Pollution degree 2
5. Ensure enough free space around unit for adequate ventilation
6. Avoid placing the device in direct sunlight.
7. Install the device in a location free of excessive dust.
8. Install the device in a room with a temperature of 15 °C to 30 °C, relative humidity 20% to 80%.
9. Do not position the device so that it is difficult to disconnect from the mains supply using the mains plug.
10. Choose a flat, stable surface capable of bearing the weight of the device.
11. Do not allow water or any foreign objects to enter the various openings of the device.

1.2.3 Electrical Installation

THIS INSTRUMENT MUST BE GROUNDED

The appropriate power supply and cord combination should be connected to the equipment BEFORE connection to the mains supply.

Before connection, please ensure that the electrical supply is suitable for the power requirements below:

Current	Voltage
1.0 A	100 V to 230 V ~ 50/60 Hz

The equipment is provided with a power supply and a selection of four mains cords, consisting of:

- Type B (US) for 120 V a.c. installations
- BS1363 style, 3-pin (UK), Type F (EU) and Type I (Aus / China) for 230 V a.c. installations

Select the power cord appropriate for your electrical installation and discard the others.

Mains Cord Replacement

Should one of the power cords not be suitable for connecting to the power supply, replace the plug with a suitable alternative.

THIS OPERATION SHOULD ONLY BE UNDERTAKEN BY A QUALIFIED ELECTRICIAN

NOTE: Refer to the equipment specification to ensure that the plug and fusing are suitable for the voltage and current stated. The cores in the mains cord are as follows:

230 V a.c.		120 V a.c.
BROWN	**LIVE/HOT**	BLACK
BLUE	**NEUTRAL**	WHITE
GREEN/YELLOW	**EARTH**	GREEN

Should the mains cord require replacement, a cable of of harmonized code H05VV-F with a cross section of 0.75 mm^2 (18 AWG) must be used. The IEC C13 connector (for connecting to the equipment power supply) must be suitable for the supply voltage and current of the equipment.

IF IN DOUBT CONSULT A QUALIFIED ELECTRICIAN

1.2.4 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.

1.2.5 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 Customer Service Office for equipment pick up and recycling.

1.3 Chemical Waste Safety

1.3.1 Chemical Waste Hazard

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

2.0 General Description

The Spex NanoSNAP is a fast, microvolume spectrophotometer that provides accurate and intuitive operational experience in only 3 seconds. It enables the measuring of samples from 190 to 1,000 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 at 3 seconds
- Wide measuring range from 190 to 1,000 nm
- Quartz sample window which protects the optical analysis system
- A nano hydrophobic coating layer on the quartz window
- Replaceable sample window avoids contamination
- Thoughtfully designed assist light
- Auto Run measurement
- Automatically creates operating history
- Cushioning design of detecting arm

2.2 Product Overview

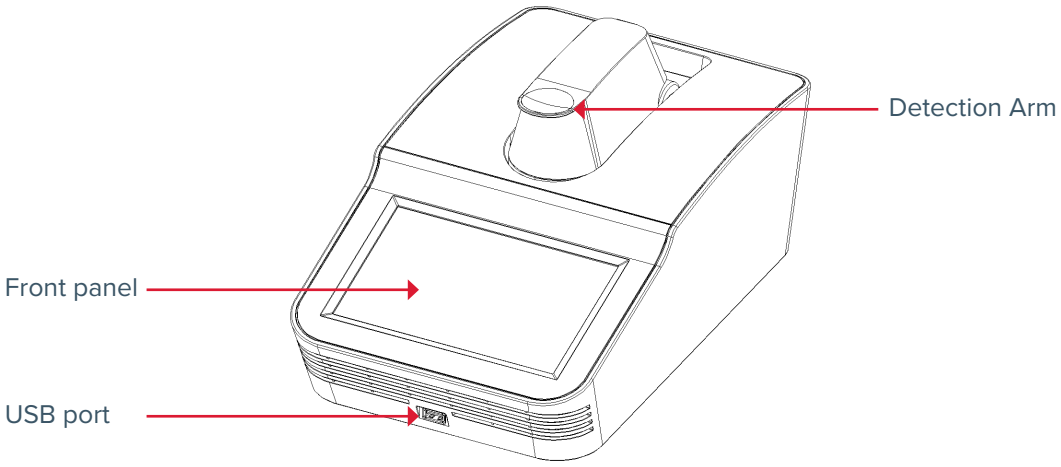


Figure 1. Front View

Table 1. Detailed description for top view.

Name	Function
Front Panel	7-inch high resolution color LCD 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.

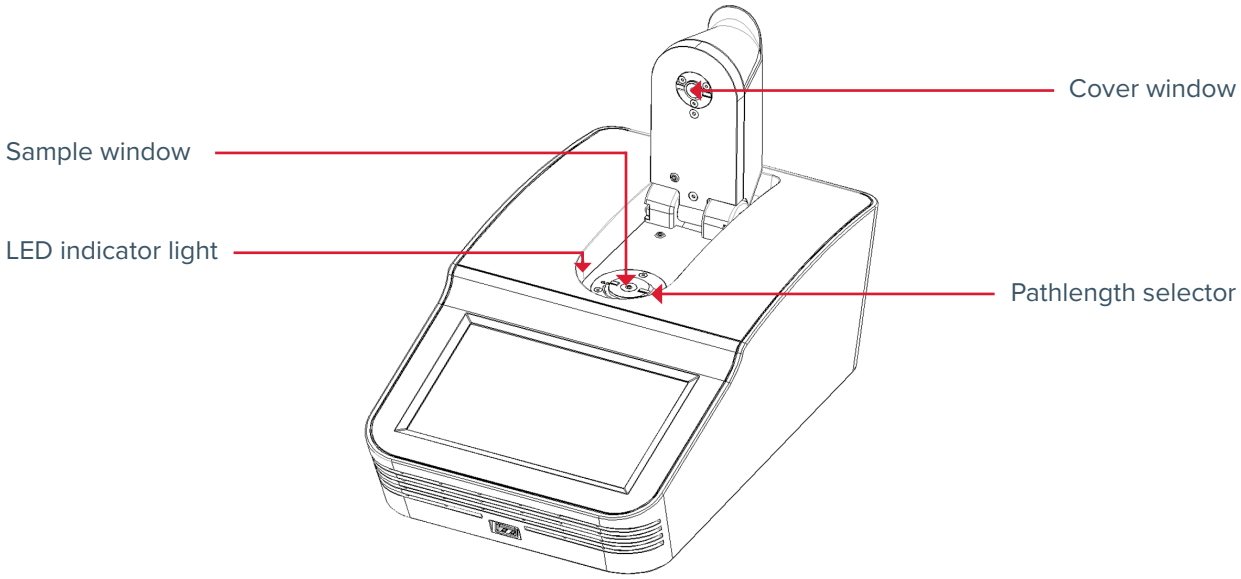


Figure 2. Front View with Opened Detection Arm

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 protects optical fibers and also reduces contamination.
Pathlength Selector	Light path of Spex NanoSNAP can be selected manually by pathlength 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.

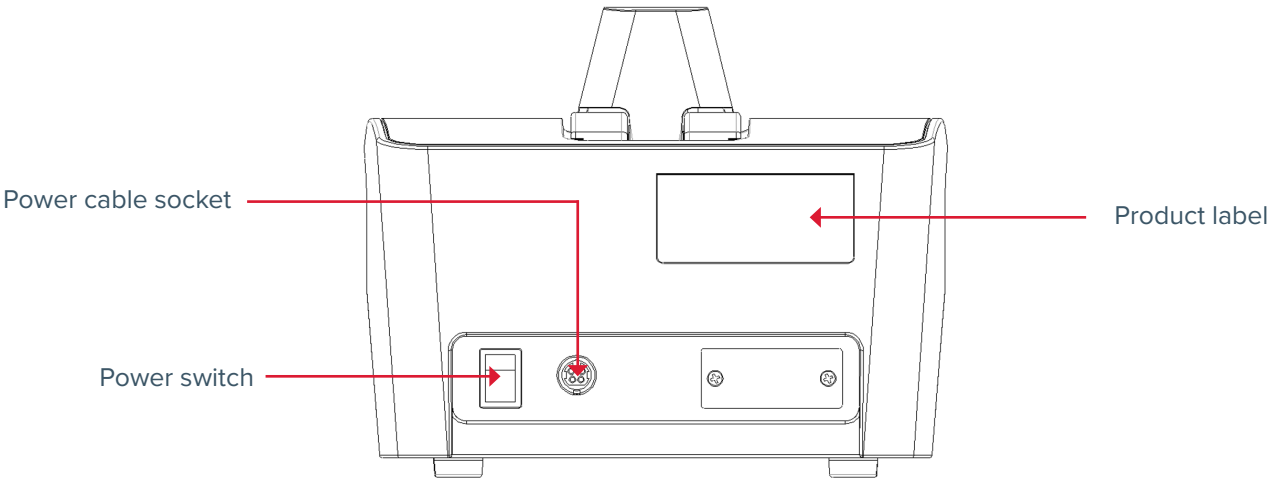


Figure 3. Rear View

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.

3.0 Getting Started

3.1 Unpacking

Once you open the Spex NanoSNAP package, confirm that all of the following items are included:

- Spex NanoSNAP spectrophotometer
- Quick-Start Guide
- Power Adapter
- Four power cords (US, UK, EU, Aus/China)
- Calibration Report

If any of the items are missing, damaged or if any incorrect items are included in the package, please contact your local Spex 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 will show the boot screen, start initiation process, and then the “Spex NanoSNAP” title will be displayed. Please **DO NOT** open the detection arm until system diagnosis is complete. Tap on the “Spex NanoSNAP” title to log into the **Main Screen** and start your operation. Tap on the Spex NanoSNAP 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 focus to plug in and out.

3.3 Main Screen

On the **Main Screen** there are some informational items indicating the status of the Spex NanoSNAP; it also contains 8 main function icons. Please refer to the following for the detailed descriptions (Figure 4, Table 4).

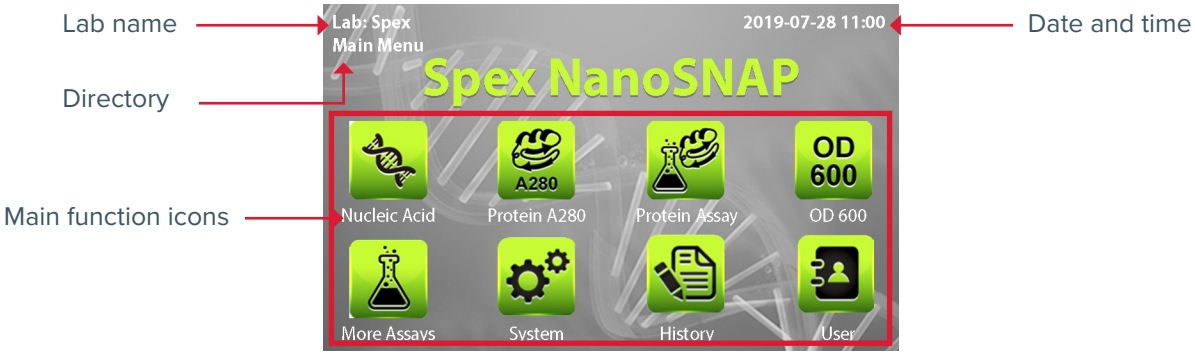


Figure 4. Main Screen Overview

Table 4. Main function icons.

Main Menu Function Icons			
	Nucleic Acid To create and edit nucleic acid protocols		**More Assays** To create and edit customized protocols
	Protein A280 To create and edit protein A280 protocols		**System** System settings
	Protein Assay To create and edit protein standard curve protocols		**History** To access stored reports
	OD 600 To create and edit OD 600 protocols		**User** User folder management

3.4 Detecting Arm Opening/Closing

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

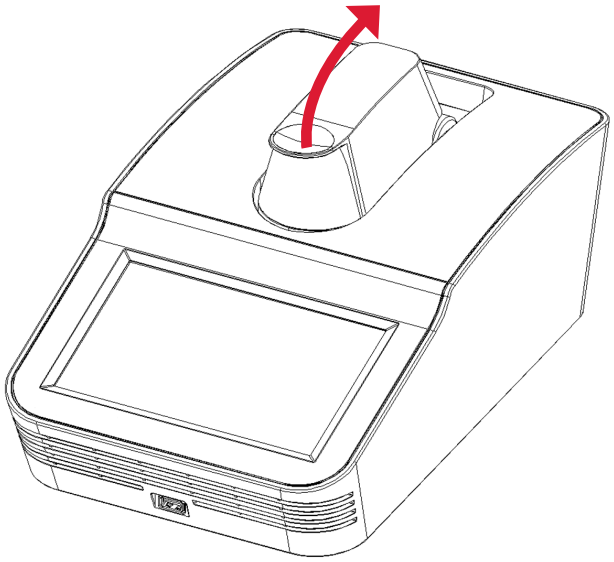


Figure 5. Opening the arm

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

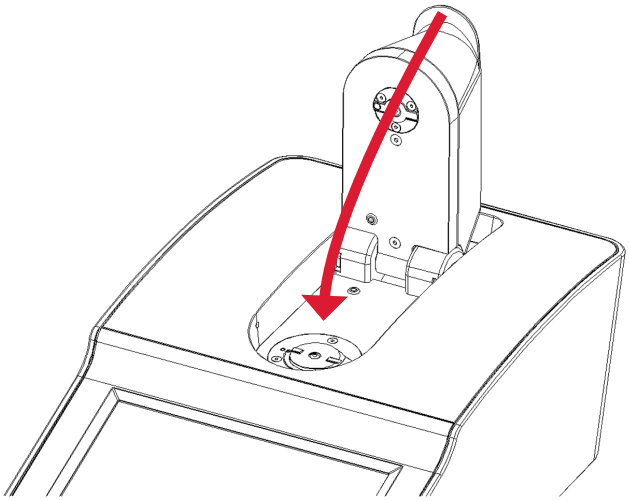


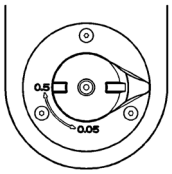
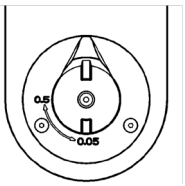
Figure 6. Closing the arm

3.5 Adjusting the Pathlength Selector

The pathlength of the Spex NanoSNAP is not automatically selected but selected manually. The metal light path selector shown down below in Table 5 is the manual pathlength selector of the Spex NanoSNAP. The measurement range of 0.5 mm pathlength 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 pathlength selector is in the right position. When the pathlength selector is in the horizontal position to the detection arm (Figure 7), it represents the 0.5 mm pathlength. In the vertical position (Figure 8), it represents the 0.05 mm pathlength. Hold the handle of the light path selector to adjust between 0.5 mm and 0.05 mm pathlength.

Table 5. Manual pathlength selector guide.

Position	Pathlength Selector	Measuring Range
 **Figure 7**	0.5 mm pathlength	From 0.04 to 30 Abs
 **Figure 8**	0.05 mm pathlength	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 icons.

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 pathlength 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 1 µL and click **Blank** to establish blank data.
6. Wipe away the blank solution. Add the sample of at least 1 µL and click **Measure**.
7. Clean the sample window and cover window with a lint-free wipe between changing samples and after the experiment is done. Use deionized water, ethanol or isopropanol if needed.

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

4.0 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 function icons.

The information tab bar has 3 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).

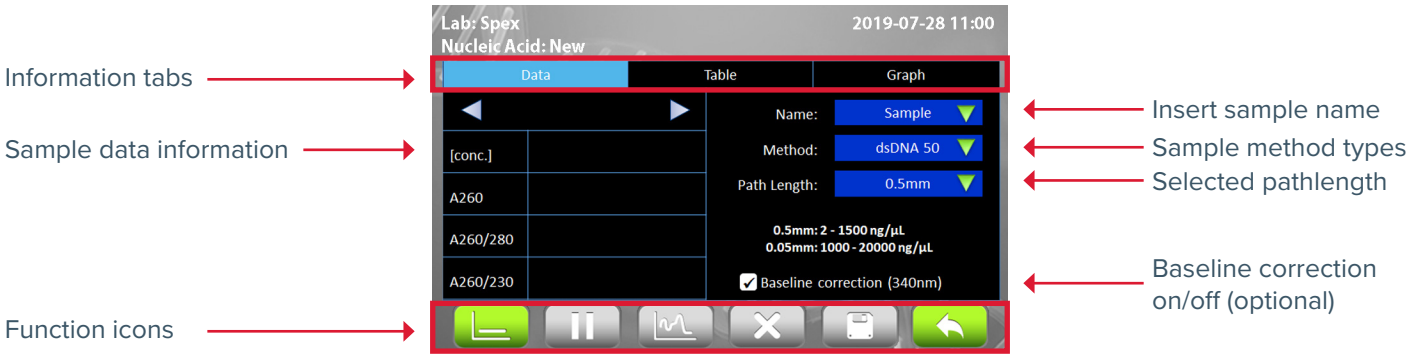


Figure 9. Data tab page

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 pathlength equivalent.
A260/280	Displays the ratio of absorbance at 260 nm and 280 nm. In dsDNA protocol, when the ratio is < 1.75, a warning icon will pop up. In RNA, a warning pops up when it is < 2.0. In ssDNA, a warning pops up when it is < 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.
Pathlength	The light path chosen by the pathlength selector will be detected automatically and length will be shown 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.

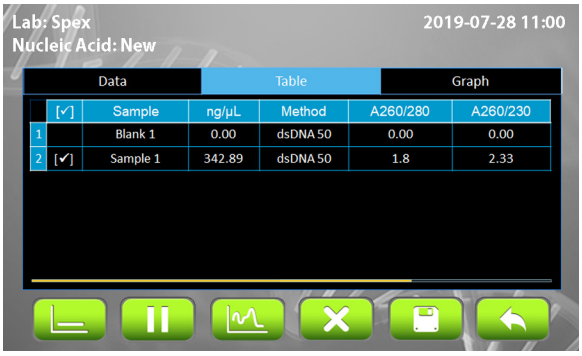


Figure 10. Table Tab Page

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 data 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- or y-axis on the graph to turn the modified graph back to default.

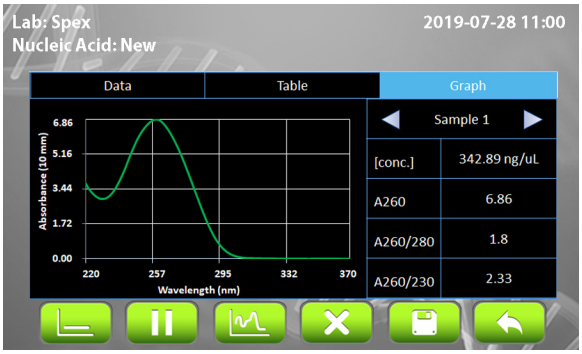
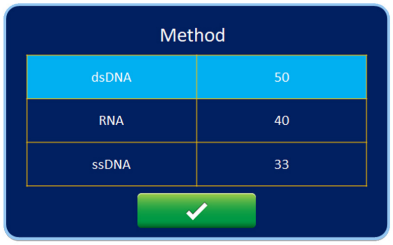


Figure 11. Graph Tab Page

4.2 Protocol Operation

1. On the main menu, tap on the **Nucleic Acid** icon to enter the 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 pathlength selector to the appropriate position. For example, the dsDNA concentration range of 0.5 mm is from 2 to 1,500 ng/µL, and 0.05 mm is from 1,000 to 20,000 ng/µL. All method ranges are shown on the Spex NanoSNAP screen.
5. Add appropriate solution of at least 1 µL and tap on the **Blank** icon to establish blank data.
6. Tap on the **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 a lint-free wipe.
8. Add your sample of at least 1 µL and tap on the **Measure** icon for sample measurement.
9. Clean the sample window and cover on the detection arm with a lint-free wipe after the experiment. Use deionized water, ethanol or isopropanol if needed.
10. The **Baseline correction** (340 nm) function is optional, and can be turned on/off any time.
11. The default of the **Auto Run** function is off. If **Auto Run** is turned on, sample measurement will be performed automatically after closing the detection arm.

Note: In Nucleic Acid, dsDNA, RNA, and ssDNA applications are offered in this protocol. If you need to test other samples, please use **Factor Method** to customize your protocol settings in **More Assays**. 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 baseline correction: $c = A260 \times \varepsilon / b$

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

c	the nucleic acid concentration in ng/µL
A260	the absorbance at 260 nm
$A_{Baseline}$	absorbance at baseline wavelength
ε	the extinction coefficient factor of nucleic acid in ng x cm/µL
b	the pathlength 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 x cm/µL
RNA	40 ng x cm/µL
ssDNA	33 ng x 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 homogeneous 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 function 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 the protocol (Figure 12), the data information parts have the features below (Table 10).

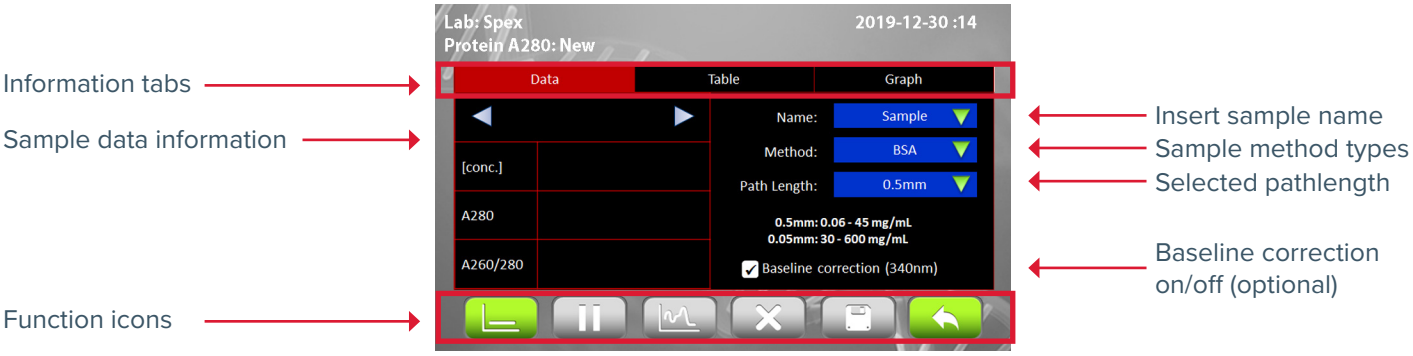


Figure 12. Data Tab Page

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	Displays the absorbance at 280 nm, which is normalized to a 10 mm pathlength equivalent.
A260/280	Displays the ratio of absorbance at 260 nm and 280 nm. When the ratio of A260/280 is > 0.6, a warning icon will pop up.
Name	The sample name can be inserted here. The default is Sample.
Method	Includes protocol types such as BSA, IgG, Lysosome, 1A = 1 mg/mL, and customized protein factor. The default is BSA.
Pathlength	The light path chosen by the pathlength selector will be detected automatically and length will be shown here.
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.

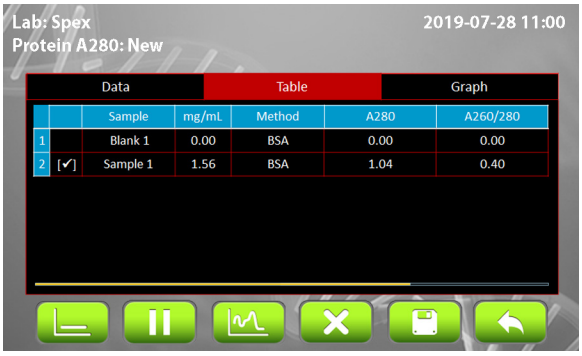


Figure 13. Table Tab Page

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 data 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- or y-axis on the graph to turn the modified graph back to default.

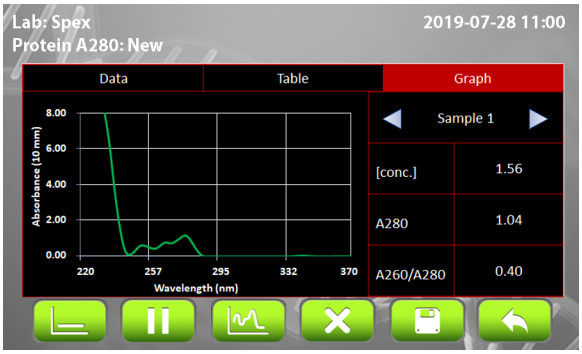
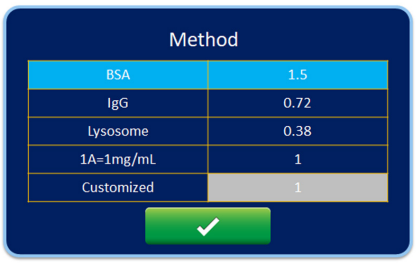


Figure 14. Graph Tab Page

5.2 Protocol Operation

1. On the main menu, tap on the **Protein A280** icon to enter the 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 pathlength 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 method ranges are shown on the Spex NanoSNAP screen.
5. Add appropriate solution of at least 1 µL and tap on the **Blank** icon to establish blank data.
6. Tap on the **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 a lint-free wipe.
8. Add your sample of at least 1 µL and tap on the **Measure** icon for sample measurement.
9. Clean the sample window and cover window on the detection arm with a lint-free wipe after the experiment. Use deionized water, ethanol or isopropanol if needed.
10. The **Baseline correction** (340 nm) function is optional and can be turned on/off any time.
11. The default of the **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, 1 A = 1 mg/mL, and customized protein factor applications are 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 baseline correction: $c = A280 \times \varepsilon / b$

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

c	the purified protein concentration in mg/mL
A280	the absorbance at 280 nm
$A_{Baseline}$	absorbance at baseline wavelength
ε	the extinction coefficient factor/purified protein factor in g x cm/L
b	the pathlength 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	Extinction Coefficient Factors (g x cm/L)	Extinction Coefficient Factors (L/g x cm)
BSA	1.50	0.667
IgG	0.72	1.37
Lysosome	0.38	0.264
1 A = 1 mg/mL	1	1

6. Application: Protein Assay

This application will measure homogeneous 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 (Table 12). This page only shows the sample data, and does not show standard data.

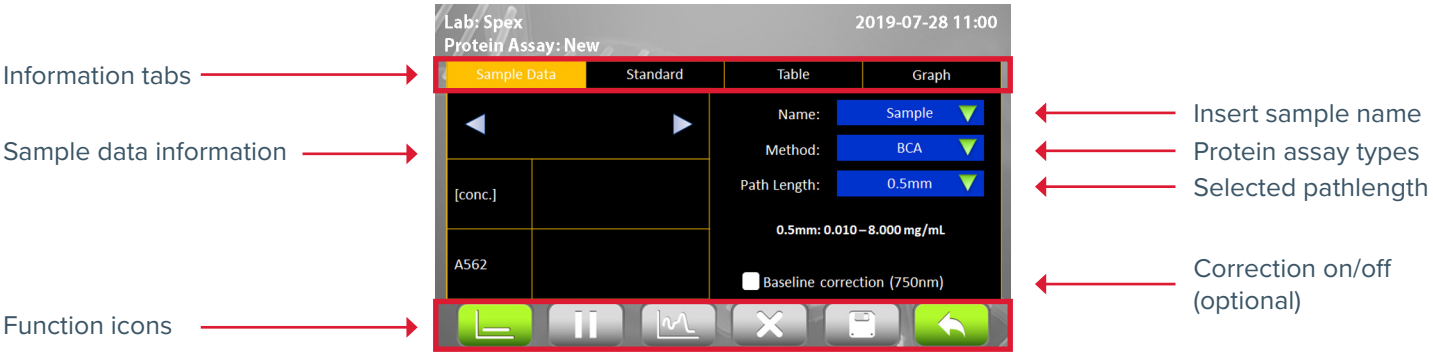


Figure 15. Sample Data Tab Page

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 pathlength 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 Lowry method. The default is BCA method.
Pathlength	The light path chosen by the pathlength selector will be detected automatically and length will be shown here. In protein assay protocol, 0.5 mm is the only available pathlength.
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 750 nm; and in the 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 standard data result. The features are shown below (Table 13).

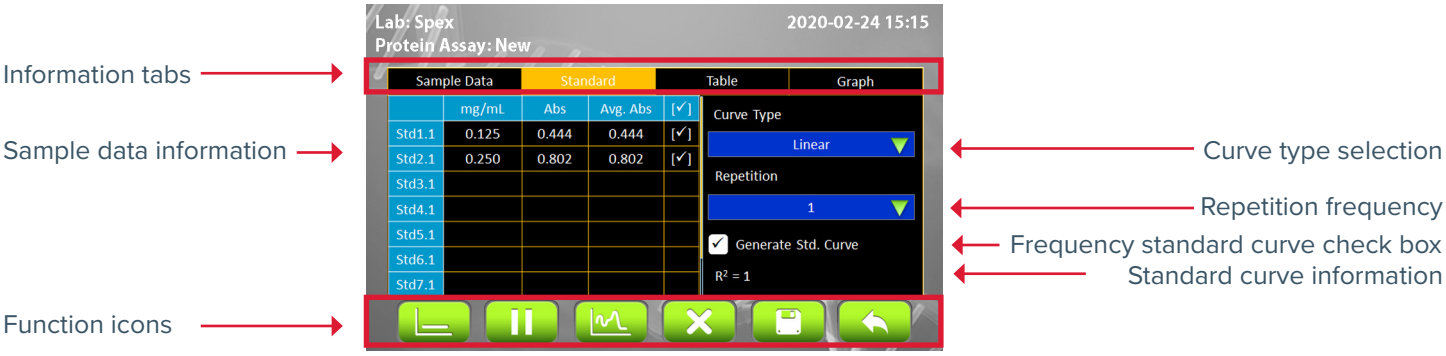


Figure 16. Standard Tab Page

Table 13. Standard tab page information.

Features	Description
mg/mL	This is the concentration column. The value is inserted by the user.
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, tab 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 has been renamed.

Note: Only one data item can be checked at one time.

6.1.4 Graph Tab Page

In the protein assay protocol, there are 2 kinds of graphs: 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- or y-axis on the graph to turn the modified graph back to default.

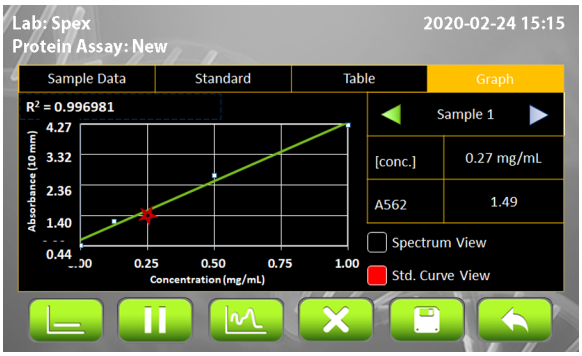


Figure 18. Graph Tab Page, Standard Curve View

6.2 Protocol Operation

1. On the main menu, tap on the **Protein Assay** icon to enter the protocol section.
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 tap on the **Blank** icon to establish blank data. The screen will automatically jump to the **Standard Curve** tab.
5. Wipe away the blank solution off the sample window and the cover window with a lint-free wipe.
6. Select the correct **Curve Type** according to your reagent.

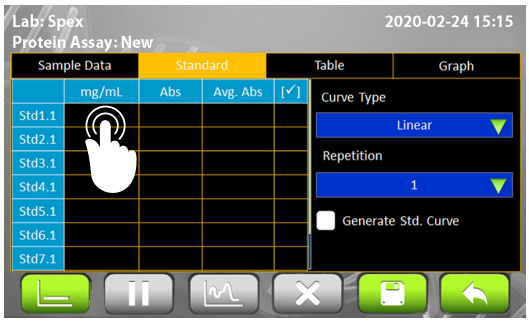
Note:

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 polynomial curve type requires minimum 3 DIFFERENT concentrations to establish standard curve.

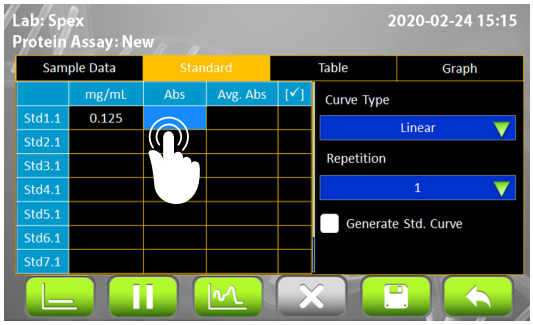
---

7. Select the repetition frequency you need in the **Repetition** bar.

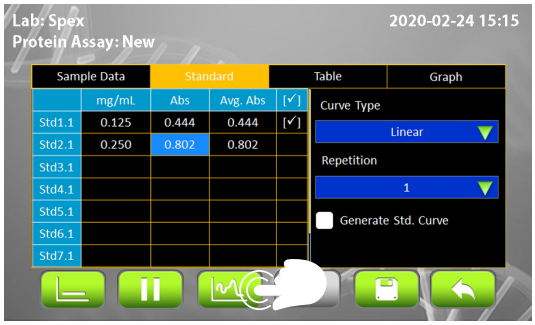
8. Tap on a cell in the **mg/mL** column to enter the concentration of your standard sample.



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

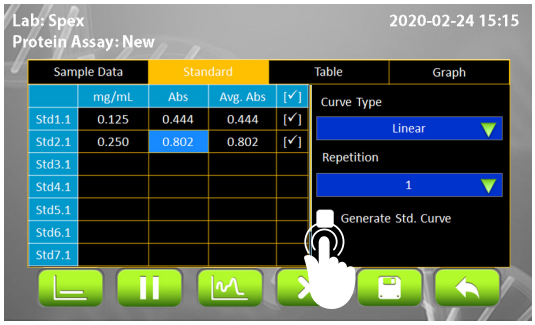


10. If you want to correct the standard absorbance, select the **Measure** icon when the indicator is on the cell you want to change.



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 the **Measure** icon to enter sample measurement.
14. After the experiment, clean the sample window and cover on the detection arm with a lint-free wipe. Use deionized water, ethanol or isopropanol if needed.
15. The correction function is optional and can be turned on/off any time.
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 kit instruction.
2. If users need to establish customized standard curve protocols, please refer to Section 8.2 (page 31).

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 pathlength 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 cell/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 function icons.

The information tab bar has 3 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 the 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 pathlength equivalent.
A (Ref.)	Displays the absorbance at self-defined wavelength which is normalized to a 10 mm pathlength 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.
Pathlength	The light path chosen by the pathlength selector will be detected automatically and length will be shown here.
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. Is 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 data item can be checked at one time.

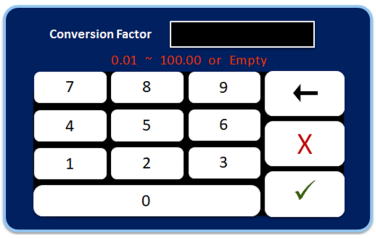
7.1.3 Graph Tab Page

The graph of measuring samples can be enlarged or minimized. The axis can be moved by dragging the graph. Long touch the x- or y-axis on the 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 the OD 600 icon to enter the 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 pathlength 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 Spex NanoSNAP screen.
5. Add appropriate solution of at least 1 µL and tap on the **Blank** icon to establish blank data.
6. Wipe away the blank solution off the sample window and the cover window with a lint-free wipe.
7. Tab on the **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 the **Measure** icon for sample measurement.
9. Clean the sample window and cover on the detection arm with a lint-free wipe after the experiment. Use deionized water, ethanol or isopropanol if needed.
10. The **Reference** (self-defined wavelength) function is optional, and can be turned on/off any time.
11. The default of the **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. Spex NanoSNAP offers the OD 600 measuring function, but it is suggested to use cuvette photometers 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).

Equation: $c = A600 \times cf/b$

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 pathlength in cm

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

8. Application: More Assays

In **More Assays**, the Spex NanoSNAP 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 settings tab page, data tab page, table tab page, and graph tab page.

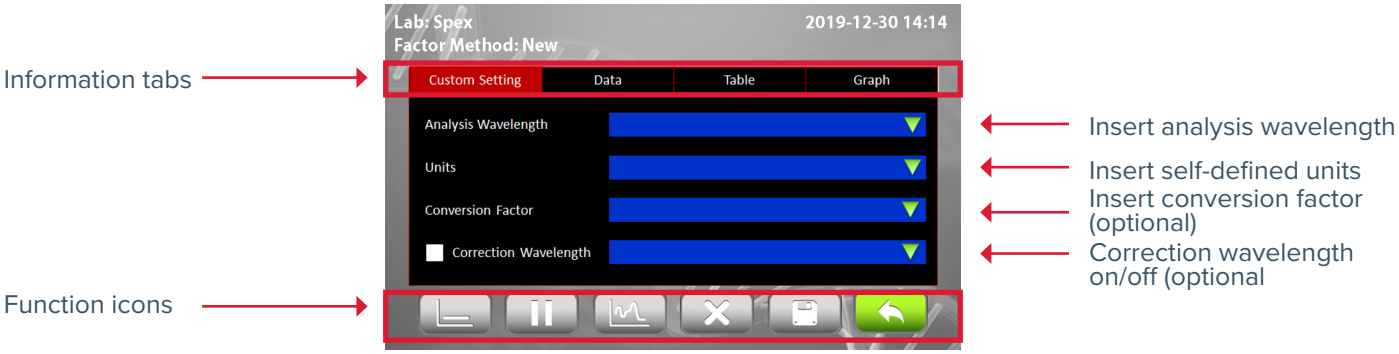


Figure 22. Custom Settings Tab Page

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) fields.

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.

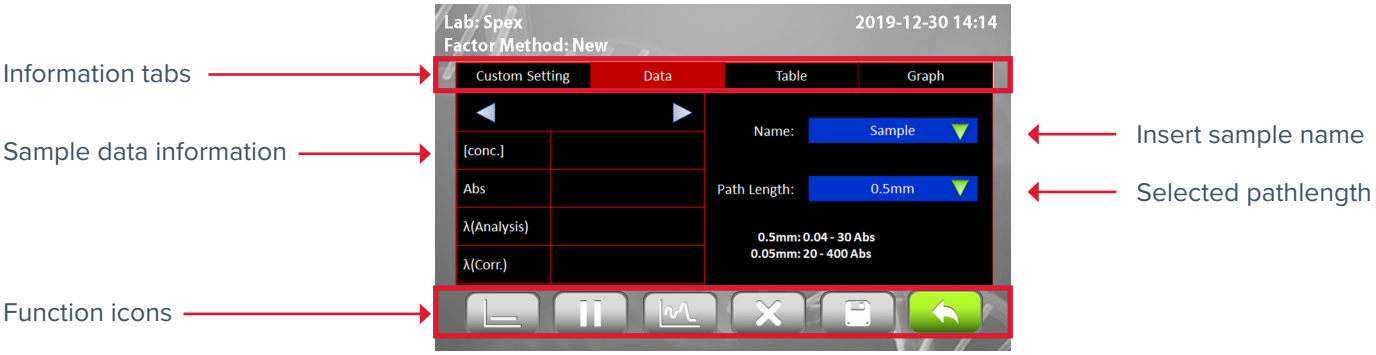


Figure 23. Data Tab Page

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 pathlength equivalent.
λ (Anlaysis)	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.
Pathlength	The light path chosen by the pathlength selector will be detected automatically and length will be shown here.

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.

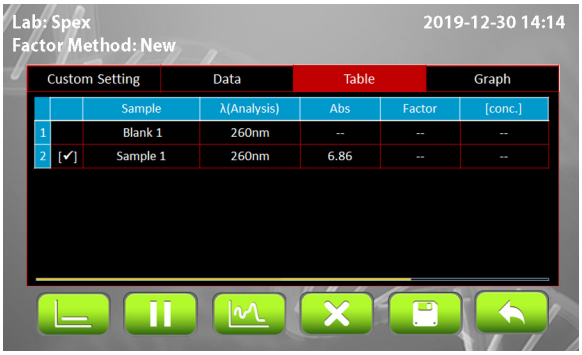


Figure 24. Table Tab Page

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 data item can be checked at one time.

The graph 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.

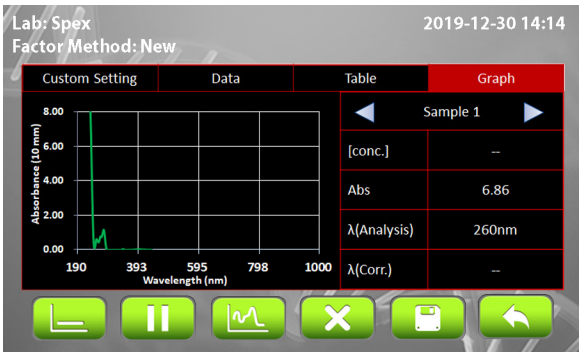


Figure 25. Graph Tab Page

8.1.2 Protocol Operation

1. On the main menu, tap on the **More Assays** icon then the **Factor Method** icon to enter the protocol section.
2. Ensure the sample window and cover window on the detection arm are clean.
3. Insert the **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 the **Blank** icon to establish blank data.
8. Wipe away the blank solution off the sample window and cover window.
9. Add your sample of at least 1 µL and select the **Measure** icon to enter sample measurement.
10. After the experiment, clean the sample window and the cover window on the detection arm with a lint-free wipe. Use deionized water, ethanol or isopropanol if needed.
11. The correction function is optional and can be turned on/off any time.
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

If 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 baseline correction: $c = A \times \varepsilon / b$

With baseline 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 pathlength in cm

8.2 Standard 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 standard curve method, the information tab bar has 5 parts: custom settings 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 and Table 17). The function icons will be activated after inserting the **Analysis Wavelength**, **Units**, and **Correction Wavelength** (optional) field.

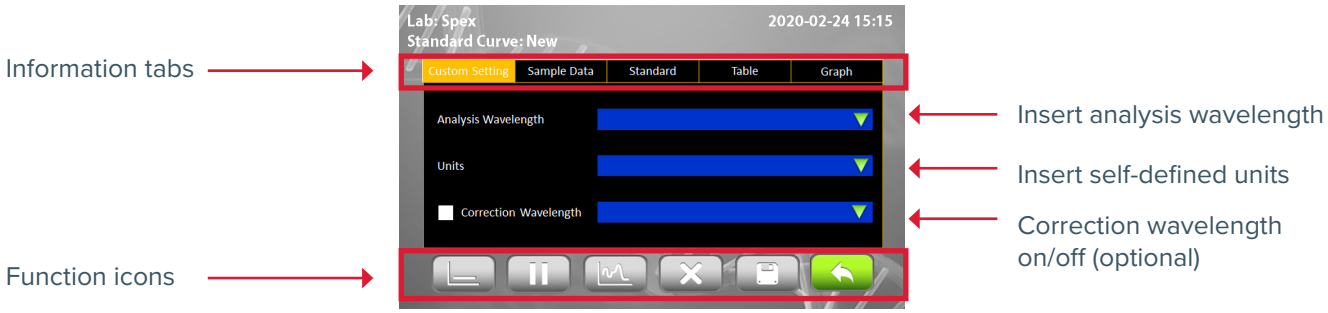


Figure 26. Custom Setting Tab Page

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.

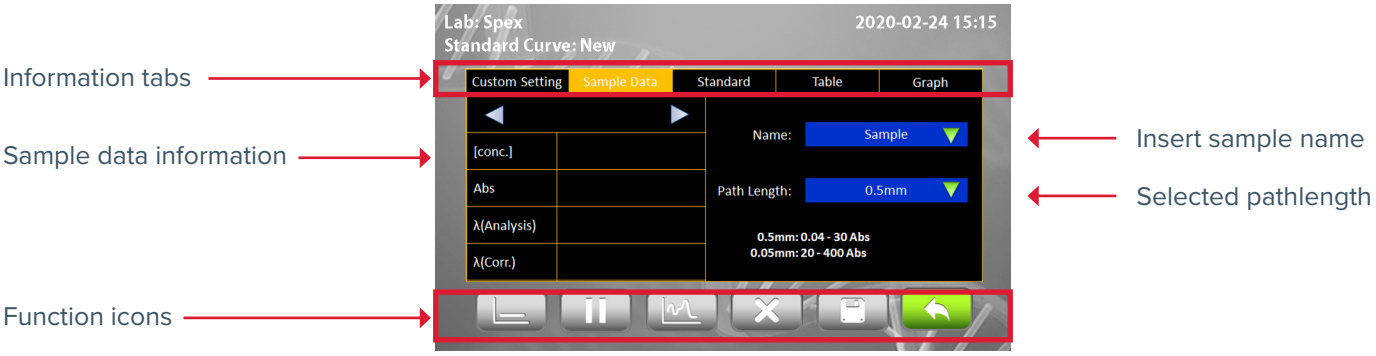


Figure 27. Sample Data Tab Page

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 pathlength equivalent.
λ (Anlaysis)	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.
Pathlength	The light path chosen by the pathlength selector will be detected automatically and length will be shown here.

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).

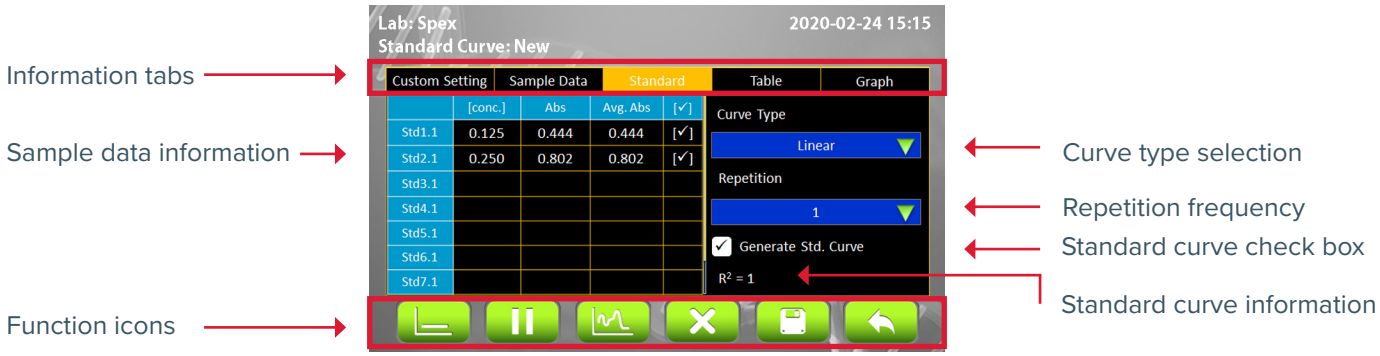


Figure 28. Standard Tab Page

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 user.
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.

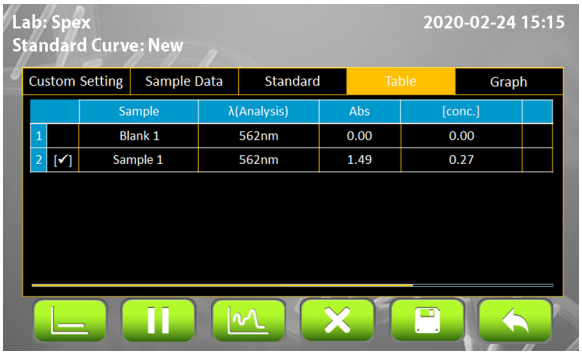


Figure 29. Table Tab Page

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 data item can be checked at one time.

In the standard curve method protocol, there are 2 kinds of graphs: 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.

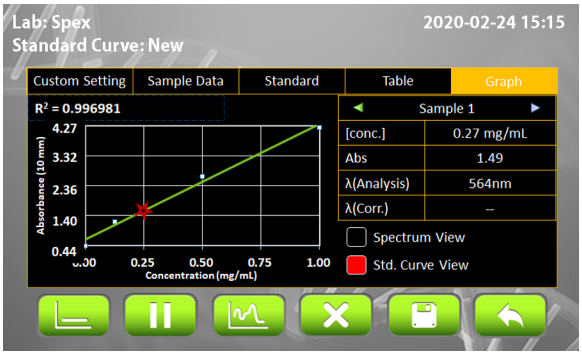


Figure 30. Graph Tab Page

8.2.2 Protocol Operation

1. On the main menu, tap on the **More Assays** icon then the **Standard Curve Method** icon to enter protocol selection.
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 the **Blank** icon to establish blank data. The screen will automatically jump to the **Standard Curve** tab.
7. Wipe away 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 polynomial 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 the **Measure** icon 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 the **Measure** icon when the indicator is on the cell you want to change.
13. You can uncheck the value if it isn't required to generate 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 the **Measure** icon to enter sample measurement.
16. After the experiment, clean the sample window and the cover window on the detection arm with a lint-free wipe. Use deionized water, ethanol or isopropanol if needed.
17. The correction function is optional and can be turned on/off any time.
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 **Standard Curve Method**, the concentration is calculated by the absorbance values measuring in the 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. Set the protocol according to Section 6: Protein Assay on page 20.

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.

In the **Custom Setting** page (Figure 31), there are 8 self-defined wavelength fields in this protocol. The setting range is from 190 nm to 1,000 nm. At least 1 user-defined wavelength is required to activate the function icons.

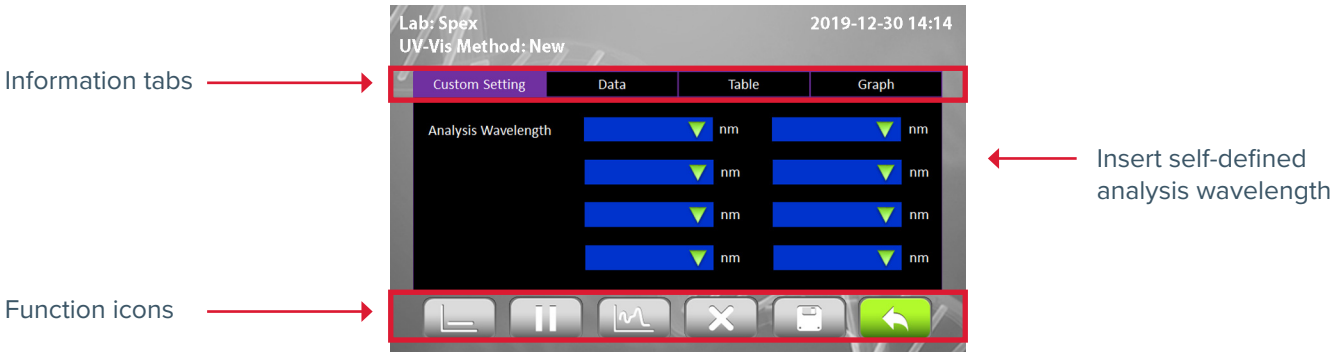


Figure 31. Custom Setting Tab Page

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.

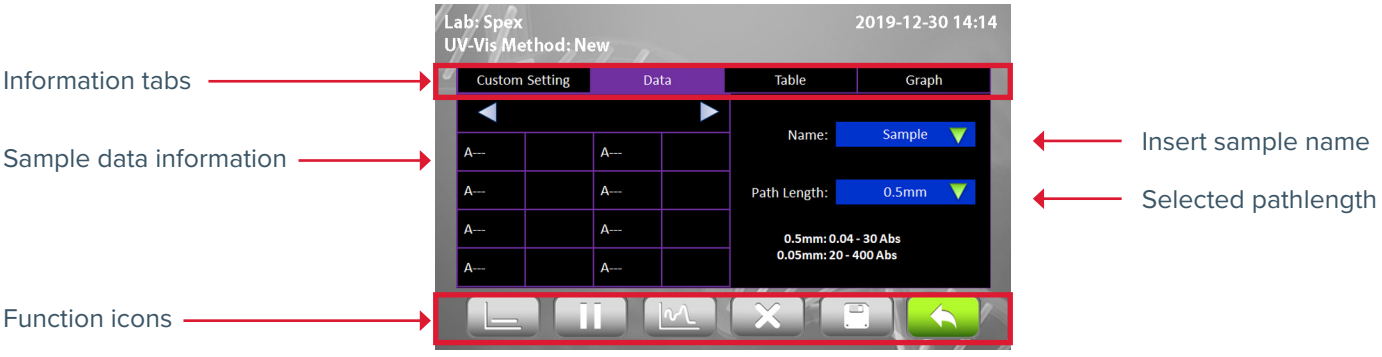


Figure 32. Data Tab Page

Table 20. Sample data tab page information.

Features	Description
A---	These columns will automatically turn to the user-defined wavelength 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.
Pathlength	The light path chosen by the pathlength selector will be detected automatically and length will be shown here.

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.

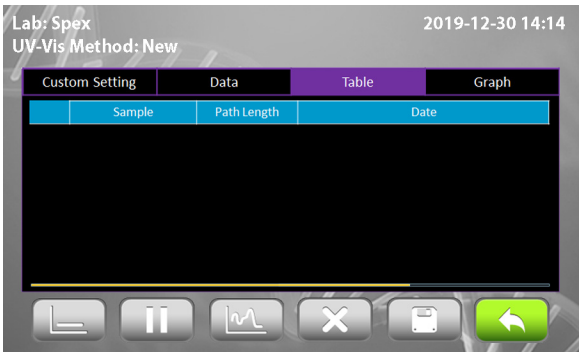


Figure 33. Table Tab Page

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 data item can be checked at one time.

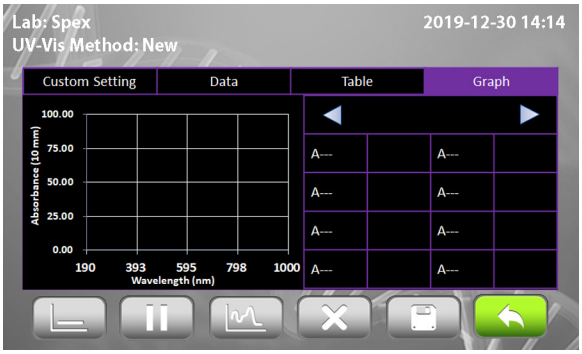


Figure 34. Graph Tab Page

The graph 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 the **More Assays** icon then the **UV-Vis** icon to enter the protocol section.

2. Ensure the sample window and cover window on the detection arm are clean.
3. Insert required **Analysis Wavelength**. Spex NanoSNAP affords a maximum of 8 wavelengths.
4. Add appropriate solution of at least 1 µL and select the **Blank** icon to establish blank data.
5. Wipe away the blank solution off the sample window and the cover window.
6. Add your sample of at least 1 µL and select the **Measure** icon to enter sample measurement.
7. After the experiment, clean the sample window and the cover window on the detection arm with a lint-free wipe. Use deionized water, ethanol or isopropanol if needed.
8. The correction function is optional, and can be turned on/off any time.
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 Settings

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 Spex NanoSNAP.

Figure 35. System Overview

Table 21. System menu setup icons.

System Menu Setup Icons			
	**Date & Time** User can change the date and time settings from here		**Self-Test** Users can do a system self-test
	**Beep Sound** User can turn ON or OFF the system buzzer from here		**About** User can check the basic information of the Spex NanoSNAP including System Version, Initialization Date and Calibration Date. The link to the Operating Manual is also here.
	**Brightness** User can adjust the brightness of the display panel according to the environment's lighting condition		**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
	**Indicator Light** User can turn ON or OFF the LED auxiliary light beside the detection arm from here		**Service** Only authorized personnel have the password to enter Service Mode and perform necessary maintenance and repairs
	**Storage** This function shows the information of total and remaining storage space		**Back** Back to previous menu

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.

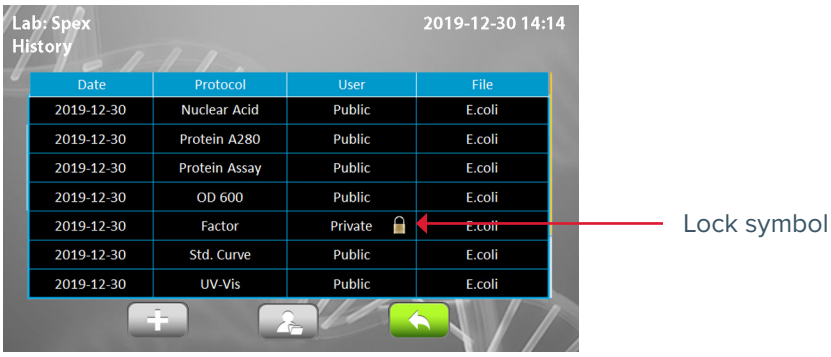


Figure 36. History List Overview

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 the 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 **Plus** icon to duplicate the report setting. The new protocol will have the same setting as the original report, but settings can still be modified.

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 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 OK to confirm the password or tap on CANCEL 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.

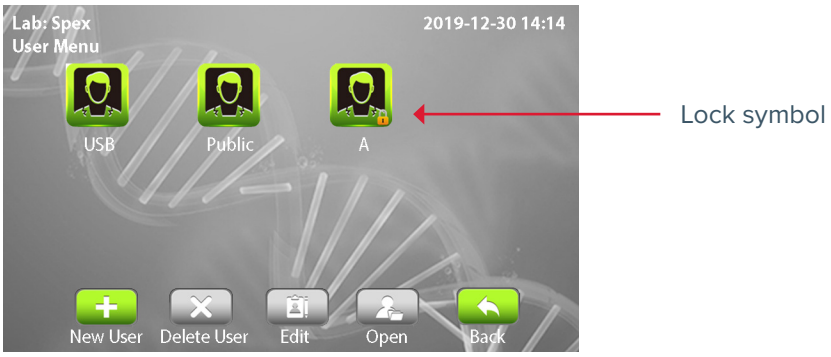


Figure 37. User Folder Overview

All protocols are stored inside the user folders. There are 8 user folders displayed on the page. If there are more than 8 user folders registered in the system, you can slide up or down on the screen to see 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 user folders. The back icon is used to return to the upper page.

11.1 Create a New User Folder

On the user folder screen, tap on the **New User** icon 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 a 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 the user folder?". Tap on ✓ to confirm the deletion. Tap on X to abort the deletion.

Note: User folders that 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, insert your USB flash drive into the front USB port and wait 5 to 10 seconds and the USB icon will pop up. (**Note**: 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 Spex NanoSNAP.) You can also use the USB flash drive to transfer the reports between the Spex NanoSNAP and your computer.

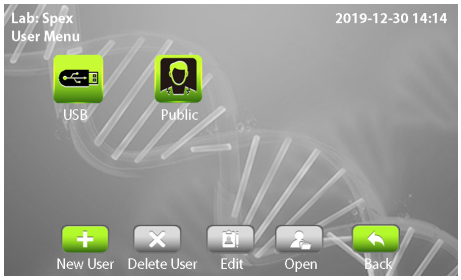


Figure 38. User Folder Overview

12. Maintenance

12.1 Cleaning the Unit

Please avoid liquid spilling onto or into the unit. Liquid may damage the Spex NanoSNAP 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

Add deionized water on the sample window, lower the detection arm and wipe with a lint-free wipe. 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 recommended 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 scree.
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 pathlength selector as it will damage the metal part and affect the pathlength.

12.3 Annual Maintenance

For the best performance, it is suggested to do annual maintenance on the Spex NanoSNAP. It includes light path confirmation and nano-coating layer recoating. Please contact your local Spex distributor for service.

12.4 Replacement

When the surface of the quartz glass has been damaged or contaminated, please contact your local Spex 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 adapter	Return the unit for service
Can't reach sample accuracy	The solutions are not homogeneous and well-mixed prior to sampling	Ensure all solutions are homogeneous and well-mixed prior to sampling
	Sample has air bubbles	Remove air bubbles from sample
	There are scratches on the surface of the 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
Pathlength selector does not work	Faulty pathlength selector mechanism	Return the unit for service
	Pathlength 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 the list of error messages in section 13.1	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 or 0.05 mm, selectable
Light Source	Pulsed Xenon flash lamp
Detector Type	2048 element CMOS
Wavelength Range	190 to 1,000 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) to 400 A
Detection Range	dsDNA: 2 to 20,000 ng/µL BSA: 0.06 to 600 mg/mL
Sample Surface Material of Construction (Lower and Upper)	Stainless steel and quartz window with hydrophobic treatment
Measurement Time	< 3 seconds
Software	
Operating System	Custom Linux based software
Registered User Folder Number	> 500 sets
User Folder Password Protection	Yes
General	
Display	7-inch color LCD with capacitive touch panel
Data Port	1 USB Type-A front port for USB flash drive
Dimensions (W x D x H)	8.1 in x 13.1 in x 6.5 in (206 mm x 333 mm x 166 mm)
Weight	7.8 lb (3.5 kg)
Glove Compatibility	All common lab gloves
Internal Storage	32 GB flash memory
Power Adapter	Input: AC 100–230 V, 50/60 Hz, 50 W Output: DC 24 V, 2.08 A
Certifications	CE, RoHS

Specifications are subject to change without prior notice.

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