Quawell

Q6000 UV-Vis Spectrophotometer

User Manual

V1.0.1 (Not available in USA)

Rev. 2015-06

Table of Contents

Introduction

Description

Quawell Q6000 is a micro-volume UV-Visible (200-900nm) spectrophotometer. With the No-Moving-Part technologies, Q6000 holds 0.5-1 μL samples between the sample surfaces and measures the sample about 3 seconds with a high degree of accuracy and reproducibility. Q6000 + cuvette can make kinetic analyzes and low concentration sample measurements using cuvette measurement mode.

Advantages

- Extremely high degree of reproducibility (at 500 ng/μL, the CV is less than 1%).
- Calibration free with CCE technologies.
- 0.5-1 μL sample only for sample measurement.
- Less measurement circle and longer light source life.
- Micro-volume and cuvette measurement modes.

CCE Technologies

CCE Technologies is one of powerful software utilities. With CCE Technologies, you are able to diagnostic and calibrate Q6000 simply and quickly (refer to Section Diagnostics).

Safety Information

- DO NOT REMOVE THE COVER!
- For use with AC ADAPTER S120S400A4 or Gs60A12
- Q6000 is for indoor use under the conditions:
- Always disconnect the instrument from line power before maintenance. Refer servicing to qualified personnel.
- Ambient operating temperature 15–35 °C
- Humidity <65%, at 25–40 °C

Installation

Computer Requirements

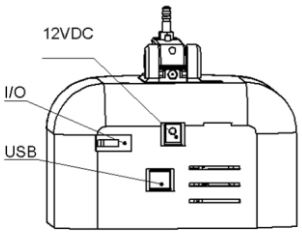
- Microsoft Windows XP, Vista, Win7/8 (32/64).
- Microsoft Excel 2003 or later.
- CPU: 400MHZ or higher.
- 128 MB RAM.
- USB 2.0 port.
- Monitor: 1024x768.

Software Setup

Note:	Do not connect the Q6000 to the PC before completely installing the software and the driver.

- Insert the CD into CD driver and open the folder corresponding to the PC system.
  - For Win XP, Vista, Win7 (8) 32-bit system, select the folder **Q6000-32 …**
  - For Win7 (8) 64-bit system, select the folder **Q6000-64 …**
- Click **setup** to copy the program to the computer **FIRST**, **AFTER FINISH**; click **OmniDriver …** to install the drivers.
- Connect the Q6000 to the computer with the USB cable. The driver will be installed automatically.
- Turn on the power switch and click the shortcut Q6000 on the desktop to run the program.

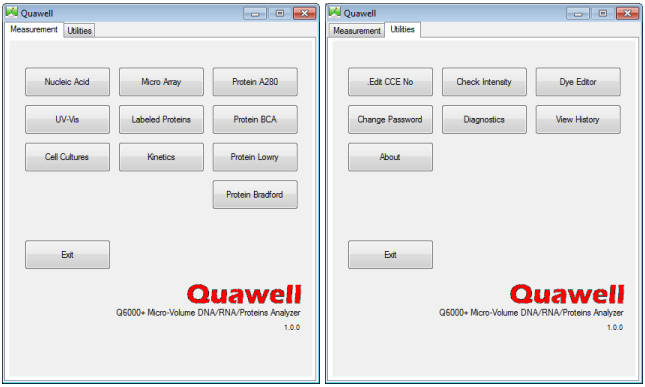
Rear panel



Software and Basic Operation

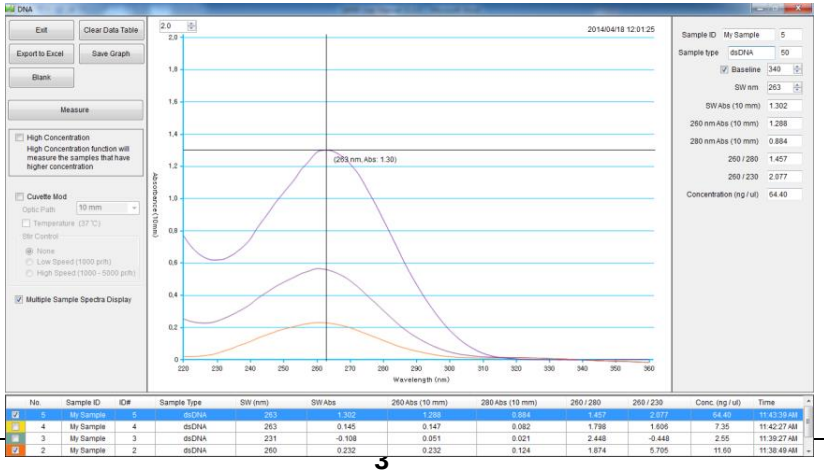
Main Menu

The main menu below contains Measurement and Utility Tab.



Screen Panels

1. **Functions panel (left):** Contains all action buttons and function selections.
2. **Graph panel:** Displays the sample data spectrum.
3. **Data panel (right):** Displays the most recent measurement sample data.
4. **Data table:** Contains the data of all measurement samples. The most recent measurement data is on the top.



Multiple Data Spectra

Check the checkbox **Multiple Sample Spectra Display** on the left panel, the multiple data spectra will be displayed on the graph area. Uncheck the checkbox appeared on the left of the data table to remove the individual spectra from the graph area.

Micro-volume Mode Measurement

Note:	• Using 1 µL samples for normal concentration measurement (< 1,500 ng/µL dsDNA) • Using 0.5 µL sample for high concentration measurement (1,500 ng/µL or higher).

1. Lift the upper arm, pipette 1 µL blank buffer onto the lower surface, close the upper arm and click **Blank** button.
2. Lift the upper arm and remove the blank buffer from the supper and lower surfaces with the dry wipe.
3. Pipette 1 µL samples onto lower surface, close the upper arm and click **Measure** to complete the measurement.
4. Lift the upper arm and remove the sample from the upper and lower surfaces, with the dry wipe.

Cuvette Mode Measurement

Note:	• The cuvette specification: 12.5 mm (L) x 12.5 mm (W) x 45 mm (H). • The cuvette Path length: 10, 5, 2 and 1 mm. • The optical beam is above 8.5 mm from the bottom of the cuvette. • Use quartz or UV transparent plastic cuvettes for UV region (<340 nm) region measurement.

1. Select the **Cuvette Mode** on the left panel. Lift the arm and Insert a cuvette with the blank buffer. Lower the arm and click the **Blank** button.
2. Lift the arm and Insert a cuvette with the sample. Lower the arm and click the **Measure** button.
3. **Heat to 37 °C:** When selected, heats the cuvette holder to 37 ±0.5 °C. It may take 0-20 minutes.
4. **Stir Control:** Stirrer on and speed selection. Low Speed: 150-300 RPM, High Speed: 500-900 RPM.

Password, change or forget password

The default password is “admin”. It is recommended that you change the password after install the program. If you forget your password, please contact your local distributor or send email to info@quawell.com to get the new password.

Software update

The software version number is on the right bottom of the main menu. Please visit our website and download the new version software. We will periodically update software with new features for free downloading.

The Best Practices

Clean measurement surfaces

1. Use a dry lab wipe to remove the liquids from both the upper and lower surfaces immediately after each measurement.
2. Ensure the sample surfaces condition as expected (refer to **Surface-Condition-Check**) before measurement.

Sample

1. Use 1 µL samples for normal concentration measurement.
2. Use 0.5 µL samples for high concentration measurement.
3. Ensure that the sample is homogeneous and vortex before measurement

Measurement

1. Use a fresh tip to deliver each sample aliquot.
2. Use a fresh aliquot sample for each measurement.
3. Repeated measurements on the same sample aliquot may result in increasing concentration.

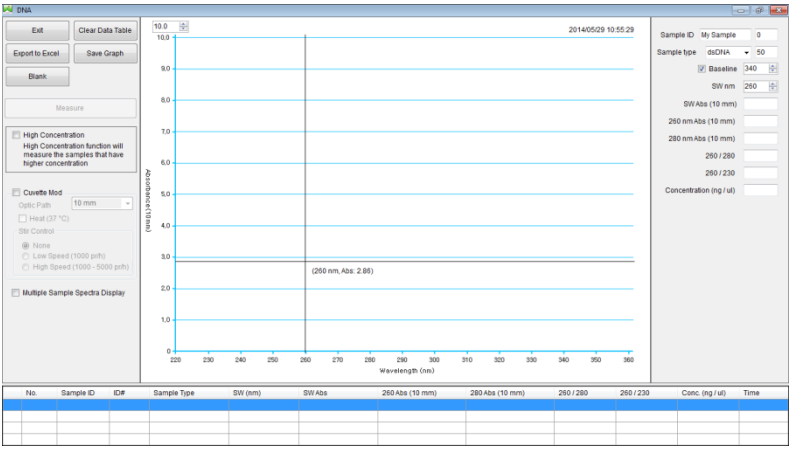
Surface-Condition-Check

1. Lift the upper arm, pipette 1 µL de-ionized onto the lower surface, close the upper arm and click **Blank** button.
2. Remove the water from both surfaces use the dry wipe.
3. Pipette 1 µL de-ionized onto the lower surface, close the arm and click **Measure** button.
4. Repeat the step 3 for 3-5 times. The absorbance should be between ± 0.04 (10 mm pathlength equivalent). If the results are not expected, clean the surfaces and repeat the steps from 1 to 3.

Nucleic Acid

Nucleic Acid Screen Features

Select **Nucleic Acid** from the main menu. The screen features will be displayed below.



- **Graph Display:** The Y-axis indicates the absorbance value and the X-axis is for the wavelength. The maximum absorbance value is automatically adjusted to the highest absorbance value.
- **Sample ID - #:** There are two windows that display the sample ID information. The left window displays the sample ID input by the user. The default is My Sample. The right window displays the number for the same sample ID. The number begins at 1 and increases by 1 for each measurement. Changing the Sample ID will automatically reset the number to 1.
- **Sample Type:** Chose the sample type for the sample to be measured. There are 3 different sample types for nucleic acids: dsDNA, ssDNA and RNA. The default is dsDNA. The sample type is disabled after blanking. The extinction coefficient of the sample selected will automatically apply to the calculation.
- **Baseline:** The default is 340 nm
- **SW nm:** The selected wavelength for the vertical lines in the graph.
- **SW Abs (10mm):** The absorbance of selected wavelength.
- **260 nm Abs (10mm):** The absorbance of sample at 260 nm.
- **280 nm Abs (10mm):** The absorbance of sample at 280 nm.
- **260/280:** The ratio of absorbance at 260 nm and 280 nm.

- **260/230:** The ratio of absorbance at 260 nm and 230 nm.
- **Concentration (ng/μL):** Sample concentration in ng/μL.

High Concentration

Note:	Use 0.5 μL for High Concentration measurement.

The Q6000 will measure dsDNA samples ≤15,000 ng/μL without dilution. Check the checkbox **High Concentration** when samples concentration is 3,500 ng/μL or higher. The instrument will automatically adjust the pathlength to 0.05 mm.

Measurement Range

Concentration	Reproducibility
1 to 15,000 ng/μL (dsDNA)	Sample range 1-100 ng/μL ± 2 ng/μL
	Sample range >100 ng/μL ± 2%

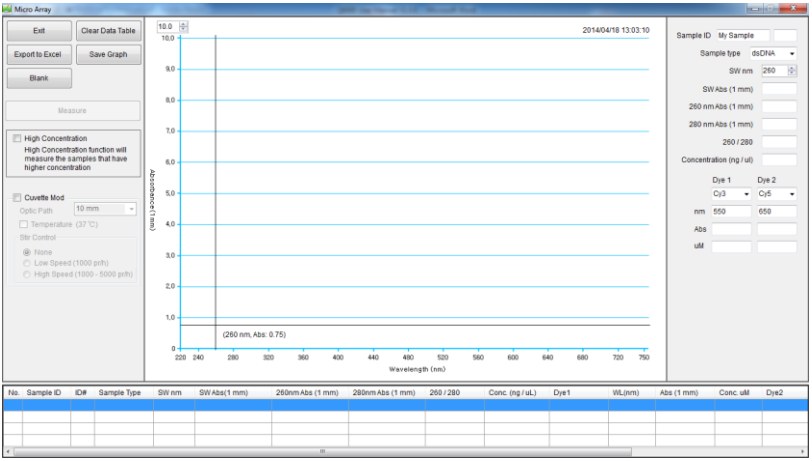
Sample Volume

There is no specific requirement for the sample volume; however for the best accuracy and reproducibility we recommend 1 μL for the normal measurement and 0.5 μL for the high concentration mode.

Microarray

Microarray Screen Features

Select Microarray from the main menu and the application interface below will appear on the screen.



- **Graph Display:** The Y-axis indicates the absorbance value and the X-axis is for the wavelength. The maximum absorbance value is automatically adjusted to the highest absorbance value. The user is also allowed to manually enter the absorbance value.
- **Sample ID - #:** There are two windows that display the sample ID information. The left window displays the sample ID input by the user. The default is “My Sample”. The right window displays the number for the same sample ID. The number begins at 1 and increases by 1 for each measurement. Changing the Sample ID will automatically reset the number to 1.
- **Sample Type:** Chose the sample type for the sample to be measured. There are 3 different sample types: dsDNA, ssDNA and RNA. The sample type is disabled after blanking.
- **Baseline:** The default is 340 nm.
- **SW nm:** The selected wavelength for the vertical lines in the graph.
- **SW Abs (10mm):** The absorbance of selected wavelength.
- **260 nm Abs (10mm):** The absorbance of sample at 260 nm.
- **280 nm Abs (10mm):** The absorbance of sample at 280 nm.

- **260/280:** The ratio of absorbance at 260 nm and 280 nm.
- **Concentration (ng/µl):** The sample concentration in ng/µL.
- **Dye1 and Dye2 Selection Windows**
  - **Dye1 or Dye2 drop-down list:** Displays the dye that is pre-predefined using the **Dye List Editor**. Please see Section 11 for the details on how to predefine the list.
  - **Abs:** absorbance of Dye1 or Dye2.
  - **Pmol/µL:** concentration of Dye1 or Dye2 in pmol/µL.

Measurement Range (Cy3)

Concentration (pmols/µL)	Reproducibility
0.2-100	± 0.2%

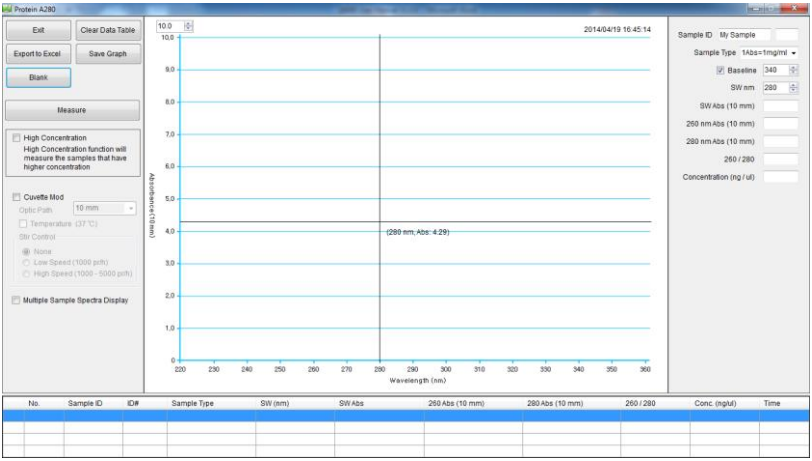
Sample Volume

There is no specific requirement for the sample volume. However for the best accuracy and reproducibility we recommend 2 µL.

Protein A280

Protein A280 Screen Features

Select Protein A280 from the Q6000 main menu and the application interface below will appear on the screen.



- **Graph Display:** The Y-axis indicates the absorbance value and the X-axis is for the wavelength. The maximum absorbance value is automatically adjusted to the highest absorbance value.
- **Sample ID - #:** There are two windows that display the sample ID information. The left window displays the sample ID input by the user. The default is My Sample. The right window displays the number for the same sample ID. The number begins at 1 and increases by 1 for each measurement. Changing the Sample ID will automatically reset the number to 1.
- **Sample Type:** Chose the sample type for the sample to be measured.
- **Baseline:** The default is 340 nm
- **SW nm:** The selected wavelength for the vertical lines in the graph.
- **SW Abs (10mm):** The absorbance of selected wavelength.
- **260 nm Abs (10mm):** The absorbance of sample at 260 nm.
- **280 nm Abs (10mm):** The absorbance of sample at 280 nm.
- **260/280:** The ratio of absorbance at 260 nm and 280 nm.
- **Concentration (mg/mL):** sample concentration in mg/mL.

Measurement Range (Purified BSA)

Concentration	Reproducibility
0.05 -100 mg/mL	sample range 0.10-10 mg/mL ± 0.10 mg/mL
	sample range >10mg/mL ±2%

Sample Volume

There is no specific requirement for the sample volume; however for the best accuracy and reproducibility we recommend 1.5 µL.

Protein Assay

BCA Method

The Bicinchoninic acid (BCA) method depends on the conversion of Cu2+ to Cu+ under alkaline conditions. The Cu+ is then detected by reaction with BCA. The reaction results in the development of an intense purple color with an absorbance maximum at 562 nm.

Lowry Method

Lowry method is also based on the conversion of Cu2+ to Cu+ under alkaline conditions. The reactions result in a strong blue color that is measured at 750 nm.

Bradford Method

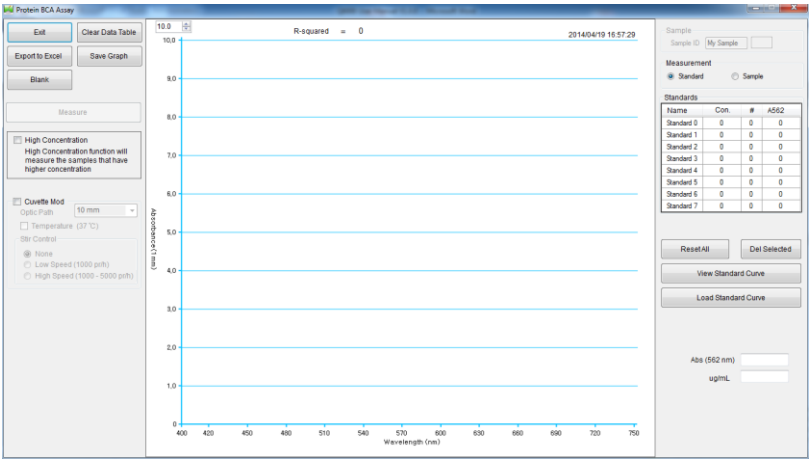
Bradford method is a common colorimetric method to determine protein concentration in a sample solution. The Bradford method of protein determination is based on the binding of a dye, Coomassie Blue G, to the protein. This binding shifts the absorption maximum of the dye from red to blue. The absorbance of the solution is measured at 595 nm and is proportional to protein concentration when compared to a standard curve.

Measurement Range

BCA	**10ug/mL-200ug/mL:** using 1:1 reagent / sample volume ratio, a minimum of 10 µL of sample and 10 µL of BCA reagent.
	200ug/mL-8mg/mL: using a 20:1 reagent / sample volume ratio, a minimum sample volume of 4 µL in 80 µL of BCA reagent.
Lowry	**200ug/mL-4mg/mL:** using a 5:1 reagent / sample volume ratio, a minimum sample volume of 20 µL and 100µL of Modified Lowry reagent
Bradford	**15ug/mL-100ug/mL:** using 1:1 reagent / sample volume ratio, a minimum of 10 µL of sample and 10 µL of Bradford reagent.
	100ug/mL-8mg/mL: using a 50:1 reagent / sample volume ratio, a minimum sample volume of 4 µL in 200 µL of Bradford reagent.

The Procedure of Protein Assay

The screen features of protein assay as below. The right pane contains the specific to the BCA, Lowry and Bradford protein assay applications. The procedures for Protein assay are the following:



Generate a standard curve

- Establish the blank value using the standard buffer.
- Enter the value of standards in the column "Con." of the Standard window on the right panel (enter 0 for Standard 0).
- Measure the standards, up to 5 measurements for each standard can be made. The number of the measurements and the average value of the absorbance will be displayed in the corresponding columns “#” and “Avg”.

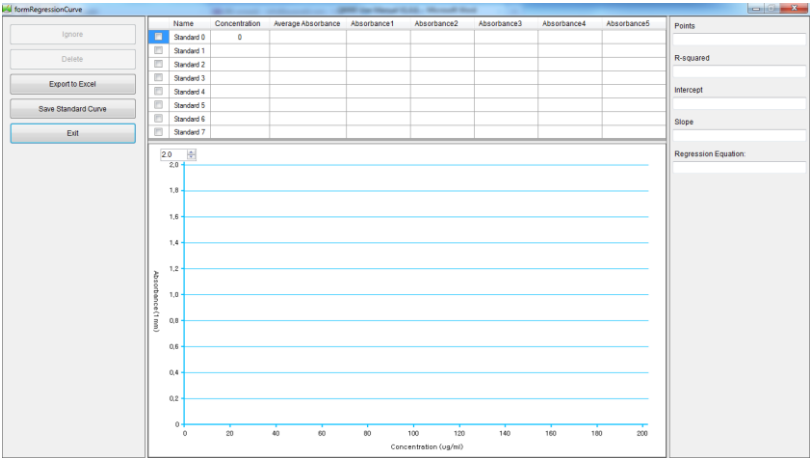
Standards

Name	Con.	#	A562
Standard 0	0	0	0
Standard 1	0	0	0
Standard 2	0	0	0
Standard 3	0	0	0
Standard 4	0	0	0
Standard 5	0	0	0
Standard 6	0	0	0
Standard 7	0	0	0

Edit Standard Measurements

Note:	The standard value can't be changed after sample value measured.

- Click View Standard Curve to load the standard curve edit screen below.



- Edit individual absorbance value - move the mouse point to the value of the absorbance in the table and left click.
- Edit standard - check the checkbox on the left of each standard point.
- Using the Delete, Ignore and Restore functions to edit your selection:

  Delete function: Click the "Delete" button to delete the selection.

  Ignore function: Click the "Ignore" button to take the selected value out from the calculation of R-squared, it is different from "Delete", the "Ignore" allow the user to restore the value and get it back to the R-squared calculation.

  Restore function: Select the ignored-value and click the "Restore" button to get the ignored-value back to the calculation of R-squared.

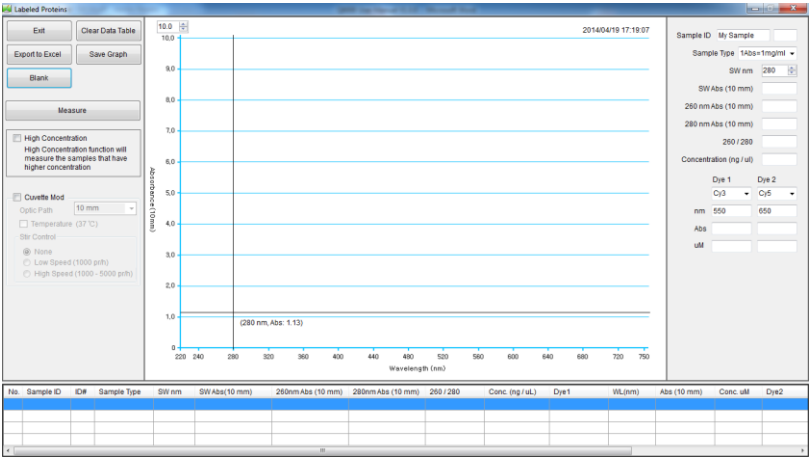
Labeled-Proteins

Overview

The Labeled-Proteins function will simultaneously measure both protein and fluorescent dye concentrations at appropriate wavelengths.

Proteins and Labels Screen Features

Select Proteins and Labels from the Q6000 main menu and the module interface will appear on the screen.



- **Graph Display**: The Y-axis indicates the absorbance value and the X-axis is for the wavelength. The maximum absorbance value is automatically adjusted to the highest absorbance value. The user is also allowed to manually enter the absorbance value.
- **Sample ID - #**: there are two windows that display the sample ID information. The left window displays the sample ID input by the user. The default is “My Sample”. The right window displays the number for the same sample ID. The number begins at 1 and increases by 1 for each measurement. Changing the Sample ID will automatically reset the number to 1.
- **Sample Type:** chose the sample type for the sample to be measured.
- **SW and Abs (10mm):** the user selected wavelength and corresponding absorbance. The wavelength can be selected by using the up/down arrows or input the number in the wavelength box. The user-selected wavelength and absorbance are not utilized in any calculations.
- **Abs280 (10mm):** absorbance of the sample at 280 nm.

- **260/280:** ratio of the absorbance at 260 nm and 280 nm.
- **mg/mL:** sample concentration in mg/mL.
- **Dye1 and Dye 2 Selection Windows**
  - Dye1 or Dye2 drop-down list: displays the dye that is pre-predefined using the Dye List Editor. See Section 11 for details on how to predefine the list.
  - Abs: absorbance of Dye1 or Dye2.
  - uM: concentration of Dye1 or Dye2 in uM.
  - Vertical Lines: the green line on the absorbance-wavelength graph indicates the peak position of the wavelength for Dye 1, and the blue vertical line indicates the peak position of the wavelength for Dye 2.

Measurement Range

Concentration	Reproducibility
0.1 -20 mg/mL (Purified BSA)	sample range 0.10-10 mg/mL: ± 0.10 mg/mL sample range >10mg/mL: ± 2%
0.2-100 uM (Cy3)	sample range 0.20-4.0 pmol/μL: ± 0.20 pmol/μL sample range >4.0 pmol/μL: ± 2%

Sample Volume

There is no specific requirement for the sample volume; however for the best accuracy and reproducibility we recommend 2 μL.

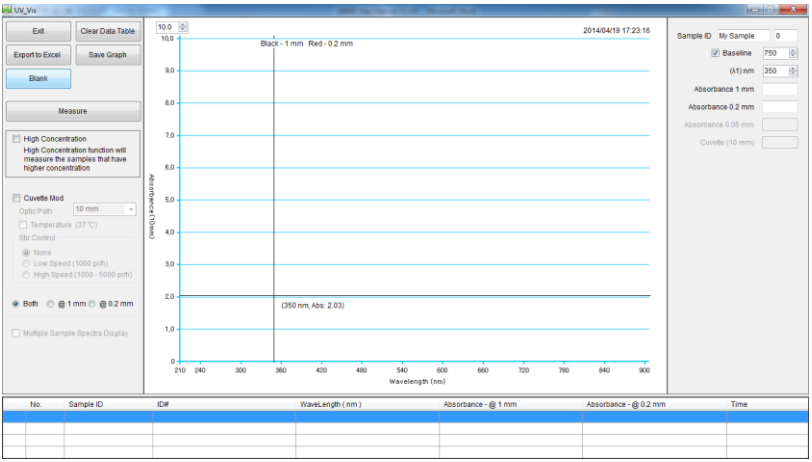
UV-Vis Measurement

Overview

The Q6000 can function as a general-use laboratory spectrophotometer. The UV-Vis module provides the operator with a sample absorbance measuring range from 200 to 850 nm.

UV-Vis Module Screen Features

Select UV-Vis from Q6000 main menu and the module interface will appear on the screen.



- **Graph Display:** The Y-axis indicates the absorbance value and the X-axis is for the wavelength. The maximum absorbance value is automatically adjusted to the highest absorbance value. The user is also allowed to manually enter the absorbance value.
- **Sample ID - #:** there are two windows that display the sample ID information. The left window displays the sample ID input by the user. The default is “My Sample”. The right window displays the ID number for that sample ID. The ID number begins at 1 and increases by 1 for each measurement. Changing the Sample ID will automatically reset the ID number to 1.
- **(λ1) nm:** select the wavelength by using the up/down arrows.
- **Absorbance 1mm:** absorbance of 1mm path at (λ1) nm.
- **Absorbance 0.2mm:** absorbance of 0.2mm path at (λ1) nm.

- **Vertical Lines:** the black vertical line on the absorbance-wavelength graph indicates the peak position of the wavelength (λ1) nm.

Sample Volume

There is no specific requirement for the sample volume; however for the best accuracy and reproducibility we recommend 1 µL.

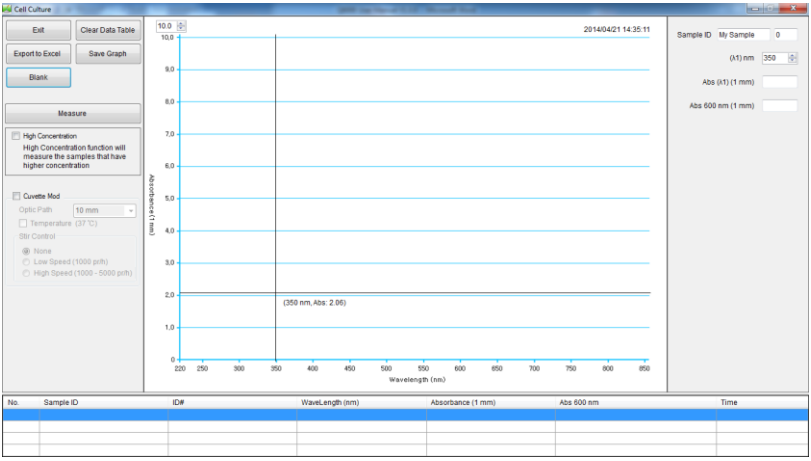
Cell Cultures (OD 600)

Overview

The Q6000 allows laboratories to monitor the density of suspended cell and microbial cultures by measuring their light scatter at 600 nm.

Cell Cultures Screen Features

Select Cell Cultures from Q6000 main menu and the interface will appear below.



- **Graph Display:** The Y-axis indicates the absorbance value and the X-axis is for the wavelength. The maximum absorbance value is automatically adjusted to the highest absorbance value.
- **Sample ID - #:** There are two windows that display the sample ID information. The left window displays the sample ID input by the user. The default is “My Sample”. The right window displays the ID number for that sample ID. The ID number begins at 1 and increases by 1 for each measurement. Changing the Sample ID will automatically reset the ID number to 1.
- **SW nm:** User select wavelength
- **Abs SW (1mm):** Absorbance at selected nm.
- **Abs 600 nm (1mm):** Absorbance at 600nm

Sample Volume

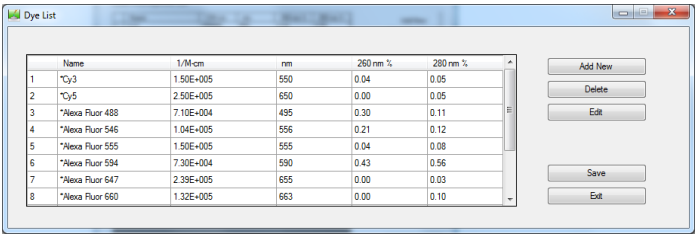
There is no specific requirement for the sample volume; however for the best accuracy and reproducibility we recommend 1 µL.

Kinetics

The predefined fluorescent dyes list

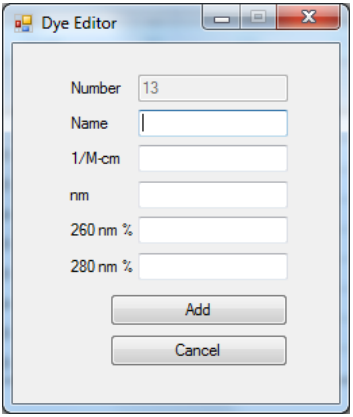
Dyes List

The list works with both the Microarray and Labeled Proteins modules. This list contains a pre-defined list of fluorescent dyes as shown below.



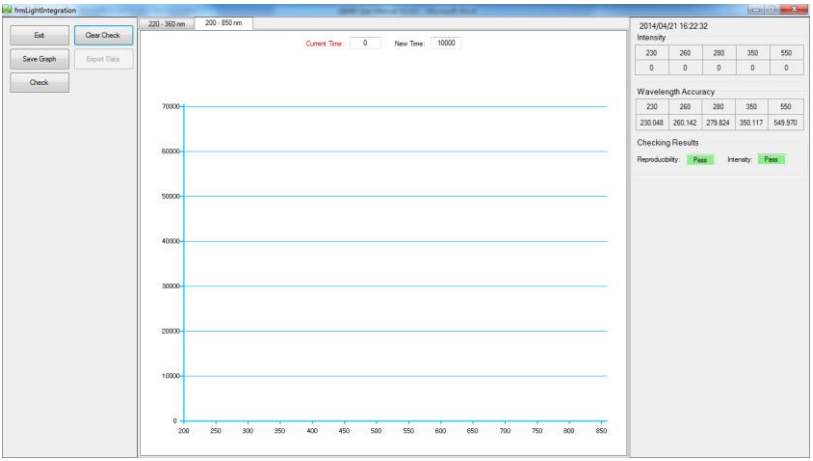
Dye Editor

Additional fluorescent dyes can be added by the user as needed.



Check Intensity

Check Intensity Screen Features



- **220-360nm tab:** Checks the light intensity between 200-360nm.
- **200-900nm tab:** Checks the light intensity between 200-850nm
- **Intensity:** Display the intensity for each wavelength.
- **Wavelength Accuracy:** Display accuracy for each wavelength.
- **Reproducibility:** Indicator for reproducibility, green-pass, red-fail.
- **Intensity:** Indicator for intensity, green-pass, red-fail.

Making Intensity Check

Note:	Before start the checking, please clean the measurement surface well.

1. Pipette 2μL de-ionized water onto the lower surface and close the upper arm. Select the wavelength region and click the Check button.
2. The Reproducibility and Intensity will display each checking results.
3. If you see the Fail and the Red background, clean the measurement surfaces and repeat the step 1-3.
4. If the above problems persist, save the graph and email to your local distributor for technical support.

Diagnostic

Diagnostic function

Diagnostic function checks the calibration of measurement pathlength as well as the reproducibility. It is recommended that you run this function every six month ensure the instrument is in the specification.

Standard Solution

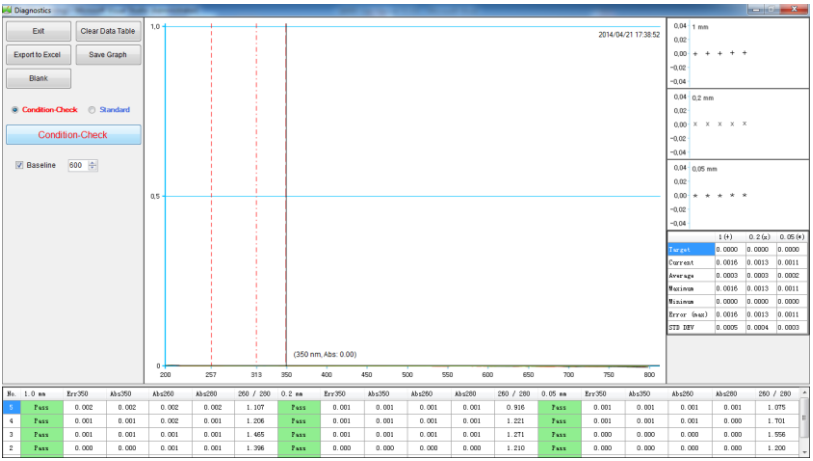
QW101 is the standard solution required for running diagnostic function. QW101 is available from your local distributor. Do not re-use QW101 after open it.

Procedure of Running Diagnostic

Note:	Clean the measurement surfaces with the de-ionized water carefully before start diagnostic.

Surfaces Condition Check

1. Select **Condition-Check**, open the upper arm and pipette 2μL de-ionized water on the lower surface, close the arm and click **Blank** button.
2. Open the upper arm and remove the water from the surfaces with the dry wipe, pipette 2 μL fresh de-ionized water on the lower surface, close the arm and click **Measure** button.
3. Repeat step 2 for 5 times. If the result of check is red, start from 1 again.



Measure the Standard

1. Select **Standard**, open the upper arm and pipette 1 µL de-ionized water on the lower surface, close the arm and click **Blank** button. Open the upper arm and remove the water from the surfaces with the dry wipe.
2. Pipette 1 µL QW101 onto the lower surface, close the arm and click **Measure** button. Remove the QW101 from surfaces with dry wipe.
3. Repeat 2 for 5-10 times.
4. Compare the values of **Abs350** (absorbance at 350 nm) on the table with the **Standard Value** below.
5. If the measurement value is not in the range below, repeat 1- 3. If the 2nd measurement is still out of range, save the results, contact your local distributor or send email to info@quawell.com.

Standard Value

	Normal	**High**
Absorbance	0.337 ± 2%	0.0337 ± 5%

Troubleshooting

Deviation in the Measurement Result

Sample Overlap

- Sample residue on either measurement surface will affect the result. We suggest that clean the surfaces with 1 µL de-ionized water after measuring highly concentrated samples.
- Running **Surface-Condition-Check** before measurement.

Sample Homogeneity

Non-homogenous samples would cause significant deviation in the data generated by any measurement system, including the spectrophotometer.

Effect of Evaporation

Sample evaporation could cause a 1-2% deviation in the sample's concentration.

Insufficient Sample Volume

- Using 1 µL samples for normal concentration measurement.
- Using 0.5 µL sample for high concentration measurement.

USB Connection Error

This error screen usually indicates that the Q6000 and PC connection failed. To correct the error, exit the program, unplug the USB cable, wait for 2-3 seconds, plug it and start the program. If the problem persists, contact your local distributor for technical support.

Maintenance

The primary Maintenance

The primary maintenance requirement of the Q6000 spectrophotometer is to keep the measurement surfaces clean. Upon completion of a measurement, wipe the sample from the upper and lower surfaces. Clean the surfaces and surrounding area with de-ionized water to prevent sample carryover and residue buildup.

Diagnostics

It is recommended that you run this function every six month ensure the instrument is in the specification.

Appendices

Q6000 Specifications

Sample Size	0.5 – 1 µL
Optic Path Length	0.5 and 0.05mm (auto selected option)
Diagnostic and Calibration	Software with CCE No.
Light Source	Xenon flash lamp
Wavelength Range	200-900 nm
Wavelength Resolution	1nm
Wavelength Accuracy	1nm
Absorbance Range	0.004 - 300
Absorbance Precision	0.002 Abs (1mm)
Absorbance Accuracy	1%
Detector Type	2048 element linear silicon CCD array
Detection Limit	2 ng/µL (dsDNA)
Max Concentration	15,000 ng/µL (dsDNA)
Measurement Cycle	~ 3 seconds
Software Compatibility	Windows® XP, Vista, Win7/8 (32 or 64)
Dimensions	145 mm x 210 mm
Weight	2.5 kg
Operating Voltage	12 VDC
Power Consumption	15 W (operating)
Surface Construction	303 stainless steel and quartz fiber
CE Approval	Units sold in Europe
Patent No.	US 7,969,575 B2

Cuvette Mode

Cuvette Specification	12.5 mm (L) x 12.5 mm (W) x 45 mm (H)
Path Length	10, 5, 2 and 1 mm
Optical Beam	8.5 mm from the bottom of the cuvette
Heat to Cuvette Holder	37 ± 0.5 °C
Stir Speed	130-900 RPM
Absorbance Range	0.04 - 750

Absorbance Calculation

When the Q6000 Spectrophotometer is “blanked”, a spectrum is taken of a reference material (blank) and stored in memory as an array of light intensities by wavelength. When a measurement of a sample is taken, the intensity of light that was transmitted through the sample is recorded. The sample intensities along with the blank intensities are used to calculate the sample absorbance according to the following equation:

$$Abs = -\log\left(\frac{\mathbf{I}_{\text{sample}}}{\mathbf{I}_{blanc}}\right)$$

Thus, the measured light intensity of both the sample and of the blank are required to calculate the absorbance at a given wavelength.

Concentration Calculation (Beer's Law)

The Beer-Lambert equation is used to correlate the calculated absorbance with concentration:

$$A = E * b * c$$

Where A is the absorbance represented in absorbance units (A), E is the wavelength-dependent molar absorptive coefficient (or extinction coefficient) with units of liter/mol-cm, b is the path length in cm, and c is the analyze concentration in moles/liter or molarities (M).

Contact information

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