



NanoDrop Micro-UV/Vis Spectrophotometers

# NanoDrop One

## User Guide

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For U.S. Technical Support, please contact:

Unity Lab Services  
Part of Thermo Fisher Scientific  
5225 Verona Road  
Madison WI 53711-4495 U.S.A.  
Telephone: 1 800 532 4752  
E-mail: [us.techsupport.analyze@thermofisher.com](mailto:us.techsupport.analyze@thermofisher.com)

For International Support, please contact:

Thermo Fisher Scientific  
Telephone: +1 608 273 5017  
E-mail: [support.madison@thermofisher.com](mailto:support.madison@thermofisher.com)

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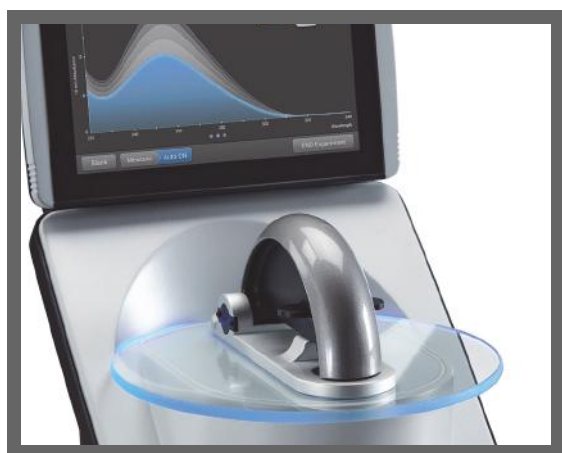
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## About the NanoDrop One Spectrophotometer



The Thermo Scientific™ NanoDrop™ One is a compact, stand-alone UV-Visible spectrophotometer developed for micro-volume analysis of purified nucleic acids and a wide variety of proteins. The patented [sample retention system](#) enables the measurement of highly concentrated samples without the need for dilutions.

The NanoDrop One system comes with preloaded software and a touchscreen display. The instrument can be connected to an optional USB label printer.

**NOTICE** Before operating a NanoDrop One instrument, please read the [safety and operating precautions](#) and then follow their recommendations when using the instrument.



### Instrument Models and Features

There are two models available for the NanoDrop One spectrophotometer...



### Optional Accessories

A number of accessories are available for the NanoDrop One instruments...



### Register Your Instrument

Register your instrument to receive e-mail updates on software and...



### Update Software

Quickly and easily download the latest NanoDrop One software...

## Instrument Models and Features

There are two models available for the NanoDrop One spectrophotometer—the NanoDrop One and the NanoDrop One<sup>C</sup>. Both models include the patented [micro-volume sample retention system](#) and general features. The NanoDrop One<sup>C</sup> model also features a cuvette holder for analyzing dilute samples using standard UV-visible cuvettes.

Both instruments come with a built-in, 7-inch Android high-resolution touchscreen preloaded with easy-to-use instrument control software. The NanoDrop One software is loaded with features to integrate with and simplify your daily workflows.



<sup>1</sup>Locate the instrument away from air vents and exhaust fans to minimize evaporation



## Touchscreen

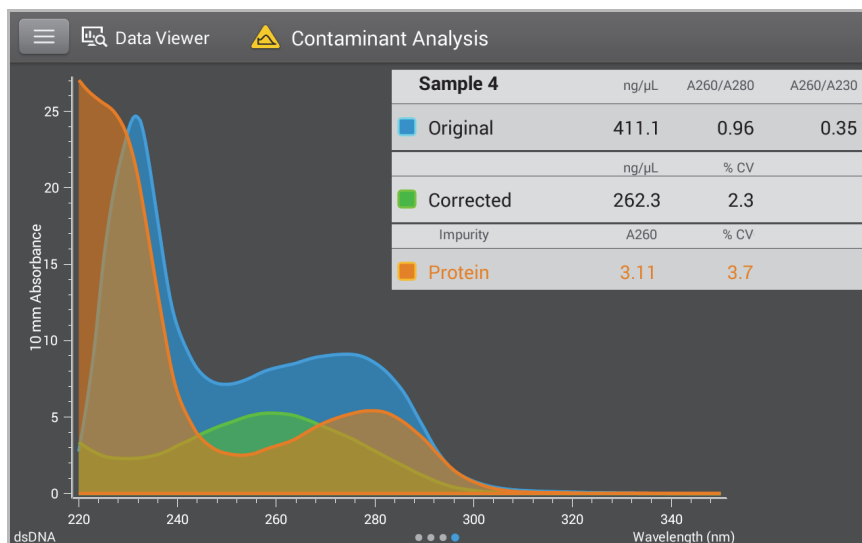


Touchscreen can slide left or right to accommodate personal preference, and tilt forward or back for optimal viewing



<sup>1</sup>Two more USB-A ports are located on instrument back panel

## NanoDrop One Software with Acclaro Sample Intelligence Technology



The Thermo Scientific™ Acclaro™ Sample Intelligence technology built into the NanoDrop One instruments provides these exclusive features to help you assess sample integrity:

- contaminant analysis to help qualify a sample before use in downstream applications
- on-demand technical support for measurements that are atypical or very low concentration
- invalid result alerts (a column sensor monitors for the presence of bubbles or reflective particles that can compromise measurement results)

## NanoDrop One<sup>C</sup> Model Additional Features



The NanoDrop One<sup>C</sup> model includes a cuvette holder for measuring dilute samples, colorimetric assays, cell cultures and kinetic studies. The cuvette system has these additional features:

- extended lower **detection limits**
- 37 °C heater option for temperature-sensitive samples and analyses
- micro-stirring option to ensure sample homogeneity and support kinetic studies

For details, see [Measure a Sample using a Cuvette](#).

## Optional Accessories

A number of accessories are available for the NanoDrop One instruments. To order an accessory, contact your local distributor or visit [our website](#).

### DYMO™ LabelWriter™ 450 USB Label Printer

Prints two 5/16-in x 4-in self-adhesive labels for transferring sample data directly into laboratory notebooks or posting on bulletin boards. The software allows [printing of data](#) from each sample measurement or from a group of samples logged and measured together.

The printer connects to the instrument (front or back) via a USB cable (included).

### PR-1 Pedestal Reconditioning Kit



Specially formulated conditioning compound that can be applied to the pedestals to restore them to a hydrophobic state (required to achieve adequate surface tension for accurate sample measurements). The kit includes conditioning compound and applicators. For more information, see [Reconditioning the Pedestals](#).

### PV-1 Performance Verification Solution

Liquid photometric standard used to check instrument performance. For more information, see [Performance Verification](#).

# Register Your Instrument



Register your instrument to receive e-mail updates on software and accessories for the NanoDrop One instruments. An Internet connection is required for registration.

### ❖ To register your instrument

1. Do one of the following:
  - From the **NanoDrop One Viewer software** running on a personal computer (PC) that is connected to the Internet, open the Help menu and choose **NanoDrop One Website**.
  - From any PC that is connected to the Internet, use any web browser to navigate to [our website](#).
2. On the website, locate NanoDrop One Registration and follow the instructions to register the instrument.

## Update Software




Quickly and easily download and install the latest NanoDrop One software and release notes from our website. Follow the steps to update or upgrade the software on your local instrument and/or install or update the NanoDrop One Viewer software on a personal computer (PC). An Internet connection is required to download software.

### To install or update NanoDrop One Viewer software

1. Do one of the following:
  - To install the Viewer software on a computer for the first time, open any web browser and find the NanoDrop website.
  - To update or upgrade the Viewer software, from the Viewer Home screen, open the Help menu and choose **NanoDrop One Website** to open our website.
2. On the NanoDrop website, locate the software downloads page.
3. Select to download NanoDrop One (PC) Viewer software (English version) and follow the instructions to download and run the installer. (A computer restart is required after the installer completes.)
4. To add a language, including software and Help systems, download and run the language pack installer (English must be installed first). (No computer restart is required after a language installer completes.)

## To update or upgrade NanoDrop One instrument software

1. Do one of the following:
  - From the **NanoDrop One Viewer software**, open the Help menu and choose **NanoDrop One Website** to open our website.
  - From any personal computer that is connected to the Internet, navigate to the NanoDrop website.
2. Insert a USB device such as a memory stick into a USB port on the computer.
3. On the NanoDrop website, locate the software downloads page, select to update or upgrade NanoDrop One operating software (English version) and follow the instructions to download the installer to the USB device.
4. To add a language, including software and Help systems, download the language pack installer(s) to the USB device.
5. Insert the USB device into any **USB port** on the NanoDrop One instrument.
6. From the instrument Home screen, tap  (Settings) > **System** > **Update Software**.

If the USB device contains more than one version of the installer, a message is displayed. Select the version to install (English installer must be run first) and tap **Update**. (An instrument restart is required after the English installer completes.)

When the installation is complete, a message similar to the following appears next to the Update Software button:

Version: 1.2.0 (currently installed version of instrument operating software)  
Database version: 1 (version of NanoDrop One database on this instrument)

7. To add a language, including software and Help systems, tap **Update Software** again, select the language and version to install and tap **Update**. (No instrument restart is required after a language installer completes.)

**Note:** To change the language, tap **Language**, select an installed language and tap **OK**. (An instrument restart is required after you change the language.)

## Applications

### Detection Limits for All Applications



**Note** Detection limits provided in the tables below are approximate and apply to micro-volume measurements only; they are based on the instrument's photometric absorbance range (10 mm equivalent) of 0–550 A. For measurements with 10 mm pathlength cuvettes, the photometric absorbance range is 0–1.5 A.

### Detection limits for standard applications

Sample Type	Lower Detection Limit	Upper Detection Limit	Typical Reproducibility <sup>a</sup>
dsDNA	2.0 ng/μL (pedestal)	27,500 ng/μL (pedestal)	±2.0 ng/μL for sample concentrations between 2.0 and 100 ng/μL samples; ±2% for samples >100 ng/μL
	0.20 ng/μL (cuvette)	75 ng/μL (cuvette)	
ssDNA	1.3 ng/μL (pedestal)	18,150 ng/μL (pedestal)	±2.0 ng/μL for sample concentrations between 2.0 and 100 ng/μL samples; ±2% for samples >100 ng/μL
	0.13 ng/μL (cuvette)	49.5 ng/μL (cuvette)	
RNA	1.6 ng/μL (pedestal)	22,000 ng/μL (pedestal)	±2.0 ng/μL for sample concentrations between 2.0 and 100 ng/μL samples; ±2% for samples >100 ng/μL
	0.16 ng/μL (cuvette)	60 ng/μL (cuvette)	

## 2 Applications

Detection Limits for All Applications

Sample Type	Lower Detection Limit	Upper Detection Limit	Typical Reproducibility <sup>a</sup>
DNA Microarray (ssDNA)	1.3 ng/μL (pedestal)	495 ng/μL (pedestal)	±2.0 ng/μL for sample concentrations between 2.0 and 100 ng/μL samples; ±2% for samples >100 ng/μL
	0.13 ng/μL (cuvette)	49.5 ng/μL (cuvette)	
Purified BSA by Protein A280	0.06 mg/mL (pedestal)	825 mg/mL (pedestal)	±0.10 mg/mL (for 0.10–10 mg/mL samples); ±2% for samples >10 mg/mL
	0.006 mg/mL (cuvette)		
IgG by Protein A280	0.03 mg/mL (pedestal)	402 mg/mL (pedestal)	
	0.003 mg/mL (cuvette)		
Purified BSA by Proteins & Labels	0.06 mg/mL (pedestal)	19 mg/mL (pedestal)	±0.10 mg/mL for 0.10–10 mg/mL samples
	0.006 mg/mL (cuvette)		
Protein BCA	0.2 mg/mL (20:1 reagent/sample volume)	8.0 mg/mL (pedestal)	2% over entire range
	0.01 mg/mL (1:1 reagent/sample volume)	0.20 mg/mL (cuvette)	0.01 mg/mL over entire range
Protein Lowry	0.2 mg/mL (pedestal)	4.0 mg/mL (pedestal)	2% over entire range
Protein Bradford	100 μg/mL (50:1 reagent/sample volume)	8000 μg/mL	±25 μg/mL for 100–500 μg/mL samples ±5% for 500–8000 μg/mL samples
	15 μg/mL (1:1 reagent/sample volume)	100 μg/μL	±4 μg/mL for 15–50 μg/mL samples ±5% for 50–125 μg/mL samples
Protein Pierce 660	50 μg/mL (15:1 reagent/sample volume)	2000 μg/mL	±3 μg/mL for 50–125 μg/mL samples ±2% for samples > 125 μg/mL
	25 μg/mL (7.5:1 reagent/sample volume)	1000 μg/mL	±3 μg/mL for 25–125 μg/mL samples ±2% for samples >125 μg/mL

<sup>a</sup> Based on five replicates (SD=ng/μL; CV=%)

**Note** To minimize instrument error with highly concentrated samples, make dilutions to ensure that measurements are made within these absorbance limits:

- For micro-volume measurements, maximum absorbance at 260 nm (for nucleic acids) or 280 nm (for proteins) should be less than 62.5 A.
- For measurements with 10 mm pathlength cuvettes, maximum absorbance at 260 nm (or 280 nm for proteins) should be less than 1.5 A, which is approximately 75 ng/μL dsDNA.



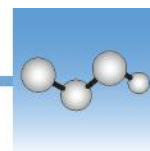
## Detection limits for pre-defined dyes

Sample Type	Lower Detection Limit	Upper Detection Limit <sup>a</sup>	Typical Reproducibility <sup>b</sup>
Cy3, Cy3.5, Alexa Fluor 555, Alexa Fluor 660	0.2 pmol/μL (pedestal)	100 pmol/μL (pedestal)	±0.20 pmol/μL for sample concentrations between 0.20 and 4.0 pmol/μL; ±2% for samples >4.0 pmol/μL
Cy5, Cy5.5, Alexa Fluor 647	0.12 pmol/μL (pedestal)	60 pmol/μL (pedestal)	±0.12 pmol/μL for sample concentrations between 0.12 and 2.4 pmol/μL; ±2% for samples >2.4 pmol/μL
Alexa Fluor 488, Alexa Fluor 594	0.4 pmol/μL (pedestal)	215 pmol/μL (pedestal)	±0.40 pmol/μL for sample concentrations between 0.40 and 8.0 pmol/μL; ±2% for samples >8.0 pmol/μL
Alexa Fluor 546	0.3 pmol/μL (pedestal)	145 pmol/μL (pedestal)	±0.30 pmol/μL for sample concentrations between 0.30 and 6.0 pmol/μL; ±2% for samples >6.0 pmol/μL

<sup>a</sup> Values are approximate

<sup>b</sup> Based on five replicates (SD=ng/μL; CV=%)





## Measure dsDNA, ssDNA or RNA

Measures the concentration of purified dsDNA, ssDNA or RNA samples that absorb at 260 nm.

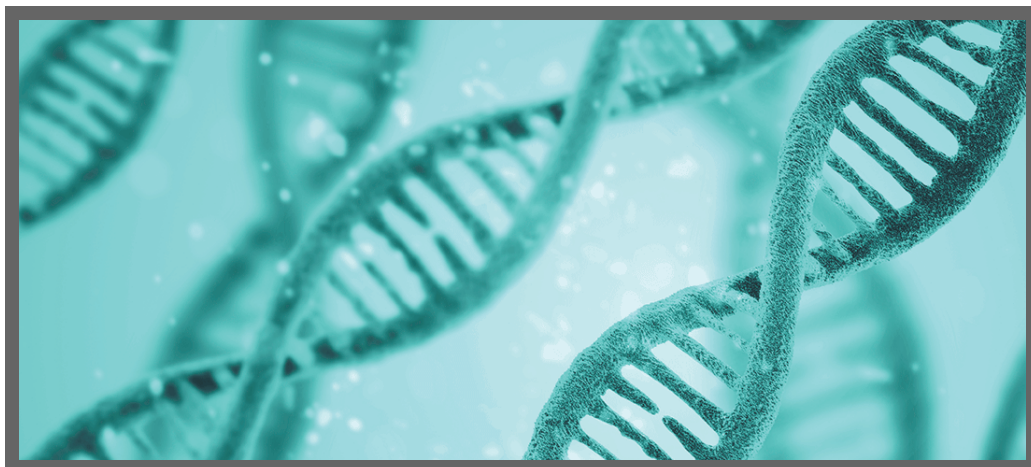
[Measure dsDNA, ssDNA or RNA](#)

[Reported Results](#)

[Settings](#)

[Detection Limits](#)

[Calculations](#)



## Measure dsDNA, ssDNA or RNA

Use the dsDNA, ssDNA and RNA applications to quantify purified double-stranded (ds) or single-stranded (ss) DNA or RNA samples. These applications report nucleic acid concentration and two absorbance ratios ( $A_{260}/A_{280}$  and  $A_{260}/A_{230}$ ). A single-point baseline correction can also be used.

## To measure dsDNA, ssDNA or RNA samples

### NOTICE

- Do not use a squirt or spray bottle on or near the instrument as liquids will flow into the instrument and may cause permanent damage.
- Do not use hydrofluoric acid (HF) on the pedestals. Fluoride ions will permanently damage the quartz fiber optic cables.

**Before you begin...**

Before taking pedestal measurements with the NanoDrop One instrument, lift the instrument arm and clean the upper and lower pedestals. At a minimum, wipe the pedestals with a new laboratory wipe. For more information, see [Cleaning the Pedestals](#).

❖ **To measure nucleic acid**

1. From the Home screen, select the **Nucleic Acids** tab and tap **dsDNA, ssDNA or RNA**, depending on the samples to be measured.
2. Specify a [baseline correction](#) if desired.
3. Pipette 1–2 µL blanking solution onto the lower pedestal and lower the arm, or insert the blanking cuvette into the cuvette holder.

**Tip:** If using a cuvette, make sure to [align the cuvette light path](#) with the instrument light path.

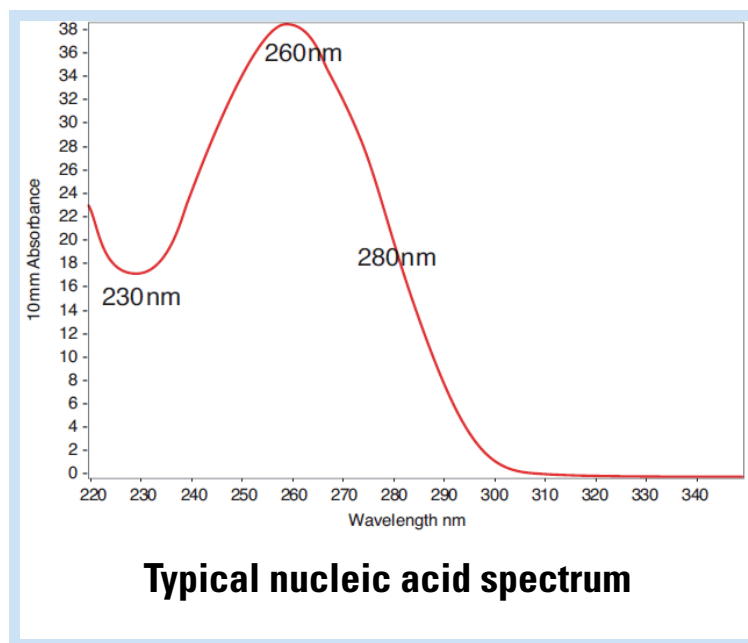
4. Tap **Blank** and wait for the measurement to complete.

**Tip:** If [Auto-Blank](#) is On, the blank measurement starts automatically after you lower the arm. (This option is not available for cuvette measurements.)

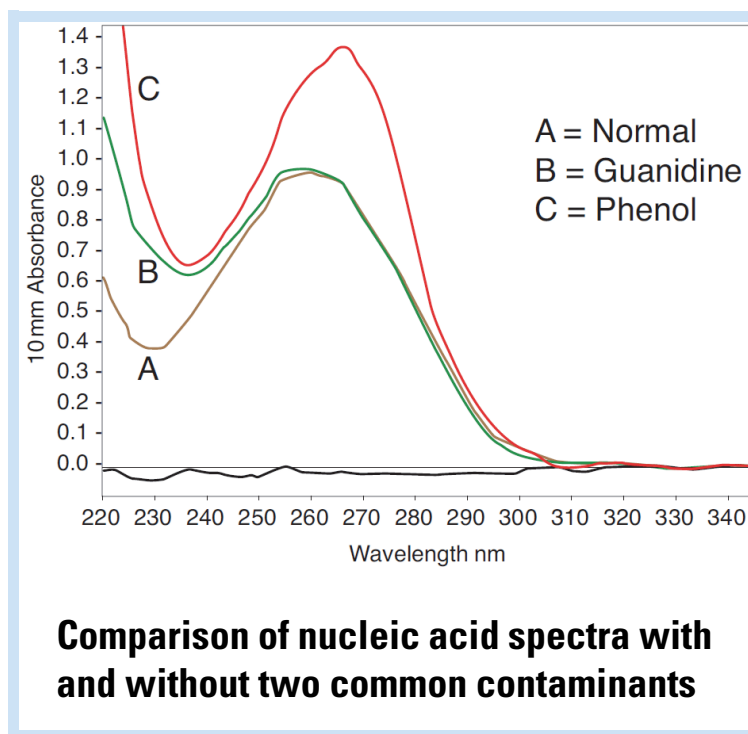
5. Lift the arm and clean both pedestals with a new laboratory wipe, or remove the blanking cuvette.
6. Pipette 1-2 µL sample solution onto the pedestal and lower the arm, or insert the sample cuvette into the cuvette holder.
7. Start the sample measurement:
  - Pedestal: If [Auto-Measure](#) is On, lower arm; if [Auto-Measure](#) is off, lower arm and tap **Measure**.
  - Cuvette: Tap **Measure**.

When the sample measurement is completed, the spectrum and reported values are displayed (see the next section).

8. When you are finished measuring samples, tap **End Experiment**.
9. Lift the arm and clean both pedestals with a new wipe, or remove the sample cuvette.



**Typical nucleic acid spectrum**



**Comparison of nucleic acid spectra with and without two common contaminants**

## Best practices for nucleic acid measurements

- Isolate and purify nucleic acid samples before measurement to remove impurities. Depending on the sample, impurities could include DNA, RNA, free nucleotides, proteins, some buffer components and dyes. See [Preparing Samples](#) for more information.

**Note** Extraction reagents such as guanidine, phenol, and EDTA contribute absorbance between 230 nm and 280 nm and will affect measurement results if present in samples (even residual amounts).

- Ensure the sample absorbance is within the instrument's [absorbance detection limits](#).
- Blank with the same buffer solution used to resuspend the analyte of interest. The blanking solution should be a similar pH and ionic strength as the analyte solution.
- Run a [blanking cycle](#) to assess the absorbance contribution of your buffer solution. If the buffer exhibits strong absorbance at or near the analysis wavelength (typically 260 nm), you may need to choose a different buffer or application. See [Choosing and Measuring a Blank](#) for more information.
- For micro-volume measurements:
  - Ensure pedestal surfaces are properly [cleaned](#) and [conditioned](#).
  - If possible, heat highly concentrated or large molecule samples, such as genomic or lambda DNA, to 63 °C (145 °F) and gently (but thoroughly) vortex before taking a measurement. Avoid introducing bubbles when mixing and pipetting.
  - Follow [best practices for micro-volume measurements](#).
  - Use a 1-2 µL sample volume. See [Recommended Sample Volumes](#) for more information.
- For cuvette measurements (NanoDrop One<sup>C</sup> instruments only), use compatible cuvettes and follow [best practices for cuvette measurements](#).

### Related Topics

- [Measure a Micro-Volume Sample](#)
- [Measure a Sample Using a Cuvette](#)
- [Best Practices for Micro-Volume Measurements](#)
- [Best Practices for Cuvette Measurements](#)
- [Prepare Samples and Blanks](#)
- [Basic Instrument Operations](#)

## Nucleic Acid Reported Results

### dsDNA measurement screen

For each measured sample, the dsDNA, ssDNA and RNA applications show the UV absorbance spectrum and a summary of the results. Here is an example:

The screenshot shows the NanoDrop One dsDNA measurement screen. On the left is a UV spectrum plot with '10mm Absorbance' on the y-axis (0 to 4) and 'Wavelength(nm)' on the x-axis (220 to 340). A blue curve shows a peak at approximately 260 nm. At the top, there is a menu icon, a sample name 'Sample 3', and 'Load #3'. A table of results is displayed on the right, with a blue highlight on the second row. At the bottom are buttons for 'Blank', 'Measure', 'OFF', and 'End Experiment'. An orange arrow points from the 'Tap row to select sample and update spectrum...' instruction to the table's expand/collapse icon.

#	ng/μL	A260/A280	A260/A230
1	220.4	1.82	2.38
2	219.5	1.82	2.38

**Annotations:**

- Menu of options; tap to open**: Points to the top-left menu icon.
- Sample name; tap to edit**: Points to the 'Sample 3' text.
- Nucleic acid concentration**: Points to the 'ng/μL' column header.
- Tap to select unit**: Points to the unit dropdown arrow.
- Purity ratios**: Points to the 'A260/A280' and 'A260/A230' column headers.
- Tap row to select sample and update spectrum; tap more rows to overlay up to five spectra. Press and hold sample row to view measurement details.**: Points to the table rows.
- Drag tab down/up to see more/less sample data**: Points to the expand/collapse icon at the bottom of the table.
- UV spectrum**: Points to the absorbance curve.
- Pinch and zoom to adjust axes; double-tap to reset**: Points to the zoom icon in the top-left corner of the plot.
- Swipe screen left to view table with more measurement results**: Points to the 'OFF' button.
- Tap to end experiment and export data**: Points to the 'End Experiment' button.

**Note** Micro-volume absorbance measurements and measurements taken with nonstandard cuvettes are normalized to a 10.0 mm pathlength equivalent.

## dsDNA, ssDNA and RNA reported values

The initial screen that appears after each measurement (see previous image) shows a summary of the reported values. To view all reported values, press and hold the sample row. Here is an example:


- sample details (application and sampling method used, i.e., pedestal or cuvette)
- [sample name](#)
- created on (date sample measurement was taken)
- [nucleic acid concentration](#)
- [A260/A280](#)
- [A260/A230](#)
- [A260](#)
- [A280](#)
- [factor](#)
- [baseline correction](#)

### Related Topics

- [Basic Instrument Operations](#)
- [Nucleic Acid Calculations](#)

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## Setting for Nucleic Acid Measurements

To show the dsDNA, ssDNA or RNA settings, from the dsDNA, ssDNA or RNA measurement screen, tap  > **Nucleic Acid Setup**.

Setting	Available Options	Description
Baseline Correction	On or off  Enter baseline correction wavelength in nm or use default value (340 nm)	<b>Optional user-defined baseline correction.</b> Can be used to correct for any offset caused by light scattering particulates by subtracting measured absorbance at specified baseline correction wavelength from absorbance values at all wavelengths in sample spectrum. As a result, absorbance of sample spectrum is zero at specified baseline correction wavelength.

### Related Topics

- [Instrument Settings](#)

## Calculations for Nucleic Acid Measurements

The nucleic acid applications use the [Beer-Lambert equation](#) to correlate absorbance with concentration. Solving Beer's law for concentration yields the equation at the right.

### Beer-Lambert Equation (solved for concentration)

$$c = A / (\epsilon * b)$$

where:

**A** = UV absorbance in absorbance units (AU)

**ε** = wavelength-dependent molar absorptivity coefficient (or extinction coefficient) in liter/mol-cm

**b** = pathlength in cm

**c** = analyte concentration in moles/liter or molarity (M)

**Note:** Dividing the measured absorbance of a sample solution by its molar extinction coefficient yields the molar concentration of the sample. See [Published Extinction Coefficients](#) for more information regarding molar vs. mass concentration values.



The Nucleic Acid applications use a modification of the Beer-Lambert equation (shown at right) to calculate sample concentration where the extinction coefficient and pathlength are combined and referred to as a "factor."

For the dsDNA, ssDNA and RNA applications, the generally accepted factors for nucleic acids are used in conjunction with Beer's Law to calculate sample concentration. For the Custom Factor application, the user-specified factor is used.

### Extinction Coefficients vs Factors

Using the terms in the Beer-Lambert equation, factor (f) is defined as:

$$\mathbf{factor\ (f) = 1/(\epsilon * b)}$$

where:

$\epsilon$  = wavelength-dependent molar extinction coefficient in ng-cm/ $\mu$ L

**b** = **sample pathlength** in cm

As a result, analyte concentration (c) is calculated as:

$$\mathbf{c = A * [1/(\epsilon * b)]}$$

or

$$\mathbf{c = A * f}$$

where:

**c** = analyte concentration in ng/ $\mu$ L

**A** = absorbance in absorbance units (A)

**f** = factor in ng-cm/ $\mu$ L (see below)

### Factors Used

- **dsDNA** (factor = 50 ng-cm/ $\mu$ L)
- **ssDNA** (factor = 33 ng-cm/ $\mu$ L)
- **RNA** (factor = 40 ng-cm/ $\mu$ L)
- **Custom Factor** (user entered factor between 15 ng-cm/ $\mu$ L and 150 ng-cm/ $\mu$ L)

Calculated nucleic acid concentrations are based on the absorbance value at 260 nm, the factor used and the sample pathlength. A single-point baseline correction (or analysis correction) may also be applied.

Concentration is reported in mass units. Calculators are available on the Internet to convert concentration from mass to molar units based on sample sequence.

Absorbance values at 260 nm, 280 nm and sometimes 230 nm are used to calculate purity ratios for the measured nucleic acid samples. Purity ratios are sensitive to the presence of contaminants in the sample, such as residual solvents and reagents typically used during sample purification.

## Measured Values

**Note:** For micro-volume absorbance measurements and measurements taken with nonstandard (other than 10 mm) cuvettes, the spectra are normalized to a 10 mm pathlength equivalent.

### A260 absorbance

- Nucleic acid absorbance values are measured at 260 nm using the normalized spectrum. This is the reported A260 value if Baseline Correction is not selected.
- If [Baseline Correction](#) is selected, the absorbance value at the correction wavelength is subtracted from the absorbance at 260 nm. The corrected absorbance at 260 nm is reported and used to calculate nucleic acid concentration.

### A230 and A280 absorbance

- Normalized and baseline-corrected (if selected) absorbance values at 230 nm and 280 nm are used to calculate A260/A230 and A260/A280 ratios.

### Sample Pathlength

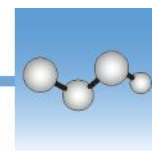
- For micro-volume measurements, the software selects the optimal pathlength (between 1.0 mm and 0.03 mm) based on sample absorbance at the analysis wavelength.
- For cuvette measurements, pathlength is determined by the cuvette Pathlength setting in the software (see [General Settings](#)).
- Displayed spectra and absorbance values are normalized to a 10 mm pathlength equivalent.

### Reported Values

- **Nucleic acid concentration.** Reported in selected unit (i.e., ng/ $\mu$ L,  $\mu$ g/ $\mu$ L or  $\mu$ g/mL). Calculations are based on modified Beer's Law equation using corrected nucleic acid absorbance value.
- **A260/A280 purity ratio.** Ratio of corrected absorbance at 260 nm to corrected absorbance at 280 nm. An A260/A280 purity ratio of  $\sim$ 1.8 is generally accepted as "pure" for DNA ( $\sim$ 2.0 for RNA). Acidic solutions may under represent the reported value by 0.2-0.3; the opposite is true for basic solutions.
- **A260/A230 purity ratio.** Ratio of corrected absorbance at 260 nm to corrected absorbance at 230 nm. An A260/A230 purity ratio between 1.8 and 2.2 is generally accepted as "pure" for DNA and RNA.

**Note:** Although purity ratios are important indicators of sample quality, the best quality indicator quality is functionality in the downstream application of interest (e.g., real-time PCR).





## Measure Microarray

Measures the concentration of purified nucleic acids that have been labeled with up to two fluorescent dyes for use in downstream microarray applications.

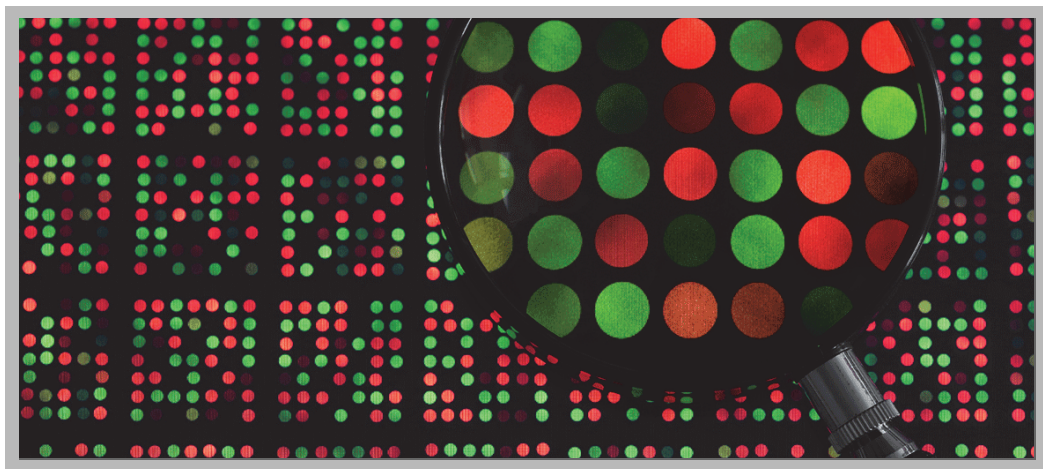
[Measure Microarray Samples](#)

[Reported Results](#)

[Settings](#)

[Detection Limits](#)

[Calculations](#)



## Measure Microarray Samples

Use the Microarray application to quantify nucleic acids that have been labeled with up to two fluorescent dyes. The application reports nucleic acid concentration, an A260/A280 ratio and the concentrations and measured absorbance values of the dye(s), allowing detection of dye concentrations as low as 0.2 picomole per microliter.

### To measure microarray samples

#### NOTICE

- Do not use a squirt or spray bottle on or near the instrument as liquids will flow into the instrument and may cause permanent damage.
- Do not use hydrofluoric acid (HF) on the pedestals. Fluoride ions will permanently damage the quartz fiber optic cables.

**Before you begin...**

Before taking pedestal measurements with the NanoDrop One instrument, lift the instrument arm and clean the upper and lower pedestals. At a minimum, wipe the pedestals with a new laboratory wipe. For more information, see [Cleaning the Pedestals](#).

❖ **To measure a microarray sample**

1. From the Home screen, select the **Nucleic Acids** tab and tap **Microarray**.
2. Specify the **sample type and factor** and the **type of dye(s)** used.

**Tip:** Select a dye from the pre-defined list or add a custom dye using the **Dye/Chromophore Editor**.

3. Pipette 1–2  $\mu\text{L}$  blanking solution onto the lower pedestal and lower the arm, or insert the blanking cuvette into the cuvette holder.

**Tip:** If using a cuvette, make sure to **align the cuvette light path** with the instrument light path.

4. Tap **Blank** and wait for the measurement to complete.

**Tip:** If **Auto-Blank** is On, the blank measurement starts automatically after you lower the arm. (This option is not available for cuvette measurements.)

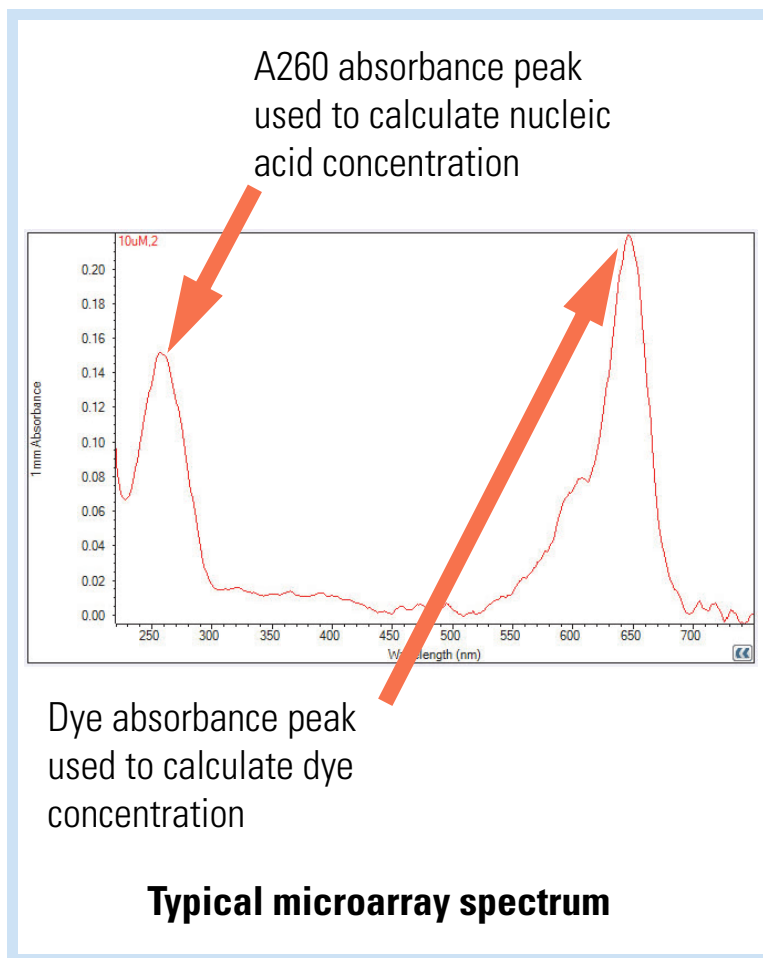
5. Lift the arm and clean both pedestals with a new laboratory wipe, or remove the blanking cuvette.
6. Pipette 1-2  $\mu\text{L}$  sample solution onto the pedestal and lower the arm, or insert the sample cuvette into the cuvette holder.

7. Start the sample measurement:


- Pedestal: If **Auto-Measure** is On, lower arm; if Auto-Measure is off, lower arm and tap **Measure**.
- Cuvette: Tap **Measure**.

When the sample measurement is completed, the spectrum and reported values are displayed (see the next section).

8. When you are finished measuring samples, tap **End Experiment**.
9. Lift the arm and clean both pedestals with a new wipe, or remove the sample cuvette.



### **Related Topics**

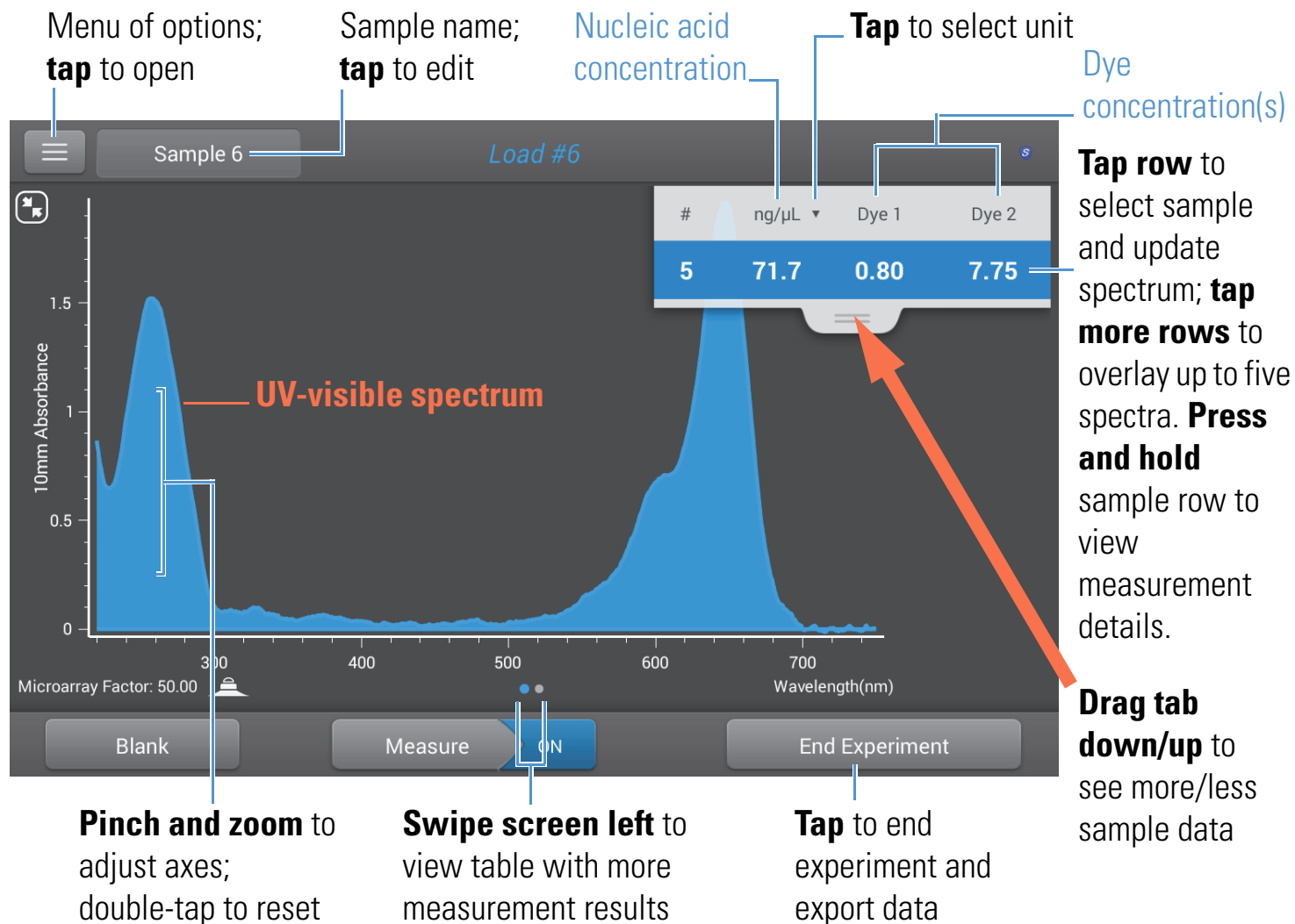
- [Best Practices for Nucleic Acid Measurements](#)
  - [Measure a Micro-Volume Sample](#)
  - [Measure a Sample Using a Cuvette](#)
  - [Best Practices for Micro-Volume Measurements](#)
  - [Best Practices for Cuvette Measurements](#)
  - [Prepare Samples and Blanks](#)
  - [Basic Instrument Operations](#)
- 



## Microarray Reported Results

### Microarray measurement screen

For each measured sample, this application shows the absorbance spectrum and a summary of the results. Here is an example:



#### Note

- A baseline correction is performed at 750 nm (absorbance value at 750 nm is subtracted from absorbance values at all wavelengths in sample spectrum).
- Micro-volume absorbance measurements and measurements taken with nonstandard cuvettes are normalized to a 10.0 mm pathlength equivalent.

## Microarray reported values

The initial screen that appears after each measurement (see previous image) shows a summary of the reported values. To view all reported values, press and hold the sample row. Here is an example:

- sample details (application used and pedestal or cuvette)
- [sample name](#)
- created on (date sample measurement was taken)
- [nucleic acid concentration](#)
- [A260](#)
- [A260/A280](#)
- [dye 1/dye 2 concentration](#)
- [sample type](#)
- [analysis correction](#)
- [factor](#)


### Related Topics

- [Basic Instrument Operations](#)
- [Microarray Calculations](#)

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## Settings for Microarray Measurements

### Microarray settings

The Microarray Setup screen appears after you select the Microarray application from the Nucleic Acids tab on the Home screen. To show the Microarray settings from the Microarray measurement screen, tap  > **Microarray Setup**.

Setting	Available Options	Description
Sample type and Factor	dsDNA (with non-editable factor of 50 ng-cm/ $\mu$ L)	Widely accepted value for double-stranded DNA
	ssDNA (with non-editable factor of 33 ng-cm/ $\mu$ L)	Widely accepted value for single-stranded DNA
	RNA (with non-editable factor of 40 ng-cm/ $\mu$ L)	Widely accepted value for RNA
	Oligo DNA with non-editable calculated factor in ng-cm/ $\mu$ L	Factor calculated from user-defined DNA base sequence. When selected, available DNA base units (i.e., G, A, T, C) appear as keys. Define sequence by tapping appropriate keys. Factor is calculated automatically based on widely accepted value for each base unit.
	Oligo RNA with non-editable calculated factor in ng-cm/ $\mu$ L	Factor calculated from user-defined RNA base sequence. When selected, available RNA base units (i.e., G, A, U, C) appear as keys. Define sequence by tapping appropriate keys. Factor is calculated automatically based on widely accepted value for each base unit.
	Custom (with user-specified factor in ng-cm/ $\mu$ L)	Enter <b>factor</b> between 15 ng-cm/ $\mu$ L and 150 ng-cm/ $\mu$ L
Dye 1/Dye 2 Type <sup>a</sup>	Cy3, 5, 3.5, or 5.5, Alexa Fluor 488, 546, 555, 594, 647, or 660	Select pre-defined dye(s) used to label sample material, or one that has been added using Dye/Chrom. Editor.
Dye 1/Dye 2 Unit	picomoles/microliter (pmol/ $\mu$ L), micromoles (uM), or millimoles (mM)	Select unit for reporting dye concentrations
Analysis Correction <sup>b</sup>	On or off	Corrects sample absorbance measurement for any offset caused by light scattering particulates by subtracting absorbance value at specified analysis correction wavelength from absorbance value at analysis wavelength. Corrected value is used to calculate sample concentration.  <b>Tip:</b> If the sample has a modification that absorbs light at 340 nm, select a different correction wavelength or turn off Analysis Correction.
	Enter analysis correction wavelength in nm or use default value (340 nm)	




<sup>a</sup> To add a custom dye or edit the list of available dyes, use the Dye/Chromophore Editor.

<sup>b</sup> The Analysis Correction affects the calculation for nucleic acid concentration only.

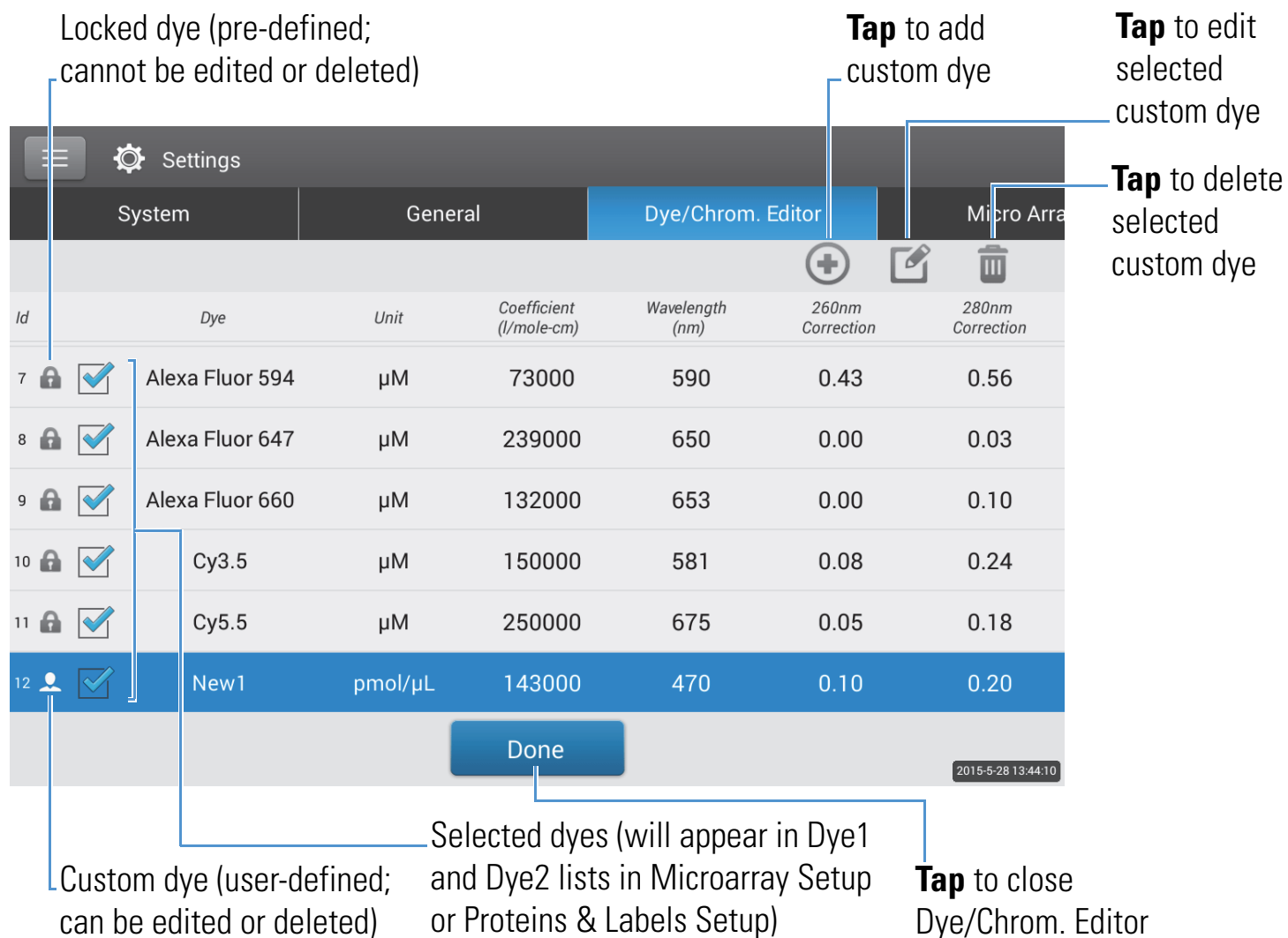
## Dye/chromophore editor

Use the Dye/Chromophore Editor to add a custom dye to the list of available dyes in [Microarray Setup](#) or [Proteins & Labels Setup](#). You can also specify which dyes are available in that list.

To access the Dye/Chromophore Editor:

- from the Home screen, tap  > **Dye/Chrom. Editor**
- from the Microarray or Proteins & Labels measurement screen, tap  >  **Settings** > **Dye/Chrom. Editor**

### Dye/Chromophore Editor



Locked dye (pre-defined; cannot be edited or deleted)

Tap to add custom dye

Tap to edit selected custom dye

Tap to delete selected custom dye

Id	Dye	Unit	Coefficient (l/mole-cm)	Wavelength (nm)	260nm Correction	280nm Correction
7	Alexa Fluor 594	µM	73000	590	0.43	0.56
8	Alexa Fluor 647	µM	239000	650	0.00	0.03
9	Alexa Fluor 660	µM	132000	653	0.00	0.10
10	Cy3.5	µM	150000	581	0.08	0.24
11	Cy5.5	µM	250000	675	0.05	0.18
12	New1	pmol/µL	143000	470	0.10	0.20

Selected dyes (will appear in Dye1 and Dye2 lists in Microarray Setup or Proteins & Labels Setup)

Custom dye (user-defined; can be edited or deleted)


Tap to close Dye/Chrom. Editor

These operations are available from the Dye/Chromophore Editor:


### Add or remove a dye

To add or remove a dye from the Dye1 or Dye2 drop-down list in [Microarray Setup](#) or [Proteins & Labels Setup](#):

- select or deselect corresponding checkbox

2		<input checked="" type="checkbox"/>	Cy3	μM	150000	550	0.04
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### Add custom dye

- tap  to show New Dye box
- enter unique **Name** for new dye (tap field to display keyboard, tap **Done** key to close keyboard)
- select default **Unit** that will be used to display dye concentration
- enter dye's **Extinction Coefficient** (or molar absorptivity constant) in L/mole-cm (typically provided by dye manufacturer)
- specify **Wavelength** in nm (between 450 nm and 700 nm) that will be used to measure dye's absorbance
- specify dye's correction values at 260 nm and 280 nm
- tap **Add Dye**


**Note** To determine dye correction values (if not available from dye manufacturer):

- use instrument to measure pure dye and note absorbance at 260 nm, 280 nm and at analysis wavelength for dye (see above)
- calculate ratio of  $A_{260}/A_{\text{dye wavelength}}$  and enter that value for 260 nm Correction
- calculate ratio of  $A_{280}/A_{\text{dye wavelength}}$  and enter that value for 280 nm Correction

When a custom dye is selected before a measurement, the dye's absorbance and concentration values are reported and the corrections are applied to the measured sample absorbance values, and to the resulting sample concentrations and purity ratios.

### Edit custom dye


**Tip** Dyes pre-defined in the software cannot be edited.

- tap to select custom dye
- tap 

- edit any entries or settings
- tap **Save Dye**

### Delete custom dye

**Tip** Dyes pre-defined in the software cannot be deleted.

- tap to select custom dye
- tap 

**NOTICE** Deleting a custom dye permanently removes the dye and all associated information from the software.

### Related Topics

- [Instrument Settings](#)

## Calculations for Microarray Measurements

As with the other nucleic acid applications, the Microarray application uses a [modification of the Beer-Lambert equation](#) to calculate sample concentration where the extinction coefficient and pathlength are combined and referred to as a “factor.” The Microarray application offers six options (shown at right) for selecting an appropriate factor for each measured sample, to be used in conjunction with Beer’s Law to calculate sample concentration.

If the factor is known, choose the Custom Factor option and enter the factor in ng-cm/μL. Otherwise, choose the option that best matches the sample solution.

**Tip:** Ideally, the factor or extinction coefficient should be determined empirically using a solution of the study nucleic acid at a known concentration using the same buffer.

### Available Options for Factors

- **dsDNA** (factor = 50 ng-cm/μL)
- **ssDNA** (factor = 33 ng-cm/μL)
- **RNA** (factor = 40 ng-cm/μL)
- **Oligo DNA** (calculated from user entered DNA nucleotide sequence)
- **Oligo RNA** (calculated from user entered RNA nucleotide sequence)
- **Custom Factor** (user entered factor between 15 ng-cm/μL and 150 ng-cm/μL)

**Note:** See [Sample Type](#) for more information.

Calculated nucleic acid concentrations are based on the absorbance value at 260 nm, the factor used and the sample pathlength. A single-point baseline correction (or analysis correction) may also be applied.

Concentration is reported in mass units. Calculators are available on the Internet to convert concentration from mass to molar units based on sample sequence.

Absorbance values at 260 nm, 280 nm and sometimes 230 nm are used to calculate purity ratios for the measured nucleic acid samples. Purity ratios are sensitive to the presence of contaminants in the sample, such as residual solvents and reagents typically used during sample purification.

Dye concentrations are calculated from the absorbance value at the dye's analysis wavelength, the dye's extinction coefficient, and the sample pathlength. A sloped-line dye correction may also be used.

## Measured Values

### A260 absorbance

**Note:** The absorbance value at 750 nm is subtracted from all wavelengths in the spectrum. As a result, the absorbance at 750 nm is zero in the displayed spectra. Also, for micro-volume absorbance measurements and measurements taken with nonstandard (other than 10 mm) cuvettes, the spectra are normalized to a 10 mm pathlength equivalent.

- Nucleic acid absorbance values for all Microarray [sample types](#) are measured at 260 nm using the 750-corrected and normalized spectrum.
- If [Analysis Correction](#) is selected, the absorbance value at the correction wavelength is subtracted from the absorbance at 260 nm.
- If one or more dyes are selected, the [dye correction values](#) at 260 nm are also subtracted from the absorbance at 260 nm.
- The final corrected absorbance at 260 nm is reported and used to calculate sample concentration.

### A280 absorbance

- 750-corrected and normalized absorbance value at 280 nm (minus the A280 dye correction) is used to calculate an A260/A280 ratio.

### Dye absorbance

- Dye absorbance values are measured at specific wavelengths. See [Dye/Chromophore Editor](#) for analysis wavelengths used.
- If Sloping Dye Correction is selected, a linear baseline is drawn between 400 nm and 750 nm and, for each dye, the absorbance value of the sloping baseline is subtracted from the absorbance value at each dye's analysis wavelength. Baseline-corrected dye absorbance values are reported and used to calculate dye concentrations.

### Dye correction

- Pre-defined dyes have known correction values for A260 and A280. See [Dye/Chromophore Editor](#) for correction values used.
- A260 dye corrections are subtracted from the [A260 absorbance value](#) used to calculate nucleic acid concentration, and from the A260 absorbance value used to calculate the [A260/A280 purity ratio](#).

### Sample Pathlength

- For micro-volume measurements, the software selects the optimal pathlength (between 1.0 mm and 0.03 mm) based on sample absorbance at the analysis wavelength.
- For cuvette measurements, pathlength is determined by the cuvette Pathlength setting in the software (see [General Settings](#)).
- Displayed spectra and absorbance values are normalized to a 10 mm pathlength equivalent.
- 

### Reported Values

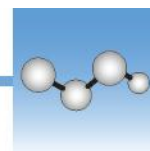
- **Nucleic acid concentration.** Reported in selected unit (i.e., ng/ $\mu$ L,  $\mu$ g/ $\mu$ L or  $\mu$ g/mL). Calculations are based on modified Beer's Law equation using corrected nucleic acid absorbance value.
- **A260/A280 purity ratio.** Ratio of corrected absorbance at 260 nm to corrected absorbance at 280 nm. An A260/A280 purity ratio of  $\sim$ 1.8 is generally accepted as "pure" for DNA ( $\sim$ 2.0 for RNA). Acidic solutions may under represent the reported value by 0.2-0.3; the opposite is true for basic solutions.
- **Dye1/Dye2 concentration.** Reported in pmol/ $\mu$ L. Calculations are based on Beer's Law equation using (sloping) baseline-corrected dye absorbance value(s).

**Note:** Although purity ratios are important indicators of sample quality, the best indicator of DNA or RNA quality is functionality in the downstream application of interest (e.g., microarray).

### Related Topics

- [Calculations for Nucleic Acid Measurements](#)





## Measure using a Custom Factor

Measures the concentration of purified nucleic acids using a custom factor for the calculations.

[Measure using Custom Factor](#)

[Reported Results](#)

[Settings](#)

[Detection Limits](#)

[Calculations](#)



## Measure Nucleic Acid using a Custom Factor

Use the Custom Factor application to quantify purified DNA or RNA samples that absorb at 260 nm with a user-defined extinction coefficient or factor. The application reports nucleic acid concentration and two absorbance ratios ( $A_{260}/A_{280}$  and  $A_{260}/A_{230}$ ). A single-point baseline correction can also be used.

### To measure nucleic acid samples using a custom factor

#### NOTICE

- Do not use a squirt or spray bottle on or near the instrument as liquids will flow into the instrument and may cause permanent damage.
- Do not use hydrofluoric acid (HF) on the pedestals. Fluoride ions will permanently damage the quartz fiber optic cables.

### Before you begin...

Before taking pedestal measurements with the NanoDrop One instrument, lift the instrument arm and clean the upper and lower pedestals. At a minimum, wipe the pedestals with a new laboratory wipe. For more information, see [Cleaning the Pedestals](#).

#### ❖ To measure using a custom factor

1. From the Home screen, select the **Nucleic Acids** tab and tap **Custom Factor**.
2. Enter the **factor** to be used for the calculations and specify a **baseline correction** if desired.
3. Pipette 1–2  $\mu\text{L}$  blanking solution onto the lower pedestal and lower the arm, or insert the blanking cuvette into the cuvette holder.

**Tip:** If using a cuvette, make sure to [align the cuvette light path](#) with the instrument light path.

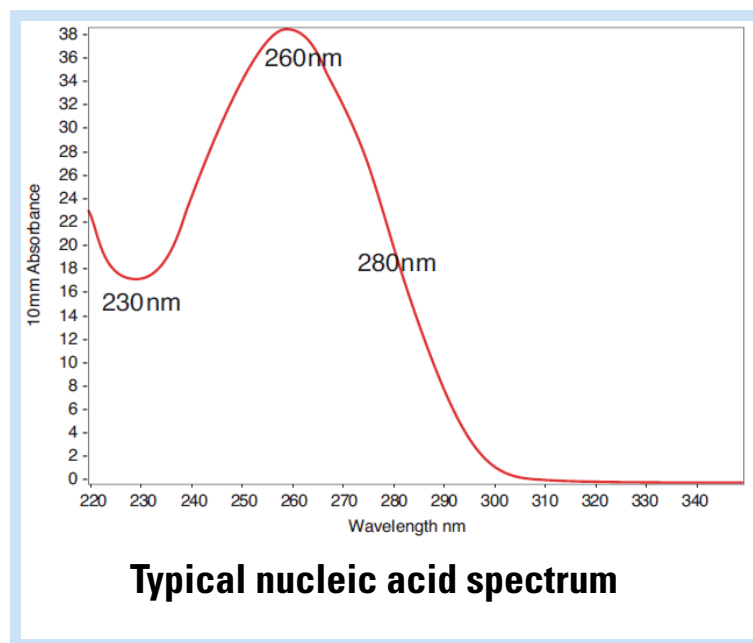
4. Tap **Blank** and wait for the measurement to complete.

**Tip:** If **Auto-Blank** is On, the blank measurement starts automatically after you lower the arm. (This option is not available for cuvette measurements.)

5. Lift the arm and clean both pedestals with a new laboratory wipe, or remove the blanking cuvette.
6. Pipette 1-2  $\mu\text{L}$  sample solution onto the pedestal and lower the arm, or insert the sample cuvette into the cuvette holder.
7. Start the sample measurement:
  - Pedestal: If **Auto-Measure** is On, lower arm; if Auto-Measure is off, lower arm and tap **Measure**.
  - Cuvette: Tap **Measure**.

When the sample measurement is completed, the spectrum and reported values are displayed (see the next section).

8. When you are finished measuring samples, tap **End Experiment**.
9. Lift the arm and clean both pedestals with a new wipe, or remove the sample cuvette.



## Related Topics

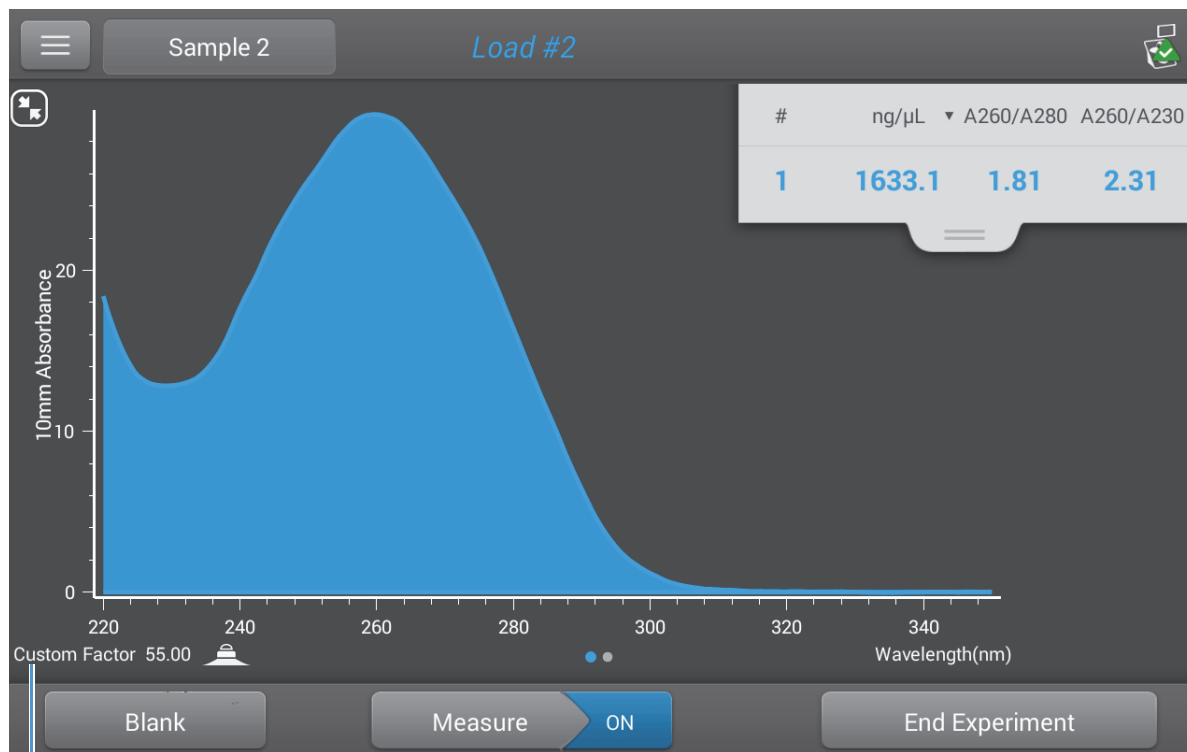
- [Measure a Micro-Volume Sample](#)
- [Measure a Sample Using a Cuvette](#)
- [Best Practices for Micro-Volume Measurements](#)
- [Best Practices for Cuvette Measurements](#)
- [Prepare Samples and Blanks](#)
- [Basic Instrument Operations](#)

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## Custom Factor Reported Results

For each measured sample, this application shows the absorbance spectrum and a summary of the results. Here is an example:

**Note** The Custom Factor measurement screen is identical to the [measurement screen for the other nucleic acid applications](#) except the Custom Factor is reported in the lower left corner (see image below).




Custom factor used to calculate nucleic acid concentration

### Related Topics

- Basic Instrument Operations
- Nucleic Acid Reported Results
- Nucleic Acid Calculations

## Settings for Nucleic Acid Measurements using a Custom Factor

To show the Custom Factor settings, tap  > **Custom Factor Setup**.

Setting	Available Options	Description
Custom Factor	Enter an integer value between 15 ng-cm/ $\mu$ L and 150 ng-cm/ $\mu$ L	Constant used to calculate nucleic acid concentration in <a href="#">modified Beer's Law equation</a> . Based on extinction coefficient and pathlength:  $f = 1/(\mathcal{E}_{260} * b)$ <p>where:  <b>f</b>= factor  <b><math>\mathcal{E}</math></b> = molar extinction coefficient at 260 nm in ng-cm/<math>\mu</math>L  <b>b</b> = <a href="#">sample pathlength</a> in cm (1 cm for nucleic acids measured with the NanoDrop One instruments)</p>
Baseline Correction	On or off  Enter baseline correction wavelength in nm or use default value (340 nm)	<b>Optional user-defined baseline correction.</b> Can be used to correct for any offset caused by light scattering particulates by subtracting measured absorbance at specified baseline correction wavelength from absorbance values at all wavelengths in sample spectrum. As a result, absorbance of sample spectrum is zero at specified baseline correction wavelength.

### Related Topics

- [Instrument Settings](#)

## Detection Limits for Nucleic Acid Measurements using a Custom Factor

The lower detection limits and reproducibility specifications for nucleic acids are provided [here](#). The upper detection limits are dependent on the [upper absorbance limit](#) of the instrument and the user-defined extinction coefficients.

### To calculate upper detection limits for nucleic acid samples

To calculate upper detection limits in ng/ $\mu$ L, use the following equation:

$$(\text{upper absorbance limit}_{\text{instrument}} * \text{extinction coefficient}_{\text{sample}})$$

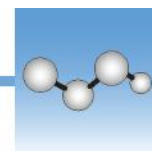
For example, for a sample measurement using an extinction coefficient of 55, the equation looks like this:

$$(550 \text{ AU} * 55 \text{ ng-cm}/\mu\text{L}) = 30,250 \text{ ng}/\mu\text{L}$$

**Note** For measurements with 10 mm pathlength cuvettes, the upper absorbance limit is 1.5 AU, which is approximately 75 ng/ $\mu$ L for dsDNA.

### Related Topics

- [Detection Limits for All Applications](#)



## Measure Oligo DNA or Oligo RNA

Measures the concentration of purified ssDNA or RNA oligonucleotides that absorb at 260 nm.

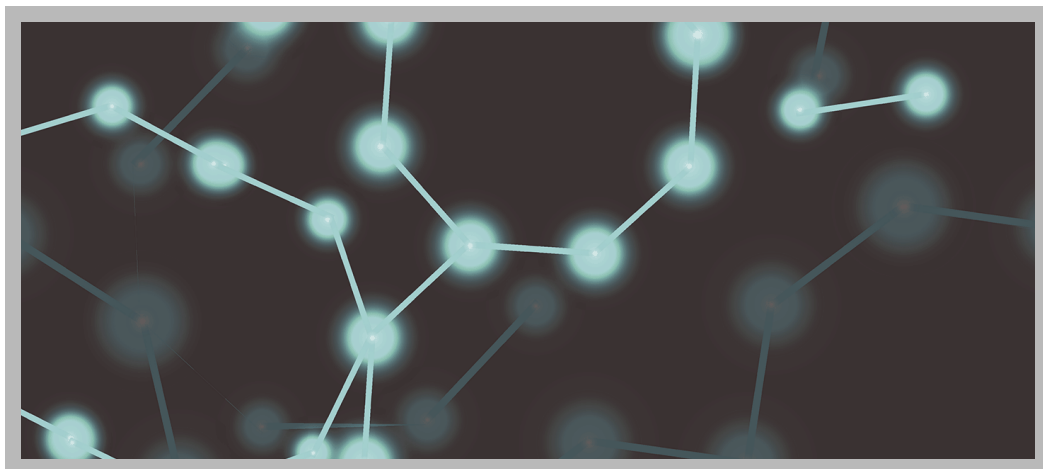
[Measure Oligo DNA or RNA](#)

[Reported Results](#)

[Settings](#)

[Detection Limits](#)

[Calculations](#)



## Measure Oligo DNA or Oligo RNA

Use the Oligo DNA and Oligo RNA applications to quantify oligonucleotides that absorb at 260 nm. Molar extinction coefficients are calculated automatically based on the user-defined base sequence of the sample. These applications report nucleic acid concentration and two absorbance ratios ( $A_{260}/A_{280}$  and  $A_{260}/A_{230}$ ). A single-point baseline correction can also be used.

**Note** If the oligonucleotide has been modified, for example with a fluorophore dye, check with the oligo manufacturer to determine if the modification contributes absorbance at 260 nm. If it does, we recommend using the [Microarray](#) application to quantify nucleic acid concentration. The Microarray application includes a correction to remove any absorbance contribution due to the dye from the oligo quantification result.

## To measure Oligo DNA or Oligo RNA samples

### NOTICE

- Do not use a squirt or spray bottle on or near the instrument as liquids will flow into the instrument and may cause permanent damage.
- Do not use hydrofluoric acid (HF) on the pedestals. Fluoride ions will permanently damage the quartz fiber optic cables.

### Before you begin...

Before taking pedestal measurements with the NanoDrop One instrument, lift the instrument arm and clean the upper and lower pedestals. At a minimum, wipe the pedestals with a new laboratory wipe. For more information, see [Cleaning the Pedestals](#).



### ❖ To measure an oligonucleotide sample

1. From the Home screen, select the **Nucleic Acids** tab and tap either **Oligo DNA** or **Oligo RNA**, as needed.
2. Specify the **Oligo base sequence** and a **baseline correction** if desired.
3. Pipette 1–2  $\mu\text{L}$  blanking solution onto the lower pedestal and lower the arm, or insert the blanking cuvette into the cuvette holder.

**Tip:** If using a cuvette, make sure to [align the cuvette light path](#) with the instrument light path.

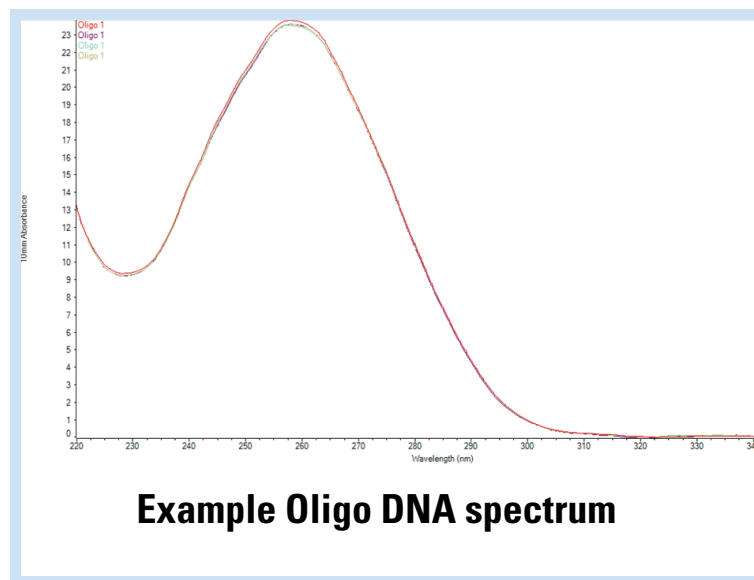
4. Tap **Blank** and wait for the measurement to complete.

**Tip:** If **Auto-Blank** is On, the blank measurement starts automatically after you lower the arm. (This option is not available for cuvette measurements.)

5. Lift the arm and clean both pedestals with a new laboratory wipe, or remove the blanking cuvette.
6. Pipette 1-2  $\mu\text{L}$  sample solution onto the pedestal and lower the arm, or insert the sample cuvette into the cuvette holder.
7. Start the sample measurement:
  - Pedestal: If **Auto-Measure** is On, lower arm; if Auto-Measure is off, lower arm and tap **Measure**.
  - Cuvette: Tap **Measure**.


When the sample measurement is completed, the spectrum and reported values are displayed (see the next section).

8. When you are finished measuring samples, tap **End Experiment**.
9. Lift the arm and clean both pedestals with a new wipe, or remove the sample cuvette.



### Related Topics

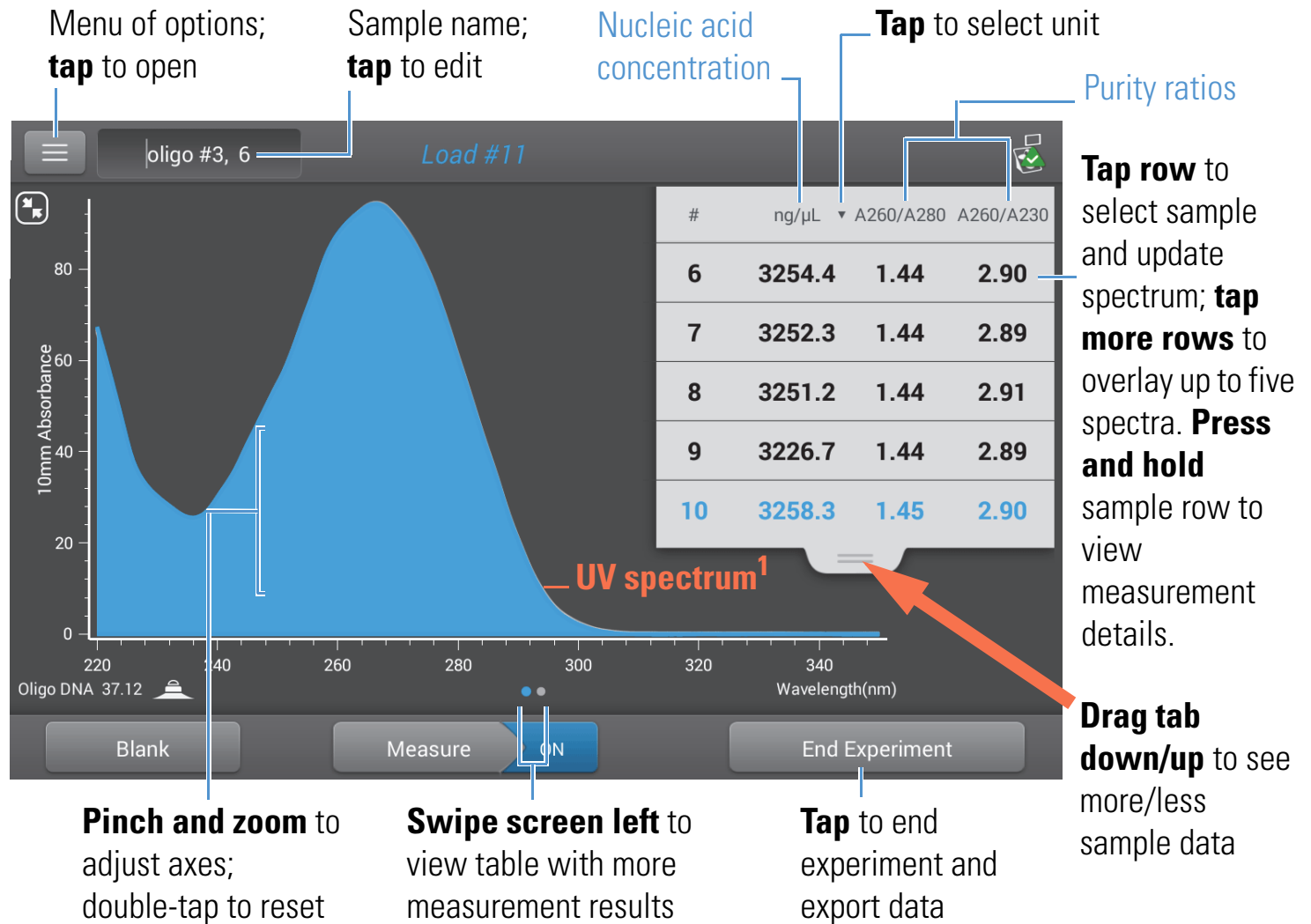
- [Best Practices for Nucleic Acid Measurements](#)

- [Measure a Micro-Volume Sample](#)
  - [Measure a Sample Using a Cuvette](#)
  - [Best Practices for Micro-Volume Measurements](#)
  - [Best Practices for Cuvette Measurements](#)
  - [Prepare Samples and Blanks](#)
  - [Basic Instrument Operations](#)
- 

## Oligo Reported Results

### Oligo DNA measurement screen

For each measured sample, the Oligo DNA and Oligo RNA applications show the UV absorbance spectrum and a summary of the results. Here is an example:



<sup>1</sup>Measured oligo: TTT TTT TTT TTT TTT TTT TTT TTT

**Note** Micro-volume absorbance measurements and measurements taken with nonstandard cuvettes are normalized to a 10.0 mm pathlength equivalent.

## Oligo DNA and Oligo RNA reported values

The initial screen that appears after each measurement (see previous image) shows a summary of the reported values. To view all reported values, press and hold the sample row. Here is an example:




- sample details (application and sampling method used, i.e., pedestal or cuvette)
- [sample name](#)
- created on (date sample measurement was taken)
- [nucleic acid concentration](#)
- [A260/A280](#)
- [A260/A230](#)
- [A260](#)
- [A280](#)
- [factor](#)
- [oligo sequence](#)
- [baseline correction](#)
- [stirrer status](#)

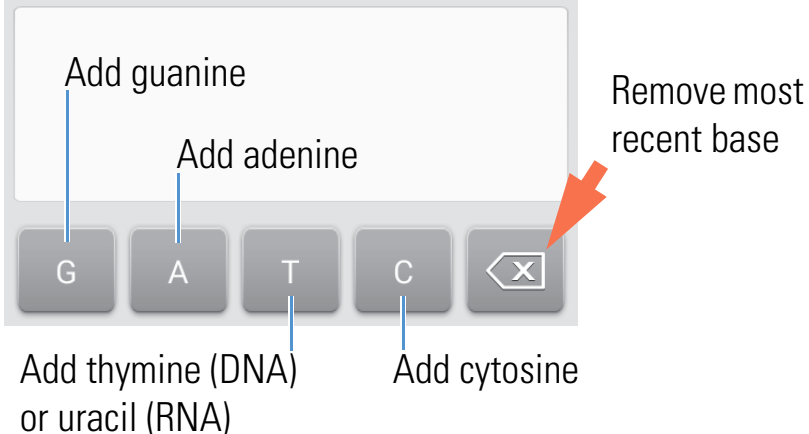
**Note** The five nucleotides that comprise DNA and RNA exhibit widely varying A260/A280 ratios. See [Oligo Purity Ratios](#) for more information.

### Related Topics

- [Basic Instrument Operations](#)
- [Oligo Calculations](#)

## Settings for Oligo DNA and Oligo RNA Measurements

The Oligo setup screen appears after you select the Oligo DNA or Oligo RNA application from the Nucleic Acids tab on the Home screen. To show the Oligo settings from the Oligo DNA or Oligo RNA measurement screen, tap  >  **Oligo DNA Setup** (or  **Oligo RNA Setup**).

Setting	Available Options	Description
Oligo Base Sequence	<p>for DNA: Use the G, A, T and C keys to specify the DNA base sequence</p> <p>for RNA: Use the G, A, U and C keys to specify the RNA base sequence</p>	<p>Specify your DNA or RNA base sequence by tapping the corresponding keys:</p> 

Each time a base is added to the sequence, the software calculates the following:

- **Factor.** Constant used to calculate oligonucleotide concentration in [modified Beer's Law equation](#). Based on extinction coefficient and pathlength:

$$f = 1/(\mathcal{E}_{260} * b)$$

where:

**f**= factor

**$\mathcal{E}$**  = molar extinction coefficient at 260 nm in ng-cm/ $\mu$ L

**b** = [sample pathlength](#) in cm (0.1 cm for nucleic acids measured with the NanoDrop One instrument)

Setting	Available Options	Description
		<ul style="list-style-type: none"> <li>• <b>Molecular Weight</b> of oligo calculated from user-defined base sequence.</li> <li>• <b>Number of Bases</b> entered.</li> <li>• <b>Molar Ext. Coefficient (260 nm)</b>. Molar extinction coefficient of oligo (in ng-cm/<math>\mu</math>L) at 260 nm calculated from entered base sequence.</li> <li>• <b>%GC</b>. Percentage of guanine and cytosine residues in total number of bases entered.</li> </ul>
Baseline Correction	On or off  Enter baseline correction wavelength in nm or use default value (340 nm)	Corrects for any offset caused by light scattering particulates by subtracting measured absorbance at specified baseline correction wavelength from absorbance values at all wavelengths in sample spectrum. As a result, absorbance of sample spectrum is zero at specified baseline correction wavelength.  <b>Tip:</b> If the sample has a modification that absorbs light at 340 nm, select a different correction wavelength or turn off Baseline Correction.

### Related Topics

- [Instrument Settings](#)

## Detection Limits for Oligo DNA and Oligo RNA Measurements

The lower detection limits and reproducibility specifications for the oligonucleotide sample types (ssDNA and RNA) are provided [here](#). The upper detection limits are dependent on the [upper absorbance limit](#) of the instrument and the extinction coefficients for the user-defined [base sequences](#).

### To calculate upper detection limits for nucleic acid samples

To calculate upper detection limits in ng/ $\mu$ L, use the following equation:

$$(\text{upper absorbance limit}_{\text{instrument}} * \text{extinction coefficient}_{\text{sample}})$$

For example, for a sample measurement using an extinction coefficient of 55, the equation looks like this:

$$(550 \text{ AU} * 55 \text{ ng-cm}/\mu\text{L}) = 30,250 \text{ ng}/\mu\text{L}$$

**Note** For measurements with 10 mm pathlength cuvettes, the upper absorbance limit is 1.5 AU, which is approximately 75 ng/ $\mu$ L for dsDNA.

## Related Topics

- [Detection Limits for All Applications](#)

## Calculations for Oligo DNA and Oligo RNA Measurements

As with the other nucleic acid applications, the Oligo applications use the [Beer-Lambert equation](#) to correlate absorbance with concentration based on the sample's extinction coefficient and pathlength. Because oligonucleotides are short, single-stranded molecules (or longer molecules of repeating sequences), their spectrum and extinction coefficient ( $\epsilon$ ) are closely dependent on base composition and sequence.

(The generally accepted extinction coefficients and factors for single-stranded DNA and RNA provide a reasonable estimate for natural, essentially randomized, sequences but not for short, synthetic oligo sequences.) To ensure the most accurate results, we use the exact value of  $\epsilon_{260}$  to calculate oligonucleotide concentration.

The NanoDrop software allows you to specify the base sequence of an oligonucleotide before it is measured. For any entered base sequence, the software uses the equation at the right to calculate the extinction coefficient.

**Tip:** The extinction coefficient is wavelength specific for each oligonucleotide and can be affected by buffer type, ionic strength and pH.

### Extinction Coefficients for Oligonucleotides

The software uses the nearest neighbor method and the following formula to calculate molar extinction coefficients for specific oligonucleotide base sequences:

$$\epsilon_{260} = \sum_1^{N-1} \epsilon_1 - \sum_2^{N-1} \epsilon_2 + \sum_1^N \epsilon_3$$

where:

$\epsilon$  = molar extinction coefficient in L/mole-cm

$\epsilon_1$  =  $\epsilon_{\text{nearest neighbor}}$

$\epsilon_2$  =  $\epsilon_{\text{individual bases}}$

$\epsilon_3$  =  $\epsilon_{\text{modifications, such as fluorescent dyes}}$

Calculated nucleic acid concentrations are based on the absorbance value at 260 nm, the factor used and the sample pathlength. A single-point baseline correction (or analysis correction) may also be applied.

Concentration is reported in mass units. Calculators are available on the Internet to convert concentration from mass to molar units based on sample sequence.

Absorbance values at 260 nm, 280 nm and sometimes 230 nm are used to calculate purity ratios for the measured nucleic acid samples. Purity ratios are sensitive to the presence of contaminants in the sample, such as residual solvents and reagents typically used during sample purification.

## Measured Values

### A260 absorbance

**Note:** For micro-volume absorbance measurements and measurements taken with nonstandard (other than 10 mm) cuvettes, the spectra are normalized to a 10 mm pathlength equivalent.

- Nucleic acid absorbance values are measured at 260 nm using the normalized spectrum. This is the reported A260 value if Baseline Correction is not selected.
- If [Baseline Correction](#) is selected, the absorbance value at the correction wavelength is subtracted from the sample absorbance at 260 nm. The corrected absorbance at 260 nm is reported and used to calculate nucleic acid concentration.

### A230, A280 absorbance

- Normalized absorbance values at 230 nm, 260 nm and 280 nm are used to calculate A260/A230 and A260/A280 ratios.

### Sample Pathlength

- For micro-volume measurements, the software selects the optimal pathlength (between 1.0 mm and 0.03 mm) based on sample absorbance at the analysis wavelength.
- For cuvette measurements, pathlength is determined by the cuvette Pathlength setting in the software (see [General Settings](#)).
- Displayed spectra and absorbance values are normalized to a 10 mm pathlength equivalent.
-



The five nucleotides that comprise DNA and RNA exhibit widely varying A260/A280 ratios. Estimated A260/A280 ratios for each independently measured nucleotide are provided below:

Guanine: 1.15

Adenine: 4.50

Cytosine: 1.51

Uracil: 4.00

Thymine: 1.47

The A260/A280 ratio for a specific nucleic acid sequence is approximately equal to the weighted average of the A260/A280 ratios for the four nucleotides present.

**Note:** RNA will typically have a higher 260/280 ratio due to the higher ratio of Uracil compared to that of Thymine.

### Reported Values

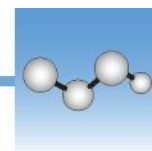
- **Nucleic acid concentration.** Reported in selected unit (i.e., ng/ $\mu$ L,  $\mu$ g/ $\mu$ L or  $\mu$ g/mL). Calculations are based on modified Beer's Law equation using corrected nucleic acid absorbance value.
- **A260/A280 purity ratio.** Ratio of corrected absorbance at 260 nm to corrected absorbance at 280 nm.
- **A260/A230 purity ratio.** Ratio of corrected absorbance at 260 nm to corrected absorbance at 230 nm.

**Note:** The traditional purity ratios (A260/A280 and A260/A230), which are used as indicators of the presence of various contaminants in nucleic acid samples, do not apply for oligonucleotides because the shapes of their spectra are highly dependent on their base compositions. See side bar for more information.

### Related Topics

- [Calculations for Nucleic Acid Measurements](#)





## Measure Protein A280

Measures the concentration of purified protein populations that absorb at 280 nm.

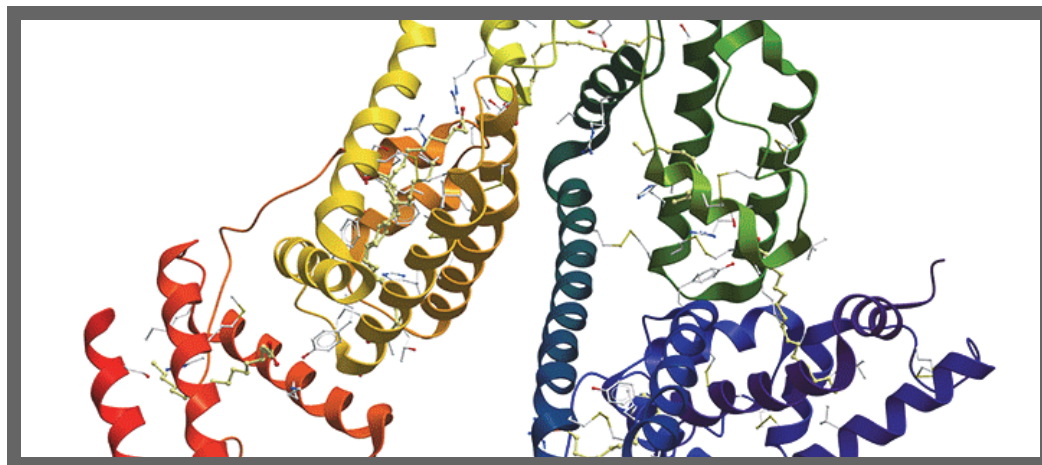
[Measure A280 Proteins](#)

[Reported Results](#)

[Settings](#)

[Detection Limits](#)

[Calculations](#)



## Measure Protein Concentration at A280

Use the Protein A280 application to quantify purified protein populations that contain amino acids such as tryptophan or tyrosine, or cys-cys disulfide bonds, which exhibit absorbance at 280 nm. This application reports protein concentration measured at 280 nm and one absorbance ratio ( $A_{260}/A_{280}$ ). A single-point baseline correction can also be used. This application does not require a standard curve.

**Note** If your samples contain mainly peptide bonds and little or no amino acids, use the [Protein A205](#) application instead of Protein A280.

## To measure Protein A280 samples

### NOTICE

- Do not use a squirt or spray bottle on or near the instrument as liquids will flow into the instrument and may cause permanent damage.
- Do not use hydrofluoric acid (HF) on the pedestals. Fluoride ions will permanently damage the quartz fiber optic cables.

**Before you begin...**

Before taking pedestal measurements with the NanoDrop One instrument, lift the instrument arm and clean the upper and lower pedestals. At a minimum, wipe the pedestals with a new laboratory wipe. For more information, see [Cleaning the Pedestals](#).

### ❖ To measure a Protein A280 sample

1. From the Home screen, select the **Proteins** tab and tap **Protein A280**.
2. Specify a **sample type** and **baseline correction** if desired.
3. Pipette 1–2  $\mu\text{L}$  blanking solution onto the lower pedestal and lower the arm, or insert the blanking cuvette into the cuvette holder.

**Tip:** If using a cuvette, make sure to **align the cuvette light path** with the instrument light path.

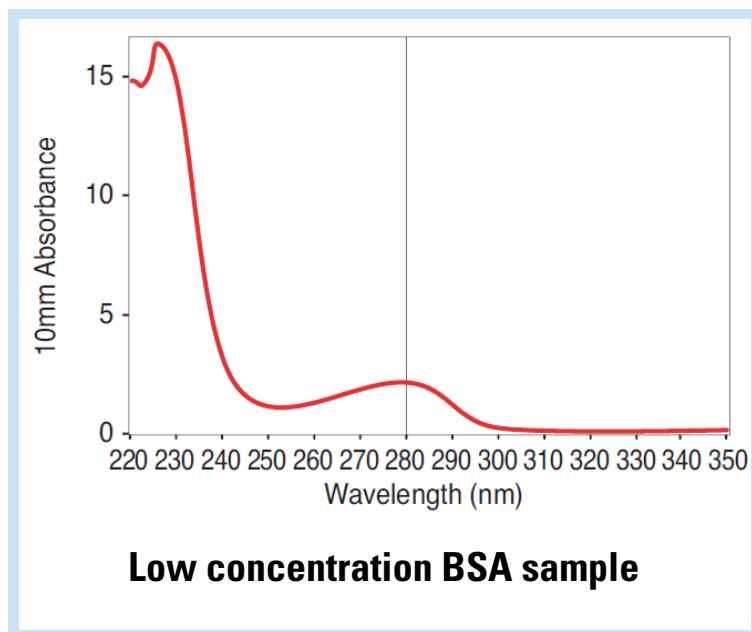
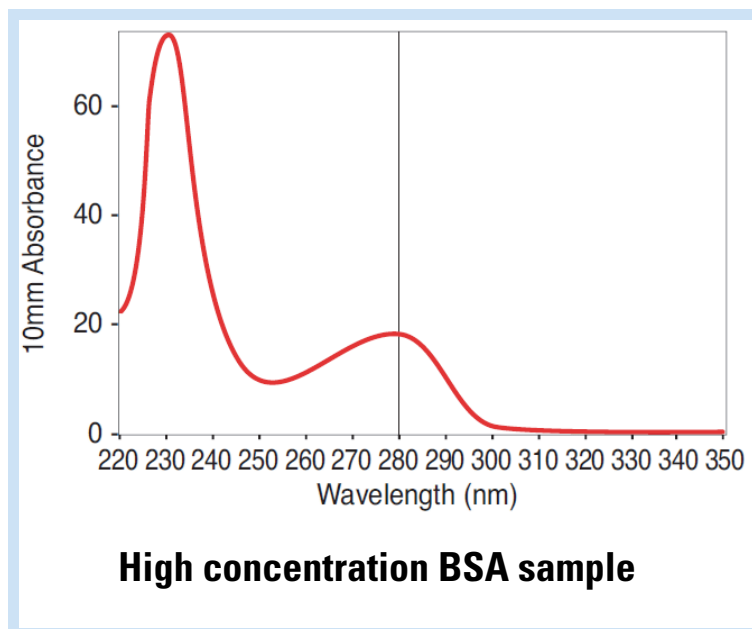
4. Tap **Blank** and wait for the measurement to complete.

**Tip:** If **Auto-Blank** is On, the blank measurement starts automatically after you lower the arm. (This option is not available for cuvette measurements.)

5. Lift the arm and clean both pedestals with a new laboratory wipe, or remove the blanking cuvette.
6. Pipette 2  $\mu\text{L}$  sample solution onto the pedestal and lower the arm, or insert the sample cuvette into the cuvette holder.
7. Start the sample measurement:
  - Pedestal: If **Auto-Measure** is On, lower arm; if Auto-Measure is off, lower arm and tap **Measure**.
  - Cuvette: Tap **Measure**

When the sample measurement is completed, the spectrum and reported values are displayed (see the next section).

8. When you are finished measuring samples, tap **End Experiment**.
9. Lift the arm and clean both pedestals with a new wipe, or remove the sample cuvette.



## Best practices for protein measurements

- Isolate and purify protein samples before measurement to remove impurities. Depending on the sample, impurities could include DNA, RNA and some buffer components. See [Preparing Samples](#) for more information.

**Note** Extraction reagents that contribute absorbance between 200 nm and 280 nm will affect measurement results if present in samples (even residual amounts).

- Ensure the sample absorbance is within the instrument's [absorbance detection limits](#).
- Choosing a blank:
  - For the Protein A280, Protein A205, and Proteins & Labels applications, blank with the same buffer solution used to resuspend the analyte of interest. The blanking solution should be a similar pH and ionic strength as the analyte solution.
  - For the Protein BCA, Protein Bradford, and Protein Lowry applications, blank with deionized water (DI H<sub>2</sub>O).
  - For the Protein Pierce 660 application, blank with the reference solution used to make the standard curve (reference solution should contain none of the standard protein stock). For more information, see [Working with standard curves](#).
- Run a [blanking cycle](#) to assess the absorbance contribution of your buffer solution. If the buffer exhibits strong absorbance at or near the analysis wavelength (typically 280 nm or 205 nm), you may need to choose a different buffer or application, such as a colorimetric assay (for example, BCA or Pierce 660). See [Choosing and Measuring a Blank](#) for more information.

**Note** Buffers such as Triton X, RIPA, and NDSB contribute significant absorbance and are not compatible with direct A280 or A205 measurements.

- For micro-volume measurements:
  - Ensure pedestal surfaces are properly [cleaned](#) and [conditioned](#). (Proteins tend to stick to pedestal surfaces.)
  - Gently (but thoroughly) vortex samples before taking a measurement. Avoid introducing bubbles when mixing and pipetting.
  - Follow [best practices for micro-volume measurements](#).
  - Use a 2 µL sample volume. See [Recommended Sample Volumes](#) for more information.
- For cuvette measurements (NanoDrop One<sup>C</sup> instruments only), use compatible cuvettes and follow [best practices for cuvette measurements](#).

### Related Topics

- [Best practices for protein measurements](#)
- [Measure a Micro-Volume Sample](#)
- [Measure a Sample Using a Cuvette](#)
- [Prepare Samples and Blanks](#)
- [Basic Instrument Operations](#)

---

## Protein A280 Reported Results

### Protein A280 measurement screen

For each measured sample, this application shows the absorbance spectrum and a summary of the results. Here is an example:

Menu of options; **tap** to open

Sample name; **tap** to edit

Protein concentration

**Tap** to select unit

Absorbance at 280 nm

Purity ratio

**UV spectrum**

#	mg/mL	A280	A260/A280
1	15.3750	10.30	0.57
2	15.6527	10.49	0.57
3	7.1125	4.77	0.55

**Tap row** to select sample and update spectrum; **tap more rows** to overlay up to five spectra. **Press and hold** sample row to view measurement details.

**Drag tab down/up** to see more/less sample data

**Pinch and zoom** to adjust axes; double-tap to reset

**Swipe screen left** to view table with more measurement results

**Tap** to end experiment and export data

**Note** Micro-volume absorbance measurements and measurements taken with nonstandard cuvettes are normalized to a 10.0 mm pathlength equivalent.

### Protein A280 reported values

The initial screen that appears after each measurement (see previous image) shows a summary of the reported values. To view all reported values, press and hold the sample row. Here is an example:




Field	Value
Application	Protein A280
Sampling method	Pedestal
Sample Name	Sample 3
Created on	9/17/2015 10:07:57 AM
Protein	7.1125 mg/mL
A280	4.77
A260/A280	0.55
Sample type	BSA
Baseline correction	340.00 nm 0.15 absorbance

### Related Topics

- [Basic Instrument Operations](#)
- [Protein A280 Calculations](#)

## Settings for Protein A280 Measurements

To show the Protein A280 settings, from the Protein A280 measurement screen, tap  > **Protein A280 Setup**.

### Protein A280 settings

The Protein A280 application provides a variety of sample type options for purified protein analysis.

Each sample type applies a unique extinction coefficient to the protein calculations. If the extinction coefficient of the sample is known, choose the **ε** + MW (molar) or **ε**1% (mass) option and enter the value. Otherwise, calculate the extinction coefficient or choose the option that best matches the sample solution. If you only need a rough estimate of protein concentration and the sample extinction coefficient is unknown, select the 1 Abs=1 mg/mL sample type option.

**Tip** Ideally, the extinction coefficient should be determined empirically using a solution of the study protein at a known concentration using the same buffer.

Setting	Available Options	Mass Ext. Coefficient (L/gm-cm)	Description
Sample type <sup>a</sup>	1 Abs = 1 mg/mL	General reference	Recommended when extinction coefficient is unknown and rough estimate of protein concentration is acceptable for a solution with no other interfering substances. Assumes 0.1% (1 mg/mL) protein solution produces 1.0A at 280 nm (where pathlength is 10 mm), i.e., <b>ε</b> 1% = 10.
	BSA	6.67	Calculates BSA (Bovine Serum Albumin) protein concentration using mass extinction coefficient ( <b>ε</b> ) of 6.67 L/gm-cm at 280 nm for 1% (i.e., 10 mg/mL) BSA solution. Assuming MW is 66,400 daltons (Da), molar extinction coefficient at 280 nm for BSA is approximately 43,824 M <sup>-1</sup> cm <sup>-1</sup> .
	IgG	13.7	Suitable for most mammalian antibodies (i.e., immunoglobulin G or IgG). Calculates protein concentration using mass extinction coefficient ( <b>ε</b> ) of 13.7 L/gm-cm at 280 nm for 1% (i.e., 10 mg/mL) IgG solution. Assuming MW is 150,000 Da, molar extinction coefficient at 280 nm for IgG is approximately 210,000 M <sup>-1</sup> cm <sup>-1</sup> .
	Lysozyme	26.4	Calculates lysozyme protein concentration using mass extinction coefficient ( <b>ε</b> ) of 26.4 L/gm-cm at 280 nm for 1% (i.e., 10 mg/mL) lysozyme solution. Assumes molar extinction coefficient for egg white lysozyme ranges between 36,000 M <sup>-1</sup> cm <sup>-1</sup> and 39,000 M <sup>-1</sup> cm <sup>-1</sup> .




Setting	Available Options	Mass Ext. Coefficient (L/gm-cm)	Description
	Other protein ( $\epsilon$ + MW)	User entered molar extinction coefficient and molecular weight	Assumes protein has known molar extinction coefficient ( $\epsilon$ ) and molecular weight (MW), where: $(\epsilon_{\text{molar}}) * 10 = (\epsilon_{\text{percent}}) * (MW_{\text{protein}})$  Enter MW in kiloDaltons (kDa) and molar extinction coefficient ( $\epsilon$ ) in $M^{-1}cm^{-1}$ divided by 1000 (i.e., $\epsilon/1000$ ). For example, for protein with molar extinction coefficient of $210,000 M^{-1}cm^{-1}$ , enter 210.
	Other protein ( $\epsilon$ 1%)	User entered mass extinction coefficient	Assumes protein has known mass extinction coefficient ( $\epsilon$ ). Enter mass extinction coefficient in L/gm-cm for 10 mg/mL ( $\epsilon$ 1%) protein solution.
Baseline Correction	On or off  Enter baseline correction wavelength in nm or use default value (340 nm)	N/A	Corrects for any offset caused by light scattering particulates by subtracting measured absorbance at specified baseline correction wavelength from absorbance values at all wavelengths in sample spectrum. As a result, absorbance of sample spectrum is zero at specified baseline correction wavelength.  <b>Tip:</b> If the sample has a modification that absorbs light at 340 nm, select a different correction wavelength or turn off Baseline Correction.

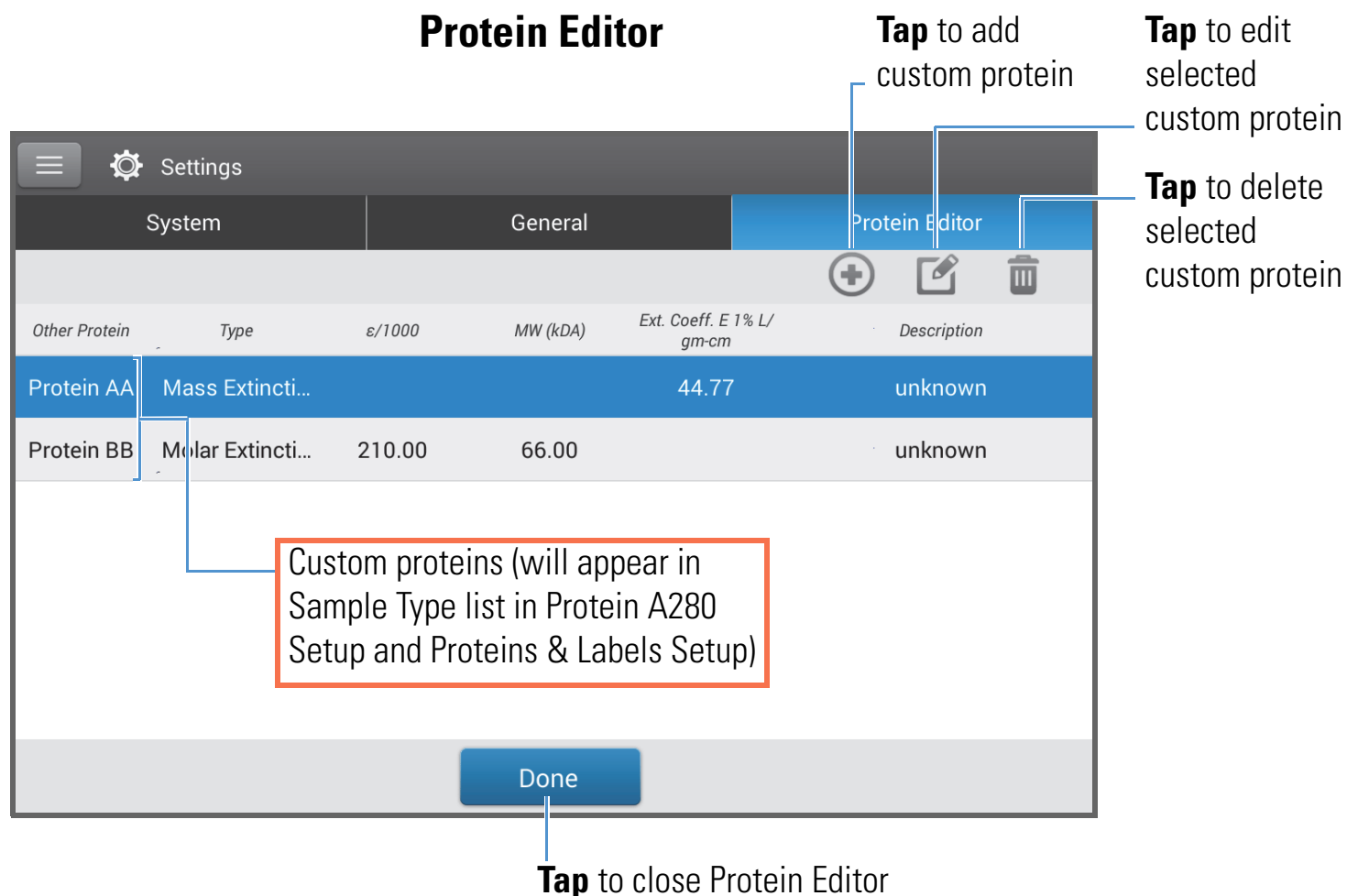
<sup>a</sup> To add or edit a custom protein, use Protein Editor.

## Protein editor

Use the Protein Editor to add a custom protein to the list of available protein sample types in [Protein A280 Setup](#) and [Proteins & Labels Setup](#).


To access the Protein Editor:

- from the Home screen, tap  > **Protein Editor**
- from the Protein A280 or Proteins & Labels measurement screen, tap  >  **Settings > Protein Editor**



These operations are available from the Protein Editor:

#### Add custom protein


- in Protein Editor, tap  to show New Protein Type box
- enter unique **Name** for new protein (tap field to display keyboard, tap **Done** key to close keyboard)
- enter **Description** for new protein
- specify whether to enter **Molar Extinction** coefficient or **Mass Extinction** coefficient for custom protein
  - if **Mass Extinction** coefficient is selected
    - enter mass extinction coefficient in L/gm-cm for 10 mg/mL (**E**1%) protein solution

**Tap** a field to show keyboard;  
to close, tap **Done** key


- if **Molar Extinction** is selected
  - enter molar extinction coefficient (**E**) in  $M^{-1}cm^{-1}$  divided by 1000 (i.e., **E**/1000). For example, for protein with molar extinction coefficient of  $210,000 M^{-1}cm^{-1}$ , enter 210
  - enter molecular weight (MW) in kiloDaltons (kDa)
- tap **OK** to close New Protein Type box

After you choose OK, the new custom protein appears in the Type list in Protein A280 Setup and Proteins & Labels Setup.

### Edit custom protein

- in Protein Editor, tap to select custom protein
- tap  to show Edit Protein Type box
- edit any entries or settings
- tap **OK**

### Delete custom protein

- in Protein Editor, tap to select custom protein
- tap 

**Note** Deleting a custom protein permanently removes the protein and all associated information from the software.

### Related Topics

- [Instrument Settings](#)

## Detection Limits for Protein A280 Measurements

Detection limits and reproducibility specifications for purified BSA proteins are provided [here](#). The BSA lower detection limit and reproducibility values apply to any protein sample type. The upper detection limits are dependent on the [upper absorbance limit](#) of the instrument and the sample's extinction coefficient.

### To calculate upper detection limits for other (non-BSA) protein sample types

To calculate upper detection limits in ng/ $\mu$ L for proteins, use the following equation:

$$(\text{upper absorbance limit}_{\text{instrument}} / \text{mass extinction coefficient}_{\text{sample}}) * 10$$

For example, if the sample's mass extinction coefficient at 280 nm is 6.67 for a 1% (10 mg/mL) solution, the equation looks like this:

$$(550 / 6.67) * 10 = 824.6 \text{ (or } \sim 825)$$

### Related Topics

- [Detection Limits for All Applications](#)

## Calculations for Protein A280 Measurements

The Protein A280 application uses the [Beer-Lambert equation](#) to correlate absorbance with concentration. Solving Beer's law for concentration yields the equation at the right.

The extinction coefficient of a peptide or protein is related to its tryptophan (W), tyrosin (Y) and cysteine (C) amino acid composition.

**Tip:** The extinction coefficient is wavelength specific for each protein and can be affected by buffer type, ionic strength and pH.

### Beer-Lambert Equation (solved for concentration)

$$c = A / (\epsilon * b)$$

where:

**A** = UV absorbance in absorbance units (AU)

**$\epsilon$**  = wavelength-dependent molar absorptivity coefficient (or extinction coefficient) in liter/mol-cm

**b** = pathlength in cm

**c** = analyte concentration in moles/liter or molarity (M)

**Note:** Dividing the measured absorbance of a sample solution by its molar extinction coefficient yields the molar concentration of the sample. See [Published Extinction Coefficients](#) for more information regarding molar vs. mass concentration values.

### Extinction Coefficients for Proteins

At 280 nm, the extinction coefficient is approximated by the weighted sum of the 280 nm molar extinction coefficients of the three constituent amino acids, as described in this equation:

$$\epsilon = (nW * 5500) + (nY * 1490) + (nC * 125)$$

where:

**$\epsilon$**  = molar extinction coefficient

**n** = number of each amino acid residue

**5500, 1490 and 125** = amino acid molar absorptivities at 280 nm

This application offers six options (shown at right) for selecting an appropriate extinction coefficient for each measured sample, to be used in conjunction with Beer's Law to calculate sample concentration.

If the extinction coefficient of the sample is known, choose the  $\epsilon$  + MW (molar) or  $\epsilon$ 1% (mass) option and enter the value. Otherwise, calculate the extinction coefficient or choose the option that best matches the sample solution.

**Tip:** Ideally, the extinction coefficient should be determined empirically using a solution of the study protein at a known concentration using the same buffer.

Most sources report extinction coefficients for proteins measured at or near 280 nm in phosphate or other physiologic buffer. These values provide sufficient accuracy for routine assessments of protein concentration.

The equation at the right shows the relationship between molar extinction coefficient ( $\epsilon_{\text{molar}}$ ) and percent extinction coefficient ( $\epsilon$ 1%).

### Available Options for Extinction Coefficient

- **1 Abs = 1 mg/mL**, where sample type and/or ext. coefficient is unknown (produces rough estimate of protein concentration)
- **BSA** (Bovine Serum Albumin, 6.67 L/gm-cm)
- **IgG** (any mammalian antibody, 13.7 L/gm-cm)
- **Lysozyme** (egg white lysozyme, 26.4 L/gm-cm)
- **Other protein ( $\epsilon$  + MW)**, user-specified molar ext. coefficient
- **Other protein ( $\epsilon$ 1%)**, user-specified mass ext. coefficient
- 

**Note:** See [Sample Type](#) for details.

### Published Extinction Coefficients

Published extinction coefficients for proteins may be reported as:

- wavelength-dependent molar absorptivity (or extinction) coefficient ( $\epsilon$ ) with units of  $M^{-1}cm^{-1}$
- percent solution extinction coefficient ( $\epsilon$ 1%) with units of  $(g/100\text{ mL})^{-1}cm^{-1}$  (i.e., 1% or 1 g/100 mL solution measured in a 1 cm cuvette)
- protein absorbance values for 0.1% (i.e., 1 mg/mL) solutions

**Tip:** Assess published values carefully to ensure unit of measure is applied correctly.

### Conversions Between $\epsilon_{\text{molar}}$ and $\epsilon$ 1%

$$(\epsilon_{\text{molar}}) * 10 = (\epsilon 1\%) * (MW_{\text{protein}})$$

Example: To determine percent solution extinction coefficient ( $\epsilon$ 1%) for a protein that has a molar extinction coefficient of  $43,824\text{ M}^{-1}cm^{-1}$  and a molecular weight (MW) of 66,400 daltons (Da), rearrange and solve the above equation as follows:

$$\epsilon 1\% = (\epsilon_{\text{molar}} * 10) / (MW_{\text{protein}})$$

$$\epsilon 1\% = (43,824 * 10) / 66,400\text{ Da}$$

$$\epsilon 1\% = 6.6\text{ g/100 mL}$$



To determine concentration (c) of a sample in mg/mL, use the equation at the right and a conversion factor of 10.

**Tip:** The NanoDrop One software includes the conversion factor when reporting protein concentrations.

### Conversions Between g/100 mL and mg/mL

$$C_{\text{protein in mg/mL}} = (A / \epsilon 1\%) * 10$$

Example: If measured absorbance for a protein sample at 280 nm relative to the reference is 5.8 A, protein concentration can be calculated as:

$$C_{\text{protein}} = (A / \epsilon 1\%) * 10$$

$$C_{\text{protein}} = (5.8/6.6 \text{ g/100 mL}) * 10$$

$$C_{\text{protein}} = 8.79 \text{ mg/mL}$$

Calculated protein concentrations are based on the absorbance value at 280 nm, the selected (or entered) extinction coefficient and the sample pathlength. A single-point baseline correction (or analysis correction) may be applied.

Concentration is reported in mass units. Calculators are available on the Internet to convert concentration from mass to molar units based on sample sequence.

Absorbance values at 260 nm and 280 nm are used to calculate purity ratios for the measured protein samples.

Purity ratios are sensitive to the presence of contaminants in the sample, such as residual solvents and reagents typically used during sample purification.

### Measured Values

#### A280 absorbance

**Note:** For micro-volume absorbance measurements and measurements taken with nonstandard (other than 10 mm) cuvettes, the spectra are normalized to a 10 mm pathlength equivalent.

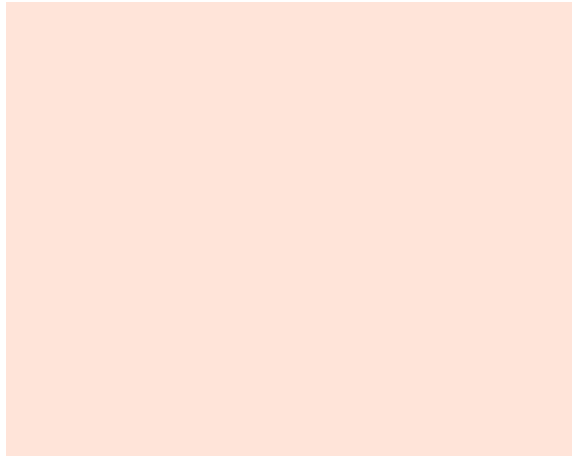
- Protein absorbance values are measured at 280 nm using the normalized spectrum. If Baseline Correction is not selected, this is the reported A280 value and the value used to calculate protein concentration.
- If [Baseline Correction](#) is selected, the normalized and baseline-corrected absorbance value at 280 nm is reported and used to calculate protein concentration.

#### A260 absorbance

- Normalized and baseline-corrected (if selected) absorbance value at 260 nm is also reported.

#### Sample Pathlength

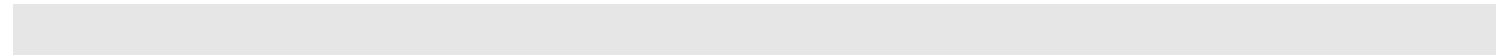
- For micro-volume measurements, the software selects the optimal pathlength (between 1.0 mm and 0.03 mm) based on sample absorbance at the analysis wavelength.
- For cuvette measurements, pathlength is determined by the cuvette Pathlength setting in the software (see [General Settings](#)).
- Displayed spectra and absorbance values are normalized to a 10 mm pathlength equivalent.

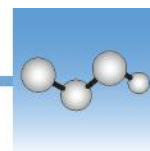


### Reported Values

- **Protein concentration.** Reported in selected unit (mg/mL or  $\mu\text{g/mL}$ ). Calculations are based on Beer-Lambert equation using corrected protein absorbance value.
- **A260/A280 purity ratio.** Ratio of corrected absorbance at 260 nm to corrected absorbance at 280 nm. An A260/A280 purity ratio of  $\sim 0.57$  is generally accepted as “pure” for proteins.

**Note:** Although purity ratios are important indicators of sample quality, the best indicator of protein quality is functionality in the downstream application of interest (e.g., real-time PCR).





## Measure Proteins and Labels

Measures the concentration of purified proteins that have been labeled with up to two fluorescent dyes.

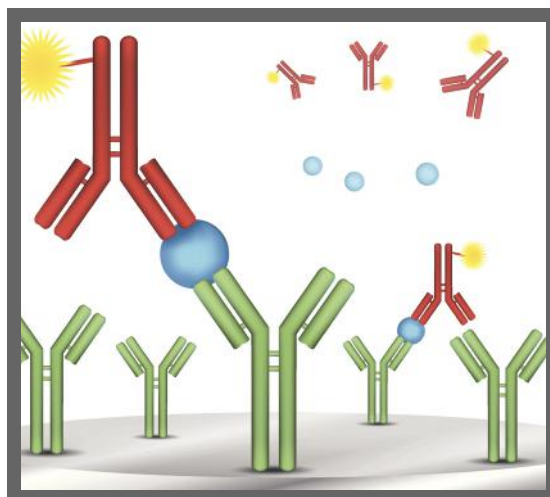
[Measure Labeled Proteins](#)

[Reported Results](#)

[Settings](#)

[Detection Limits](#)

[Calculations](#)



## Measure Labeled Protein Samples

Use the Proteins and Labels application to quantify proteins and fluorescent dyes for protein array conjugates, as well as metalloproteins such as hemoglobin, using wavelength ratios. This application reports protein concentration measured at 280 nm, an A269/A280 absorbance ratio, and the concentrations and measured absorbance values of the dyes, allowing detection of dye concentrations as low as 0.2 picomole per microliter. This information is useful for evaluating protein/dye conjugation (degree of labeling) for use in downstream applications.

## To measure labeled protein samples

### NOTICE

- Do not use a squirt or spray bottle on or near the instrument as liquids will flow into the instrument and may cause permanent damage.
- Do not use hydrofluoric acid (HF) on the pedestals. Fluoride ions will permanently damage the quartz fiber optic cables.

**Before you begin...**

Before taking pedestal measurements with the NanoDrop One instrument, lift the instrument arm and clean the upper and lower pedestals. At a minimum, wipe the pedestals with a new laboratory wipe. For more information, see [Cleaning the Pedestals](#).

❖ **To measure a labeled protein sample**

1. From the Home screen, select the **Proteins** tab and then tap **Protein & Labels**.
2. Specify the **sample type** and the **type of dye(s)** used.

**Tip:** Select a dye from the pre-defined list or add a custom dye using the **Dye/Chromophore Editor**.

3. Pipette 1–2  $\mu\text{L}$  of the blanking solution onto the lower pedestal and lower the arm, or insert the blanking cuvette into the cuvette holder.

**Tip:** If using a cuvette, make sure to **align the cuvette light path** with the instrument light path.

4. Tap **Blank** and wait for the measurement to complete.

**Tip:** If **Auto-Blank** is On, the blank measurement starts automatically after you lower the arm. (This option is not available for cuvette measurements.)

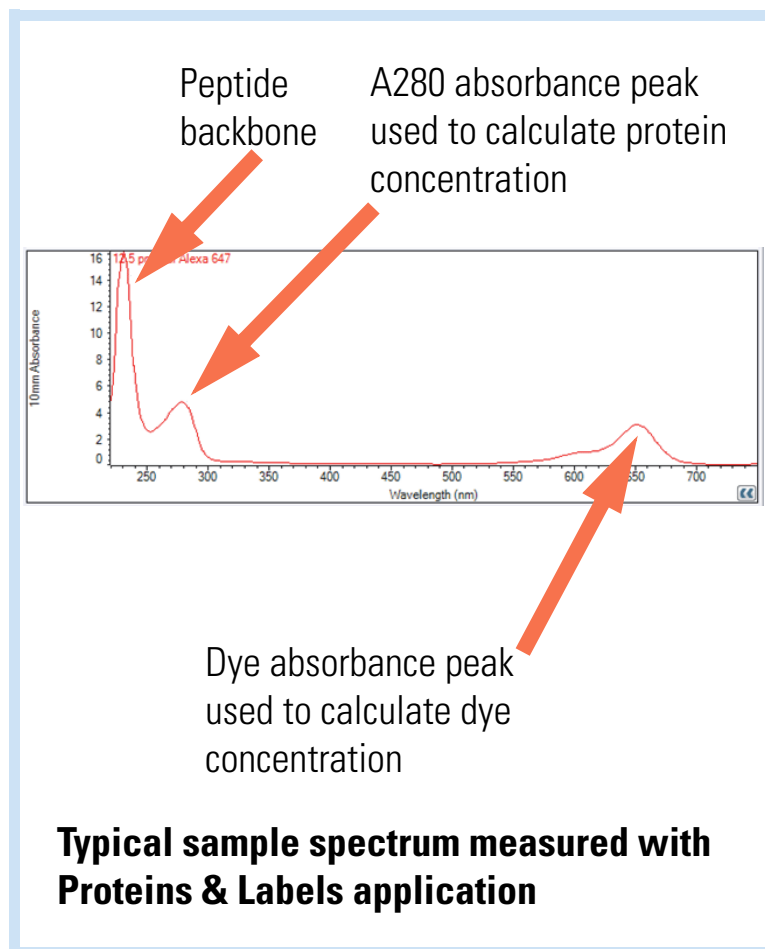
5. Lift the arm and clean both pedestals with a new laboratory wipe, or remove the blanking cuvette.
6. Pipette 2  $\mu\text{L}$  sample solution onto the pedestal and lower the arm, or insert the sample cuvette into the cuvette holder.

7. Start the sample measurement:

- Pedestal: If **Auto-Measure** is On, lower arm; if Auto-Measure is off, lower arm and tap **Measure**.
- Cuvette: Tap **Measure**

When the sample measurement is completed, the spectrum and reported values are displayed (see the next section).

8. When you are finished measuring samples, tap **End Experiment**.
9. Lift the arm and clean both pedestals with a new wipe, or remove the sample cuvette.



### Related Topics

- [Best practices for protein measurements](#)
- [Measure a Micro-Volume Sample](#)
- [Measure a Sample Using a Cuvette](#)
- [Prepare Samples and Blanks](#)
- [Basic Instrument Operations](#)

---

## Proteins & Labels Reported Results

### Proteins & Labels measurement screen

For each measured sample, this application shows the absorbance spectrum and a summary of the results. Here is an example:

Menu of options; **tap** to open

Sample name; **tap** to edit

Protein concentration

**Tap** to select unit

Dye concentration(s)

**Tap row** to select sample and update spectrum; **tap more rows** to overlay up to five spectra. **Press and hold** sample row to view measurement details.

**Drag tab down/up** to see more/less sample data

**Pinch and zoom** to adjust axes; double-tap to reset

**Swipe screen left** to view table with more measurement results

**Tap** to end experiment and export data

**UV-visible spectrum**

#	mg/mL	Dye 1	Dye 2
20	0.1962	0.45	0.00

**Note**

- A baseline correction is performed at 750 nm (absorbance value at 750 nm is subtracted from absorbance values at all wavelengths in sample spectrum).
- Micro-volume absorbance measurements and measurements taken with nonstandard cuvettes are normalized to a 10.0 mm pathlength equivalent.

## Proteins & Labels reported values

The initial screen that appears after each measurement (see previous image) shows a summary of the reported values. To view all reported values, press and hold the sample row. Here is an example:

### Reported values for Proteins & Labels application

- Sample details (application and sampling method used, i.e., pedestal or cuvette)
- [Sample Name](#)
- Creation date
- [Protein](#)
- [A280](#)
- [Sample Type](#)
- [Dye 1/Dye 2](#)
- [Sloping Dye Correction](#)
- [Analysis Correction](#)

### Related Topics

- [Basic Instrument Operations](#)
- [Proteins & Labels calculations](#)

---

## Settings for Proteins and Labels Measurements

To show the Proteins & Labels settings, from the Proteins & Labels measurement screen, tap



> **Proteins & Labels Setup.**



Setting	Available Options	Mass Ext. Coefficient (L/gm-cm)	Description
Sample type <sup>a</sup>	1 Abs = 1 mg/mL	General reference	<a href="#">Tap here</a> for detailed description of each available setting.
	BSA	6.67	Each sample type applies a unique extinction coefficient to the protein calculations. If the extinction coefficient of the sample is known, choose the <b>ε</b> + MW (molar) or <b>ε</b> 1% (mass) option and enter the value. Otherwise, calculate the extinction coefficient or choose the option that best matches the sample solution. If you only need a rough estimate of protein concentration and the sample extinction coefficient is unknown, select the 1 Abs=1 mg/mL sample type option.
	IgG	13.7	
	Lysozyme	26.4	
	Other protein ( <b>ε</b> + MW)	user-entered molar extinction coefficient/molecular weight	
Other protein ( <b>ε</b> 1%)	User entered mass extinction coefficient	<b>Tip:</b> Ideally, the extinction coefficient should be determined empirically using a solution of the study protein at a known concentration using the same buffer.	
Analysis Correction <sup>b</sup>	On or off	N/A	Corrects sample absorbance measurement for any offset caused by light scattering particulates by subtracting absorbance value at specified analysis correction wavelength from absorbance value at analysis wavelength. Corrected value is used to calculate sample concentration.  <b>Tip:</b> If the sample has a modification that absorbs light at 340 nm, select a different correction wavelength or turn off Analysis Correction.
	Enter analysis correction wavelength in nm or use default value (340 nm)		
Dye 1/Dye 2 Type <sup>c</sup>	Cy3, 5, 3.5, or 5.5, Alexa Fluor 488, 546, 555, 594, 647, or 660	See <a href="#">Dye/Chromophore Editor</a> for specific values for each dye	Select pre-defined dye used to label sample material, or one that has been added using <a href="#">Dye/Chrom. Editor</a> .
Dye 1/Dye 2 Unit	picomoles/microliter (pmol/uL), micromoles (uM), or millimoles (mM)	not applicable	Select unit for reporting dye concentrations.
Sloping Dye Correction <sup>d</sup>	On or off		Corrects dye absorbance measurements for any offset caused by light scattering particulates by subtracting absorbance value of a sloping baseline from 400 nm to 750 nm from absorbance value at dye's analysis wavelength.

<sup>a</sup> To add or edit a custom protein, use [Protein Editor](#).

<sup>b</sup> Analysis Correction affects calculation for protein concentration only.

<sup>c</sup> To add custom dye or edit list of available dyes, use [Dye/Chromophore Editor](#).

<sup>d</sup> Sloping Dye Correction affects calculations for dye concentration only.

### Related Topics

- [Instrument Settings](#)
- [Protein Editor](#)
- [Dye/Chromophore Editor](#)

## Detection Limits for Proteins and Labels Measurements

Detection limits and reproducibility specifications for purified BSA proteins and dyes that are pre-defined in the software are provided [here](#). The BSA lower detection limit and reproducibility values apply to any protein sample type. The upper detection limits are dependent on the [upper absorbance limit](#) of the instrument and the sample's extinction coefficient.

### To calculate upper detection limits for other (non-BSA) protein sample types

To calculate upper detection limits in ng/ $\mu$ L for proteins, use the following equation:

$$(\text{upper absorbance limit}_{\text{instrument}} / \text{mass extinction coefficient}_{\text{sample}}) * 10$$

For example, if the sample's mass extinction coefficient at 280 nm is 6.67 for a 1% (10 mg/mL) solution, the equation looks like this:

$$(550 / 6.67) * 10 = 824.6 \text{ (or } \sim 825)$$

### Related Topics

- [Detection Limits for All Applications](#)

## Calculations for Proteins and Labels Measurements

As with the other protein applications, Proteins & Labels uses the [Beer-Lambert equation](#) to correlate absorbance with concentration based on the sample's extinction coefficient and pathlength.

This application offers six options (shown at right) for selecting an appropriate extinction coefficient for each measured sample, to be used in conjunction with Beer's Law to calculate sample concentration.

If the extinction coefficient of the sample is known, choose the  $\epsilon$  + MW (molar) or  $\epsilon$ 1% (mass) option and enter the value. Otherwise, calculate the extinction coefficient or choose the option that best matches the sample solution.

**Tip:** Ideally, the extinction coefficient should be determined empirically using a solution of the study protein at a known concentration using the same buffer.

Calculated protein concentrations are based on the absorbance value at 280 nm, the selected (or entered) extinction coefficient and the sample pathlength. A single-point baseline correction (or analysis correction) may be applied.

Concentration is reported in mass units. Calculators are available on the Internet to convert concentration from mass to molar units based on sample sequence.

### Available Options for Extinction Coefficient

- **1 Abs = 1 mg/mL**, where sample type and/or ext. coefficient is unknown (produces rough estimate of protein concentration)
- **BSA** (Bovine Serum Albumin, 6.67 L/gm-cm)
- **IgG** (any mammalian antibody, 13.7 L/gm-cm)
- **Lysozyme** (egg white lysozyme, 26.4 L/gm-cm)
- **Other protein ( $\epsilon$  + MW)**, user-specified molar ext. coefficient
- **Other protein ( $\epsilon$ 1%)**, user-specified mass ext. coefficient

**Note:** See [Sample Type](#) for details.

### Measured Values

#### A280 absorbance

**Note:** The absorbance value at 750 nm is subtracted from all wavelengths in the spectrum. As a result, the absorbance at 750 nm is zero in the displayed spectra. Also, for micro-volume absorbance measurements and measurements taken with nonstandard (other than 10 mm) cuvettes, the spectra are normalized to a 10 mm pathlength equivalent.

- Protein absorbance values are measured at 280 nm using the 750 nm-corrected and normalized spectrum. If Analysis Correction and Dye Correction are not selected, this is the reported A280 value and the value used to calculate protein concentration.
- If [Analysis Correction](#) is selected, the 750-corrected, normalized and analysis-corrected absorbance value at 280 nm is reported and used to calculate protein concentration.
- If a Dye is used, the 750-corrected, normalized, analysis-corrected and [dye-corrected](#) absorbance value at 280 nm is reported and used to calculate protein concentration.

Dye concentrations are calculated from the absorbance value at the dye's analysis wavelength, the dye's extinction coefficient, and the sample pathlength. A sloped-line dye correction may also be used.

### Dye absorbance

- Dye absorbance values are measured at specific wavelengths. See [Dye/Chromophore Editor](#) for analysis wavelengths used.
- If Sloping Dye Correction is selected, a linear baseline is drawn between 400 nm and 750 nm and, for each dye, the absorbance value of the sloping baseline is subtracted from the absorbance value at each dye's analysis wavelength. Baseline-corrected dye absorbance values are reported and used to calculate dye concentrations.

### Dye correction

- Pre-defined dyes have known correction values for A260 and A280. See [Dye/Chromophore Editor](#) for correction values used.
- A280 dye correction is subtracted from [A280 absorbance value](#) used to calculate protein concentration.

### Sample Pathlength

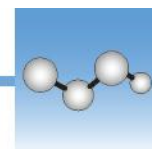
- For micro-volume measurements, the software selects the optimal pathlength (between 1.0 mm and 0.03 mm) based on sample absorbance at the analysis wavelength.
- For cuvette measurements, pathlength is determined by the cuvette Pathlength setting in the software (see [General Settings](#)).
- Displayed spectra and absorbance values are normalized to a 10 mm pathlength equivalent.

### Reported Values

- **Protein concentration.** Reported in selected unit (mg/mL or  $\mu\text{g/mL}$ ). Calculations are based on Beer-Lambert equation using corrected protein absorbance value.
- **Dye1/Dye2 concentration.** Reported in  $\text{pmol}/\mu\text{L}$ . Calculations are based on Beer's Law equation using (sloping) baseline-corrected dye absorbance value(s).

### Related Topics

- [Beer-Lambert Equation](#)
- [Protein A280 Calculations](#)



## Measure Protein A205

Measures the concentration of purified protein populations that absorb at 205 nm.

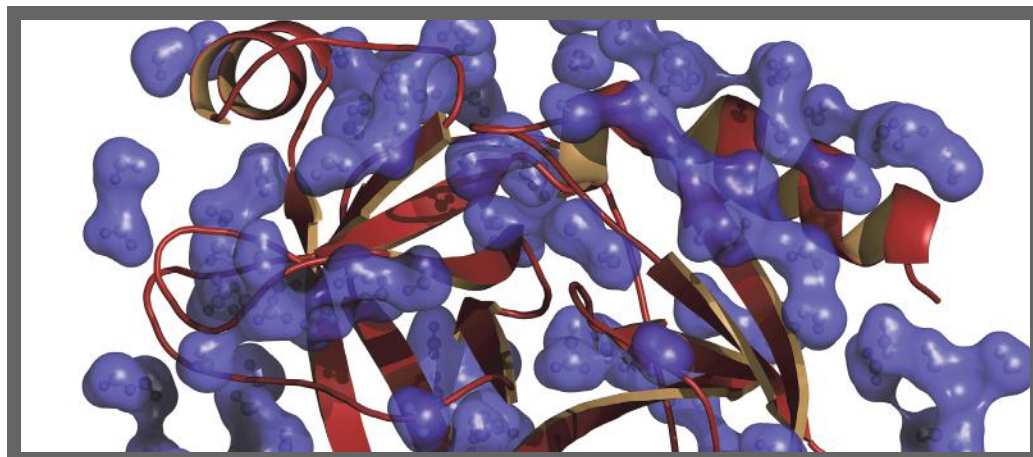
[Measure A205 Proteins](#)

[Reported Results](#)

[Settings](#)

[Detection Limits](#)

[Calculations](#)



## Measure Protein Concentration at A205

Use the Protein A205 application to quantify purified peptides and other proteins that contain peptide bonds, which exhibit absorbance at 205 nm. This application reports protein concentration and two absorbance values (A205 and A280). A single-point baseline correction can also be used. This application does not require a standard curve.

**Note** If your samples contain mainly amino acids such as tryptophan or tyrosine, or cys-cys disulfide bonds, use the [Protein A280](#) application instead of Protein A205.

## To measure Protein A205 samples

### NOTICE

- Do not use a squirt or spray bottle on or near the instrument as liquids will flow into the instrument and may cause permanent damage.
- Do not use hydrofluoric acid (HF) on the pedestals. Fluoride ions will permanently damage the quartz fiber optic cables.

**Before you begin...**

Before taking pedestal measurements with the NanoDrop One instrument, lift the instrument arm and clean the upper and lower pedestals. At a minimum, wipe the pedestals with a new laboratory wipe. For more information, see [Cleaning the Pedestals](#).

**❖ To measure a Protein A205 sample**

1. From the Home screen, select the **Proteins** tab and then tap **Protein A205**.
2. Specify a [sample type](#) and [baseline correction](#) if desired.
3. Pipette 1–2  $\mu\text{L}$  of the blanking solution onto the lower pedestal and lower the arm, or insert the blanking cuvette into the cuvette holder.

**Tip:** If using a cuvette, make sure to [align the cuvette light path](#) with the instrument light path.

4. Tap **Blank** and wait for the measurement to complete.

**Tip:** If [Auto-Blank](#) is On, the blank measurement starts automatically after you lower the arm. (This option is not available for cuvette measurements.)

5. Lift the arm and clean both pedestals with a new laboratory wipe, or remove the blanking cuvette.
6. Pipette 2  $\mu\text{L}$  sample solution onto the pedestal and lower the arm, or insert the sample cuvette into the cuvette holder.
7. Start the sample measurement:
  - Pedestal: If [Auto-Measure](#) is On, lower arm; if Auto-Measure is off, lower arm and tap **Measure**.
  - Cuvette: Tap **Measure**

When the sample measurement is completed, the spectrum and reported values are displayed (see the next section).

8. When you are finished measuring samples, tap **End Experiment**.
9. Lift the arm and clean both pedestals with a new wipe, or remove the sample cuvette.

**Related Topics**

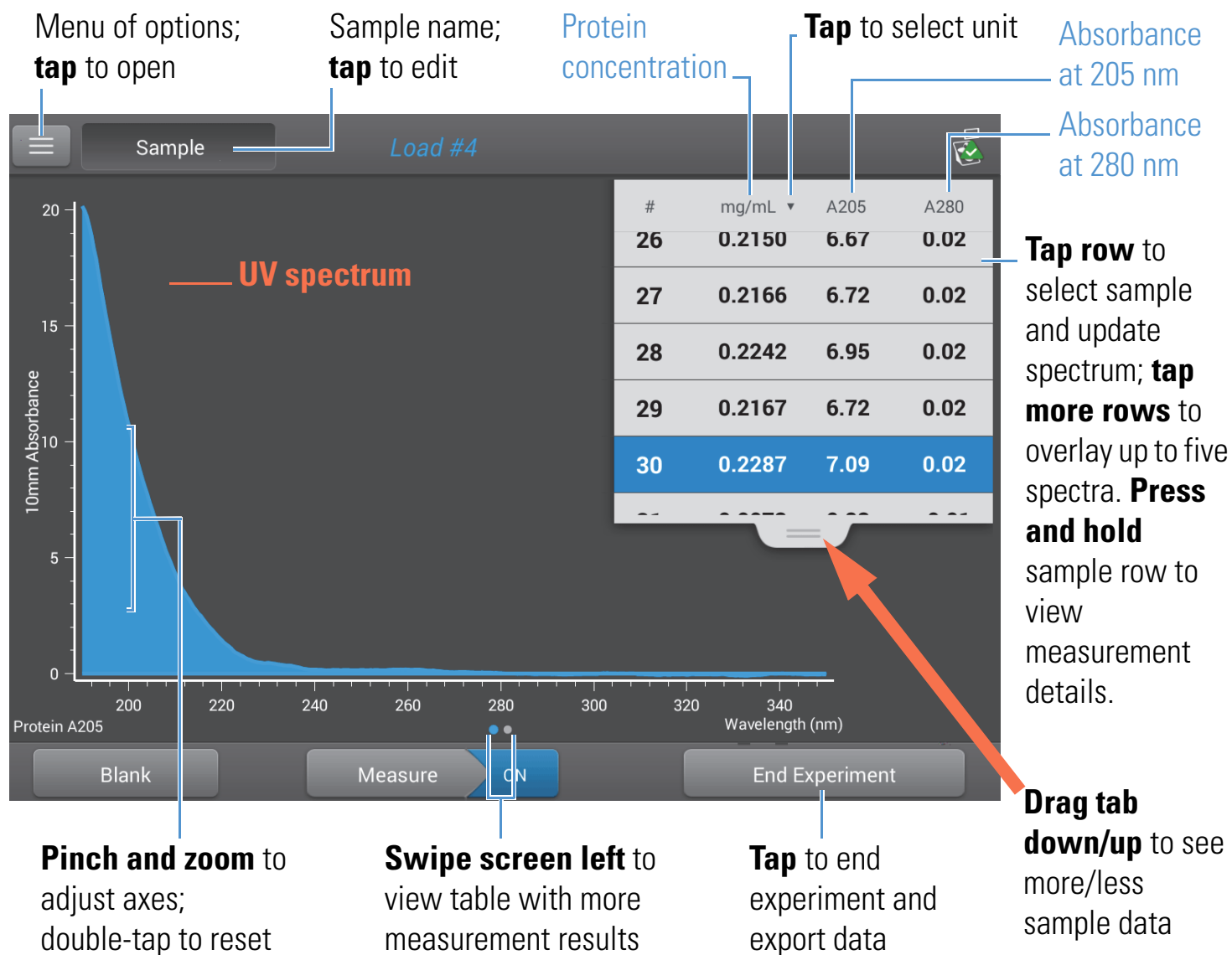
- [Best Practices for Protein Measurements](#)
- [Measure a Micro-Volume Sample](#)
- [Measure a Sample Using a Cuvette](#)

- Prepare Samples and Blanks
  - Basic Instrument Operations
- 

## Protein A205 Reported Results

### Protein A205 measurement screen

For each measured sample, this application shows the absorbance spectrum and a summary of the results. Here is an example:

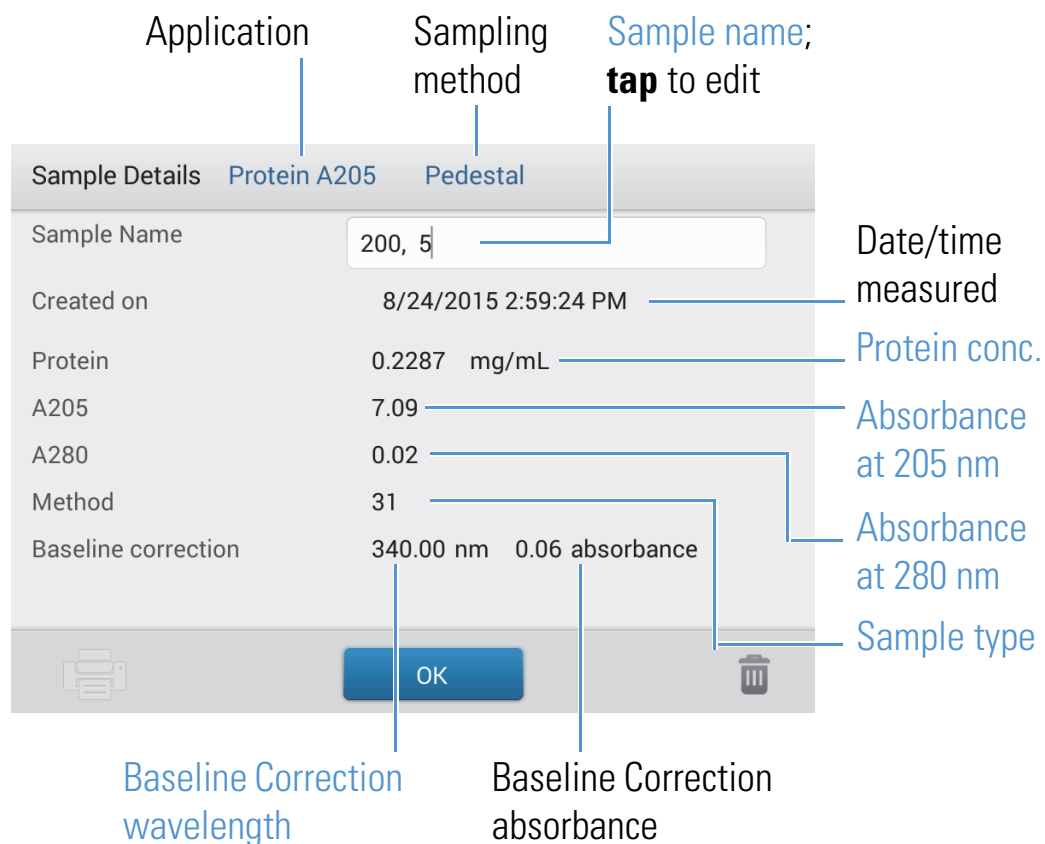


**Note** Micro-volume absorbance measurements and measurements taken with nonstandard cuvettes are normalized to a 10.0 mm pathlength equivalent.



## Protein A205 reported values


The initial screen that appears after each measurement (see previous image) shows a summary of the reported values. To view all reported values, press and hold the sample row. Here is an example:



### Related Topics

- [Basic Instrument Operations](#)
- [Protein A205 Calculations](#)

## Settings for Protein A205 Measurements

To show the Protein A205 settings, from the Protein A205 measurement screen, tap  > **Protein A205 Setup**.

Setting	Available Options	Mass Ext. Coefficient (L/gm-cm)	Description
Sample type	31	31	Assumes $\epsilon$ 0.1% (1 mg/mL) at 205 nm = 31
	Scopes	$27 + 120 * (A280/A205)$	Assumes $\epsilon$ 0.1% (1 mg/mL) at 205 nm = $27 + 120 * (A280/A205)$
	Other protein ( $\epsilon$ 1%)	User entered mass extinction coefficient	Assumes protein has known mass extinction coefficient ( $\epsilon$ ). Enter mass extinction coefficient in L/gm-cm for 1 mg/mL ( $\epsilon$ 0.1%) protein solution.
Baseline Correction	On or off  Enter baseline correction wavelength in nm or use default value (340 nm)	N/A	<p>Corrects for any offset caused by light scattering particulates by subtracting measured absorbance at specified baseline correction wavelength from absorbance values at all wavelengths in sample spectrum. As a result, absorbance of sample spectrum is zero at specified baseline correction wavelength.</p> <p><b>Tip:</b> If the sample has a modification that absorbs light at 340 nm, select a different correction wavelength or turn off Baseline Correction.</p>

### Related Topics

- [Instrument Settings](#)

## Calculations for Protein A205 Measurements

As with the other protein applications, Proteins A205 uses the [Beer-Lambert equation](#) to correlate absorbance with concentration based on the sample's extinction coefficient and pathlength.

This application offers three options (shown at right) for selecting an appropriate extinction coefficient for each measured sample, to be used in conjunction with Beer's Law to calculate sample concentration.

If the extinction coefficient of the sample is known, choose the **ε1%** (mass) option and enter the value. Otherwise, calculate the extinction coefficient or choose the option that best matches the sample solution.

**Tip:** Ideally, the extinction coefficient should be determined empirically using a solution of the study protein at a known concentration using the same buffer.

Calculated protein concentrations are based on the absorbance value at 205 nm, the selected (or entered) extinction coefficient and the sample pathlength. A single-point baseline correction may also be applied.

Concentration is reported in mass units. Calculators are available on the Internet to convert concentration from mass to molar units based on the sample sequence.

### Available Options for Extinction Coefficient

- **31**, assumes **ε0.1%** (1 mg/mL) at 205 nm = 31
- **Scopes**, assumes **ε0.1%** (1 mg/mL) at 205 nm = 27 + 120 \* (A280/A205)
- **Other protein**, enter mass extinction coefficient in L/gm-cm for 1 mg/mL (**ε0.1%**) protein solution

**Note:** See [Sample Type](#) for details.

### Measured Values

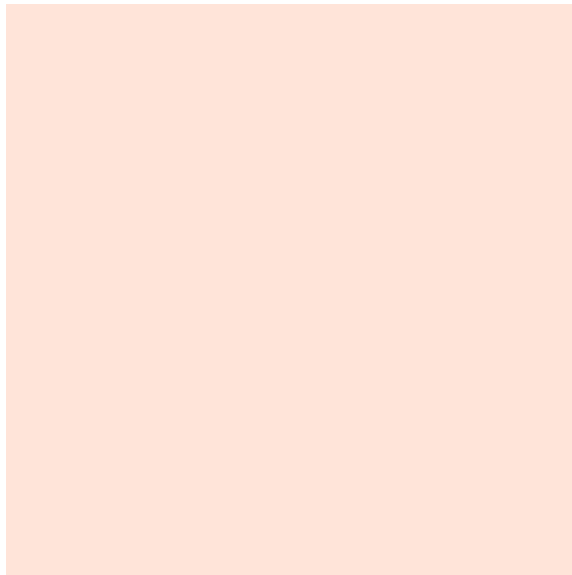
#### A205 absorbance

**Note:** For micro-volume absorbance measurements and measurements taken with nonstandard (other than 10 mm) cuvettes, the spectra are normalized to a 10 mm pathlength equivalent.

- Protein absorbance values are measured at 205 nm using the normalized spectrum. If Baseline Correction is not selected, this is the reported A205 value and the value used to calculate protein concentration.
- If [Baseline Correction](#) is selected, the normalized and baseline-corrected absorbance value at 205 nm is reported and used to calculate protein concentration.

#### A280 absorbance

- Normalized and baseline-corrected (if selected) absorbance value at 280 nm is also reported.



### Sample Pathlength

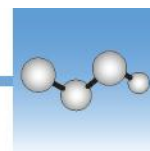
- For micro-volume measurements, the software selects the optimal pathlength (between 1.0 mm and 0.03 mm) based on sample absorbance at the analysis wavelength.
- For cuvette measurements, pathlength is determined by the cuvette Pathlength setting in the software (see [General Settings](#)).
- Displayed spectra and absorbance values are normalized to a 10 mm pathlength equivalent.

### Reported Values

- **Protein concentration.** Reported in selected unit (mg/mL or  $\mu\text{g/mL}$ ). Calculations are based on Beer-Lambert equation using corrected protein absorbance value.

### Related Topics

- [Beer-Lambert Equation](#)
- [Protein A280 Calculations](#)



## Measure Protein BCA

Measures total protein concentration of unpurified protein samples using a bicinchoninic acid colorimetric detection reagent.

[Measure Total Protein](#)

[Reported Results](#)

[Settings](#)

[Detection Limits](#)



## Measure Total Protein Concentration

The Protein BCA assay uses bicinchoninic acid as a colorimetric detection reagent to determine total protein concentration in unpurified protein samples. This application is useful for measuring dilute protein solutions or proteins in the presence of components that exhibit significant absorbance between 200 nm and 280 nm, which rules out direct protein measurements at 280 nm or 205 nm. This application measures absorbance at 562 nm and uses a standard curve to calculate protein concentration. A single-point baseline correction is applied.

### Theory of Protein BCA assay

The Protein BCA assay uses bicinchoninic acid (BCA) as the detection reagent for  $\text{Cu}^{+1}$ , which is formed when  $\text{Cu}^{+2}$  is reduced by certain proteins in an alkaline environment. A purple reaction product is formed by the chelation of two molecules of BCA with one cuprous ion ( $\text{Cu}^{+1}$ ). The resulting Cu-BCA chelate formed in the presence of protein is measured at 562 nm and baseline-corrected using the absorbance value at 750 nm. Pre-formulated kits of BCA reagent and  $\text{CuSO}_4$  are available from us or a local distributor.

## Protein assay kits and protocols

Please refer to the NanoDrop website for up-to-date kits and protocols for the NanoDrop One instruments. Follow the assay kit manufacturer's recommendations for all standards and samples (unknowns). Ensure each is subjected to the same timing and temperature throughout the assay.

Protein standards for generating a standard curve may also be provided by the kit manufacturer. Since the NanoDrop One pedestals can measure higher protein concentrations than traditional cuvette-based spectrophotometers, you may need to supply your own protein standards at higher concentrations than provided by the manufacturer. For example, additional standards may be required to ensure the standard curve covers the dynamic range of the assay and the expected range of the unknown samples.

## Working with standard curves

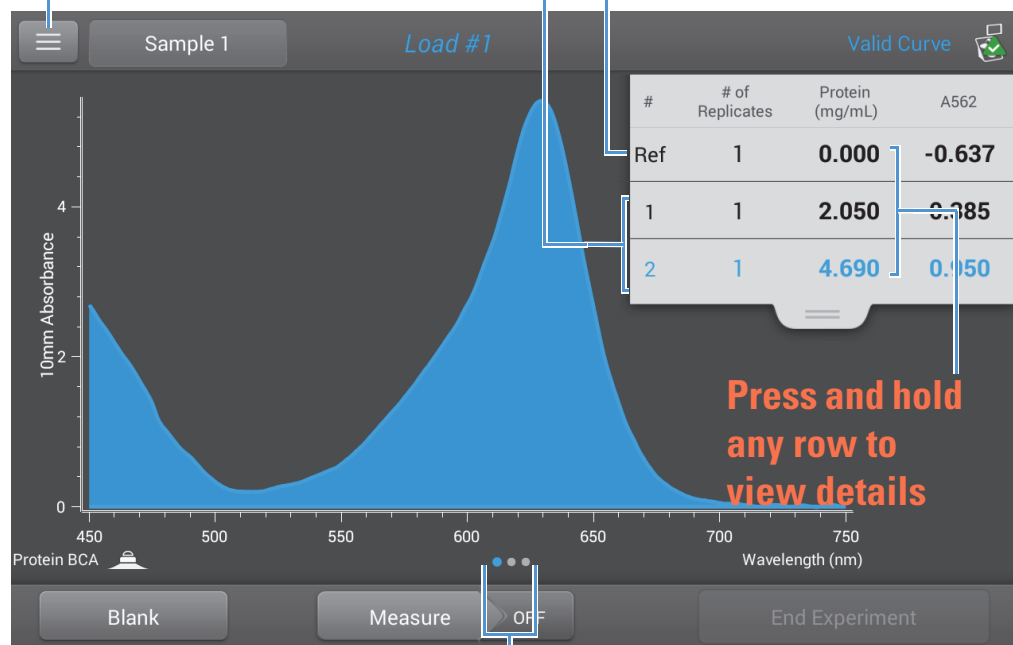
A standard curve is required for colorimetric protein analysis.

- Each experiment requires a new standard curve.
- Prepare standards and unknown samples the same way. See the kit manufacturer's guidelines and recommendations.
  - **All reference and standards solutions** should be the same buffer used to resuspend the samples plus the same volume of reagent added to the samples.
  - **First standard** is a reference measurement. The reference solution should contain none of the analyte of interest. (The reference measurement is not the same as a blank measurement. This application requires both.)
  - **Concentration range of the standards** must cover the dynamic range of the assay and the expected range of the unknown samples. Sample analyte concentrations are not extrapolated beyond the concentration of the highest standard.
- Use the application setup screen to enter concentration values for the standards and to specify how standards and samples will be measured (number of replicates, etc.).
  - Depending on the [Curve Type](#) setting, a standard curve can be generated using two or more standards.
  - The software **requires one reference measurement** and allows **up to 7 standards**.
  - **Concentration values for standards** can be entered in any order but the standards must be measured in the order in which they were entered; however, best practice dictates that standards be measured from the lowest concentration of the standard analyte stock to the highest.

- For all colorimetric assays except Protein Pierce 660, **blank the instrument** with DI H<sub>2</sub>O (deionized water). For Protein Pierce 660, blank with the reference solution (see below).
- **Measure the reference and all standards** before you start analyzing samples. (After the first sample has been measured, no additional changes are allowed to the standard curve.)

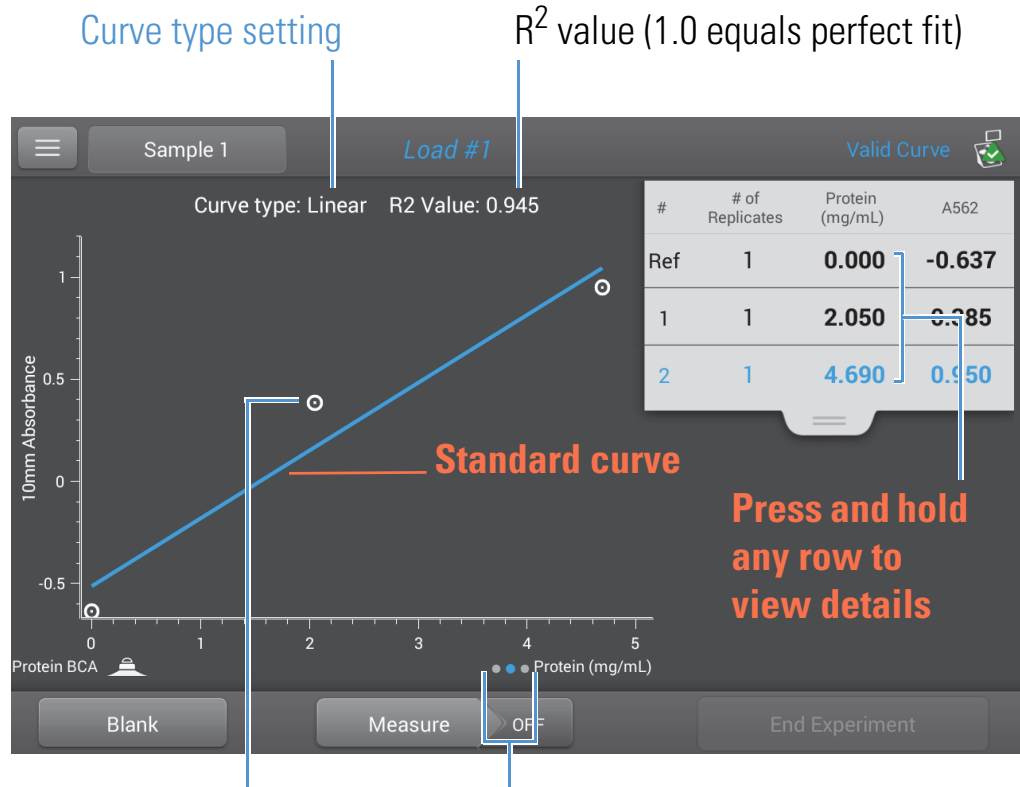
As you measure the standards, a measurement screen appears, similar to the measurement screens for samples.

Menu; **tap** Standard concentrations and absorbance values Reference concentration and absorbance value



**Swipe left one screen**  
to view standard curve

Swipe left one screen to see the standard curve as you build it. Here is an example:



White circles indicate data points for standards

Swipe left one screen to view data table for standards

The  $R^2$  value indicates how well the standard curve fits the standard data points (1.0 is a perfect fit; all points lie exactly on the curve).



**Swipe left one screen** to see the data table for the standards. Here is an example:

#	# of Replicates	Standard Name	Protein (mg/mL)	A562
Ref	1	Reference	0.000	-0.637
1	1	Standard	2.050	0.385
2	1	Standard	4.690	0.950

**Press and hold any row to view details**

Protein BCA

Blank Measure OFF End Experiment

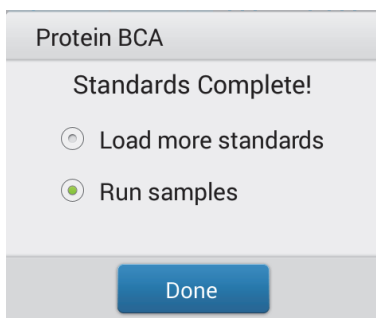
**Press and hold** a row in any of the previous screens to view details about an individual standard. Here is an example:

Standard Details	Protein BCA	Pedestal
Standard Name	Standard	
Created on	9/30/2015 6:58:37 PM	
Protein (mg/mL):	4.690	
A562:	0.950	
R2 Value:	0.945	

**Tap to delete this measurement**

OK

After the minimum number of standards has been measured for the selected curve type, a message similar to the following appears:




**Load more standards:** returns to the setup screen where you can add or edit the concentration value for any standard and then measure the standard.


**Run samples:** continues to sample measurement screen, after which standards can no longer be edited.

- You can add, edit or delete a standard any time before the first sample measurement.


### Add standard

- from standards measurement screen, tap  > [application name] Setup
- tap the next empty Concentration field and enter the concentration value for the new standard
- tap **Done**

### Edit standard

- from standards measurement screen, tap  > [application name] Setup
- tap the Concentration field and edit the concentration value
- tap **Done**

### Delete standard

- from standards measurement screen, standard curve screen, or standards data table, press and hold the row to show Standard Details box
- tap 

The standard no longer appears in the table on the measurement screen and its concentration value no longer appears on the setup screen.

**Note** You can use this method to delete the reference measurement; however, a new reference must be measured immediately afterwards.

- After the minimum number of standards has been measured for the selected curve type, the message “Invalid Curve” changes to “Valid Curve.” (This occurs even when additional standards have been defined but not yet measured.) If the “Invalid Curve” message remains after all entered standards have been measured, try:
  - selecting a different curve type
  - remeasuring standards using the correct standard material

**Valid Curve indicator:** This is only an indicator that the required minimum number of points has been established for the selected curve type. It does not validate the integrity of the curve. For example, additional standards may be required to cover the expected assay concentration range.

## To measure Protein BCA standards and samples

### NOTICE

- Do not use a squirt or spray bottle on or near the instrument as liquids will flow into the instrument and may cause permanent damage.
- Do not use hydrofluoric acid (HF) on the pedestals. Fluoride ions will permanently damage the quartz fiber optic cables.

### Before you begin...

Before taking pedestal measurements with the NanoDrop One instrument, lift the instrument arm and clean the upper and lower pedestals. At a minimum, wipe the pedestals with a new laboratory wipe. For more information, see [Cleaning the Pedestals](#).

### ❖ To measure Protein BCA standards and samples

1. From the Home screen, select the **Proteins** tab and tap **Protein BCA**.
2. Specify a [curve type](#) and number of [replicates for each standard](#) and enter the [concentration of each standard](#).

**Tip:** For this assay, we recommend setting **Curve Type** to “Linear”.

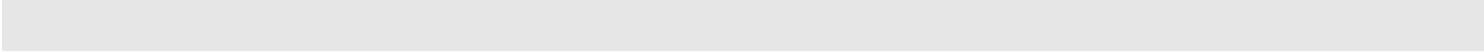
3. Measure blank:
  - pipette 2 µL DI H<sub>2</sub>O onto lower pedestal and lower arm, or insert DI H<sub>2</sub>O blanking cuvette into cuvette holder

**Tip:** If using a cuvette, make sure to [align cuvette light path](#) with instrument light path.

- tap **Blank** and wait for measurement to complete
  - lift arm and clean both pedestals with new laboratory wipe, or remove cuvette
4. Measure reference standard:
- pipette 2  $\mu$ L reference solution onto pedestal, or insert reference cuvette (reference solution should contain none of the standard protein stock, see [Working With Standard Curves](#) for details)
  - lower arm to start measurement (or tap **Measure** if Auto-Measure is off)
  - lift arm and clean both pedestals with new wipe, or remove cuvette
  - if Replicates setting is greater than 1, repeat measurement
5. Measure remaining standards:
- pipette 2  $\mu$ L standard 1 onto pedestal, or insert standard 1 cuvette
  - lower arm to start measurement (or tap **Measure** if Auto-Measure is off)
  - lift arm and clean both pedestals with new wipe, or remove cuvette
  - if Replicates setting is greater than 1, repeat measurement
  - repeat substeps above for each additional standard (when specified number of standards and replicates have been measured, a message asks whether to load more standards or begin measuring samples)
  - if finished measuring standards, tap **Done** (swipe left to view standard curve)
6. Measure samples:
- pipette 2  $\mu$ L sample 1 onto pedestal, or insert sample 1 cuvette
  - lower arm to start measurement (or tap **Measure** if Auto-Measure is off)
  - lift arm and clean both pedestals with new wipe, or remove cuvette
  - if Replicates setting is greater than 1, repeat measurement
7. When you are finished measuring samples, tap **End Experiment**.
8. Lift the arm and clean both pedestals with a new wipe, or remove the sample cuvette.

### Related Topics

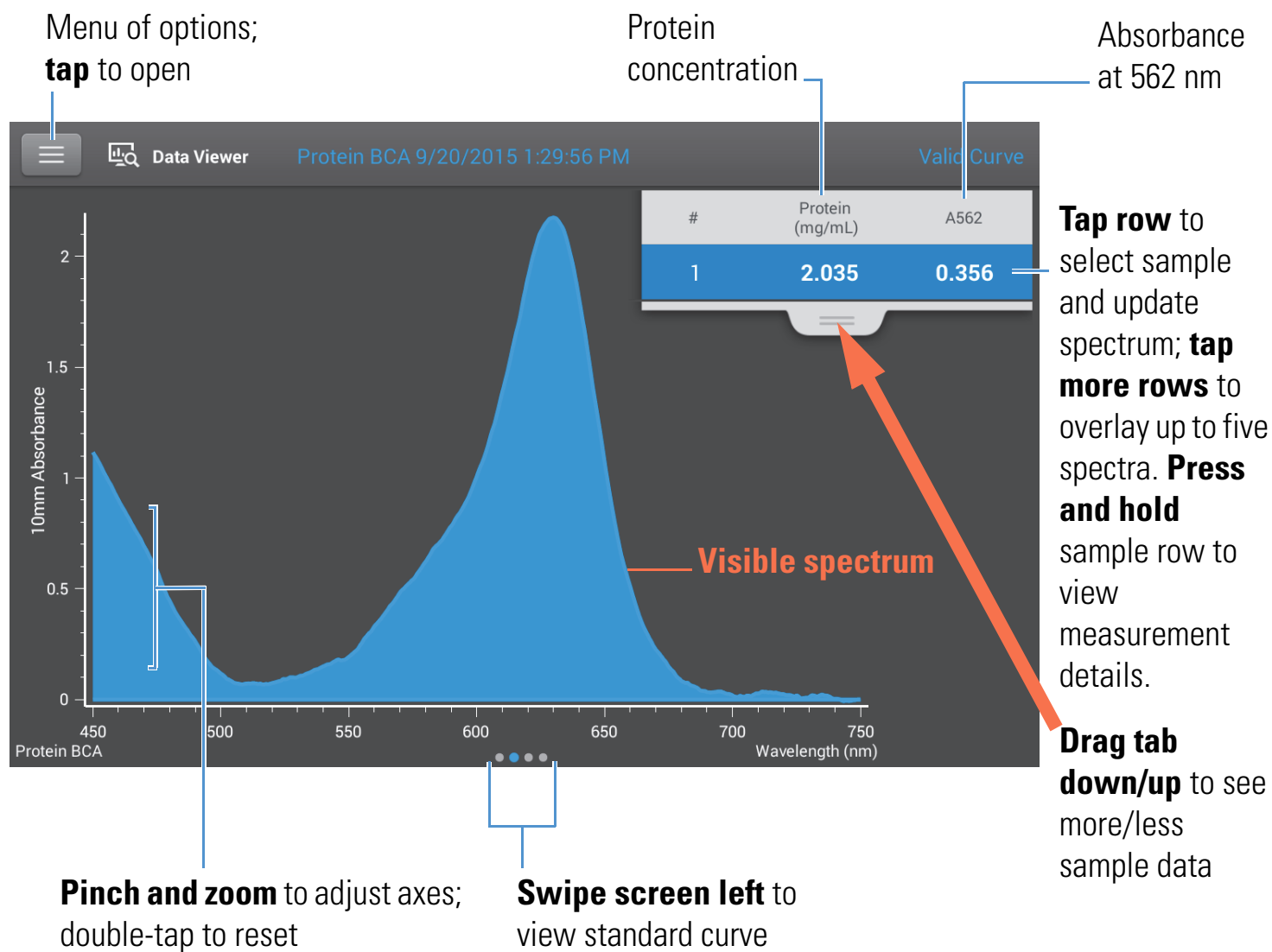
- [Best practices for protein measurements](#)
- [Measure a Micro-Volume Sample](#)
- [Measure a Sample Using a Cuvette](#)

- Prepare Samples and Blanks
  - Basic Instrument Operations
- 

## Protein BCA Reported Results

### Protein BCA measurement screen (shown from Data Viewer)

For each measured sample and standard, this application shows the visible absorbance spectrum and a summary of the results. The standard curve is also available by swiping left from the measurement screen (or in the [Data Viewer](#) as shown below).



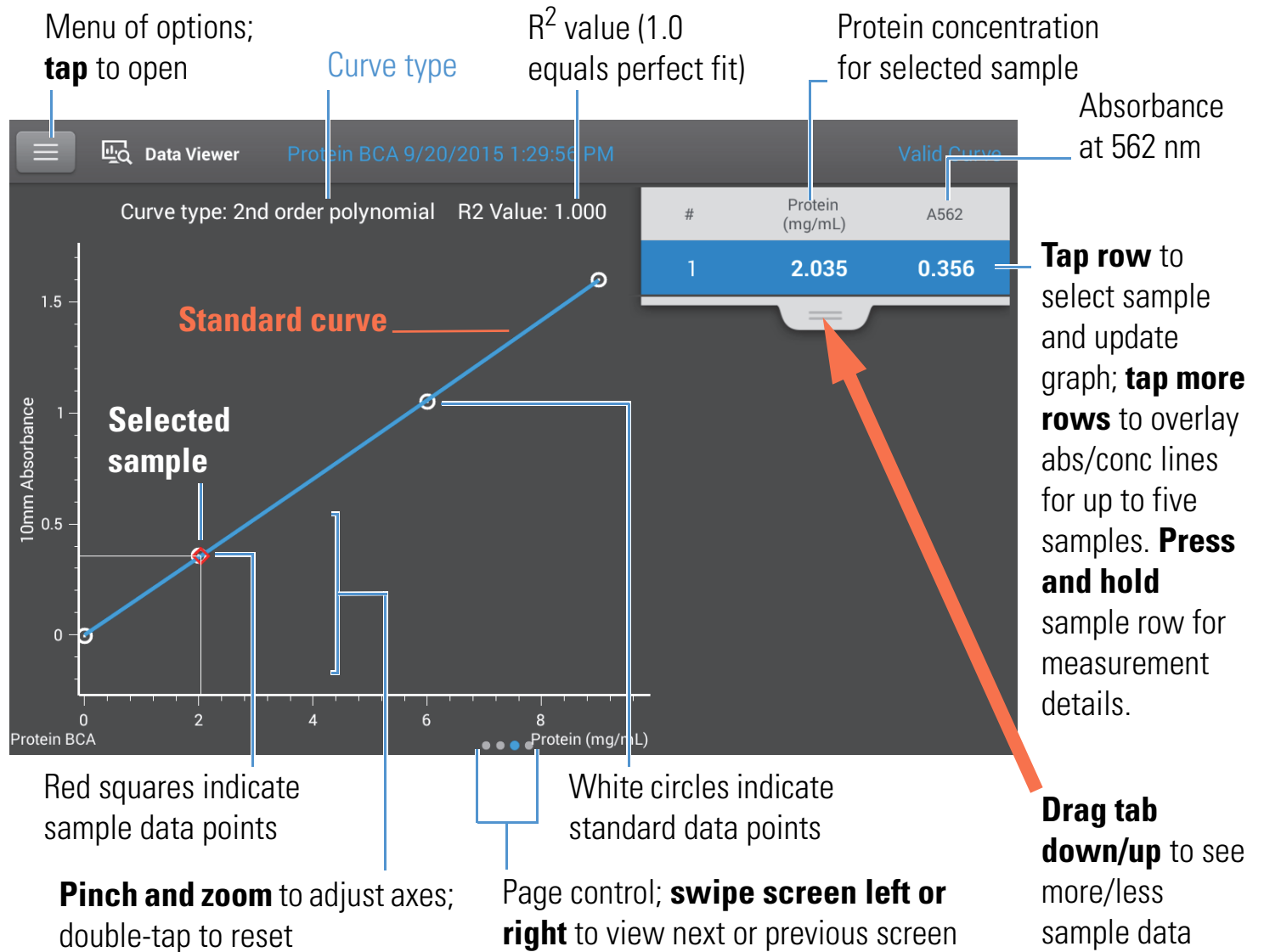
**Note**

- A baseline correction is performed at 750 nm (absorbance value at 750 nm is subtracted from absorbance values at all wavelengths in sample spectrum).
- Micro-volume absorbance measurements and measurements taken with nonstandard cuvettes are normalized to a 10.0 mm pathlength equivalent.

## Protein BCA standard curve screen

The standard curve screen shows graphically the relationship between the measured standards, the calculated standard curve, and the measured absorbance and calculated concentration for a selected sample. A horizontal line connects the sample absorbance value on the Y-axis to the standard curve. A vertical line connects that point to the sample concentration value on the X-axis.

The  $R^2$  value indicates how well the standard curve fits the standard data points (1.0 is a perfect fit; that is, all points lie exactly on the curve).





## Protein BCA reported values

The initial screen that appears after each measurement and the standards screen (see previous image) show a summary of the reported values. To view all reported values, press and hold the sample row. Here is an example:

The screenshot shows a 'Sample Details' screen with the following data and annotations:

Field	Value	Annotation
Sample Name	Sample 1	Sample name; tap to edit
Created on	9/20/2015 6:29:56 PM	Date/time measured
Protein (mg/mL):	2.035	Protein conc.
A562:	0.356	Absorbance at 562 nm
Baseline correction	750.00 nm 0.04 absorbance	Baseline correction wavelength (750.00 nm) and Baseline correction absorbance (0.04)

Additional annotations on the screen include 'Sampling method' pointing to 'Pedestal' and 'OK' button.

### Related Topics

- [Basic Instrument Operations](#)
- [Protein A280 Calculations](#)

## Settings for Protein BCA Measurements

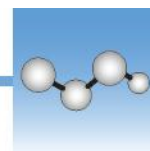
To show the Protein BCA settings, from the Protein BCA measurement screen, tap  > **Protein BCA Setup**.

**Note** You can edit the Curve Type setting when measuring standards by changing the list box at the top of the application measurement screen. You can edit the concentration value for a standard from the application setup screen. After the first sample measurement, these settings cannot be changed.

Setting	Description
Curve Type	Specify type of equation used to create standard curve from standard concentration values. Available options: <ul style="list-style-type: none"> <li>– <b>Linear:</b> Draws the linear least squares line through all measured standards (requires reference measurement and at least one standard)</li> <li>– <b>Interpolation:</b> Draws a series of straight lines to connect all measured standards (requires reference measurement and at least one standard)</li> <li>– <b>2<sup>nd</sup> order polynomial:</b> Draws the 2<sup>nd</sup> order least squares polynomial using all measured standards (requires reference measurement and at least two standards)</li> <li>– <b>3<sup>rd</sup> order polynomial:</b> Draws the 3<sup>rd</sup> order least squares polynomial using all measured standards (requires reference measurement and at least three standards)</li> </ul>
Replicates	Enter number of measurements of the reference or the same standard or sample that are averaged together to produce its associated concentration value.  <b>Note:</b> Replicates setting cannot be changed after the first standard has been measured.
Standards	Enter actual concentration value of each standard.  <b>Note:</b> Concentration values can be entered in any order but the standards must be measured in the order they were entered.

### Related Topics

- [Instrument Settings](#)



## Measure Protein Bradford

Measures total protein concentration of unpurified protein samples using a Coomassie Blue dye colorimetric detection reagent.

[Measure Total Protein](#)

[Reported Results](#)

[Settings](#)

[Detection Limits](#)



## Measure Total Protein Concentration

The Protein Bradford assay uses Coomassie Blue dye as a colorimetric detection reagent to determine total protein concentration in unpurified protein samples. This application is useful for measuring dilute protein solutions that require lower detection sensitivity or proteins in the presence of components that exhibit significant absorbance between 200 nm and 280 nm, which rules out direct protein measurements at 280 nm or 205 nm. This application measures absorbance at 595 nm and uses a standard curve to calculate protein concentration. See [Working with Standard Curves](#) for more information. A single-point baseline correction is applied.

### Theory of Protein Bradford assay

The Protein Bradford assay uses the protein-induced absorbance shift of Coomassie Blue dye to determine total protein concentration. The bound protein-dye complex is measured at 595 nm and baseline-corrected using the absorbance value at 750 nm. Pre-formulated kits of stabilized reagent mixture containing Coomassie Blue dye, alcohol, and surfactant are available from us or a local distributor.

To maximize reliability with the Protein Bradford assay:

- **Work quickly and do not allow prepared standards or samples to sit longer than necessary.** Coomassie dye-dye and Coomassie dye-protein aggregates can form particulates with increasing development time, resulting in significant fluctuations in absorbance readings.
- **Measure standards and samples in triplicate** using a new aliquot for each measurement. For pedestal measurements, the total analyte (protein-dye) signal at 595 nm is limited to ~0.150A due to the pedestal's 1.0 mm pathlength, the Coomassie dye concentration, and the acidic pH.

**Note** If you have a NanoDrop One<sup>C</sup> model instrument, using the cuvette option will result in a higher absorbance signal.

## Protein assay kits and protocols

Please refer to the NanoDrop website for up-to-date kits and protocols for the NanoDrop One instruments. Follow the assay kit manufacturer's recommendations for all standards and samples (unknowns). Ensure each is subjected to the same timing and temperature throughout the assay.

Protein standards for generating a standard curve may also be provided by the kit manufacturer. Since the NanoDrop One pedestals can measure higher protein concentrations than traditional cuvette-based spectrophotometers, you may need to supply your own protein standards at higher concentrations than provided by the manufacturer. For example, additional standards may be required to ensure the standard curve covers the dynamic range of the assay and the expected range of the unknown samples.

## To measure Protein Bradford standards and samples

### NOTICE

- Do not use a squirt or spray bottle on or near the instrument as liquids will flow into the instrument and may cause permanent damage.
- Do not use hydrofluoric acid (HF) on the pedestals. Fluoride ions will permanently damage the quartz fiber optic cables.

**Before you begin...**

Before taking pedestal measurements with the NanoDrop One instrument, lift the instrument arm and clean the upper and lower pedestals. At a minimum, wipe the pedestals with a new laboratory wipe. For more information, see [Cleaning the Pedestals](#).

**❖ To measure Protein Bradford standards and samples**

1. From the Home screen, select the **Proteins** tab and tap **Protein Bradford**.
2. Specify a [curve type](#) and number of [replicates for each standard](#) and enter the [concentration of each standard](#).

**Tip:** For this assay, set **Curve Type** to “2nd Order Polynomial” and **Replicates** to 3.

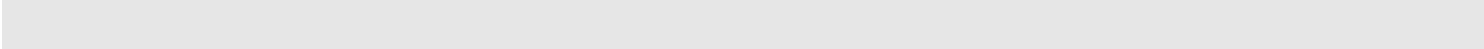
3. Measure blank:
  - pipette 2  $\mu\text{L}$  DI  $\text{H}_2\text{O}$  onto lower pedestal and lower arm, or insert DI  $\text{H}_2\text{O}$  blanking cuvette into cuvette holder

**Tip:** If using a cuvette, make sure to [align cuvette light path](#) with instrument light path.

- tap **Blank** and wait for measurement to complete
  - lift arm and clean both pedestals with new laboratory wipe, or remove cuvette
4. Measure reference standard:
- pipette 2  $\mu$ L reference solution onto pedestal, or insert reference cuvette (reference solution should contain none of the standard protein stock, see [Working With Standard Curves](#) for details)
  - lower arm to start measurement (or tap **Measure** if Auto-Measure is off)
  - lift arm and clean both pedestals with new wipe, or remove cuvette
  - if Replicates setting is greater than 1, repeat measurement
5. Measure remaining standards:
- pipette 2  $\mu$ L standard 1 onto pedestal, or insert standard 1 cuvette
  - lower arm to start measurement (or tap **Measure** if Auto-Measure is off)
  - lift arm and clean both pedestals with new wipe, or remove cuvette
  - if Replicates setting is greater than 1, repeat measurement
  - repeat substeps above for each additional standard (when specified number of standards and replicates have been measured, a message asks whether to load more standards or begin measuring samples)
  - if finished measuring standards, tap **Done** (swipe left to view standard curve)
6. Measure samples:
- pipette 2  $\mu$ L sample 1 onto pedestal, or insert sample 1 cuvette
  - lower arm to start measurement (or tap **Measure** if Auto-Measure is off)
  - lift arm and clean both pedestals with new wipe, or remove cuvette
  - if Replicates setting is greater than 1, repeat measurement
7. When you are finished measuring samples, tap **End Experiment**.
8. Lift the arm and clean both pedestals with a new wipe, or remove the sample cuvette.

### Related Topics

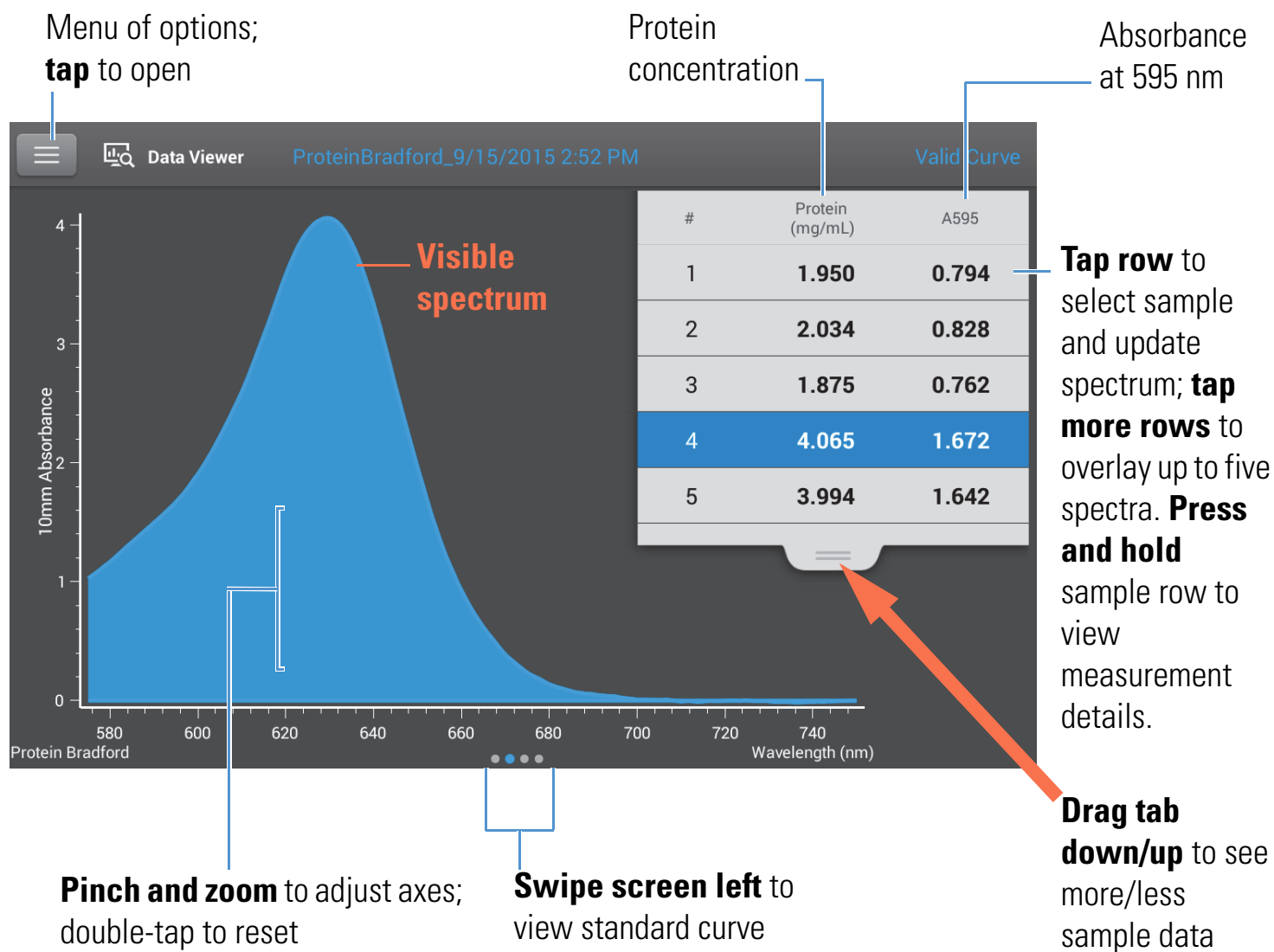
- [Working with standard curves](#)
- [Best practices for protein measurements](#)
- [Measure a Micro-Volume Sample](#)

- Measure a Sample Using a Cuvette
  - Prepare Samples and Blanks
  - Basic Instrument Operations
- 

## Protein Bradford Reported Results

### Protein Bradford measurement screen (shown from Data Viewer)

For each measured sample and standard, this application shows the visible absorbance spectrum and a summary of the results. The standard curve is also available by swiping left from the measurement screen (or in the [Data Viewer](#) as shown below).





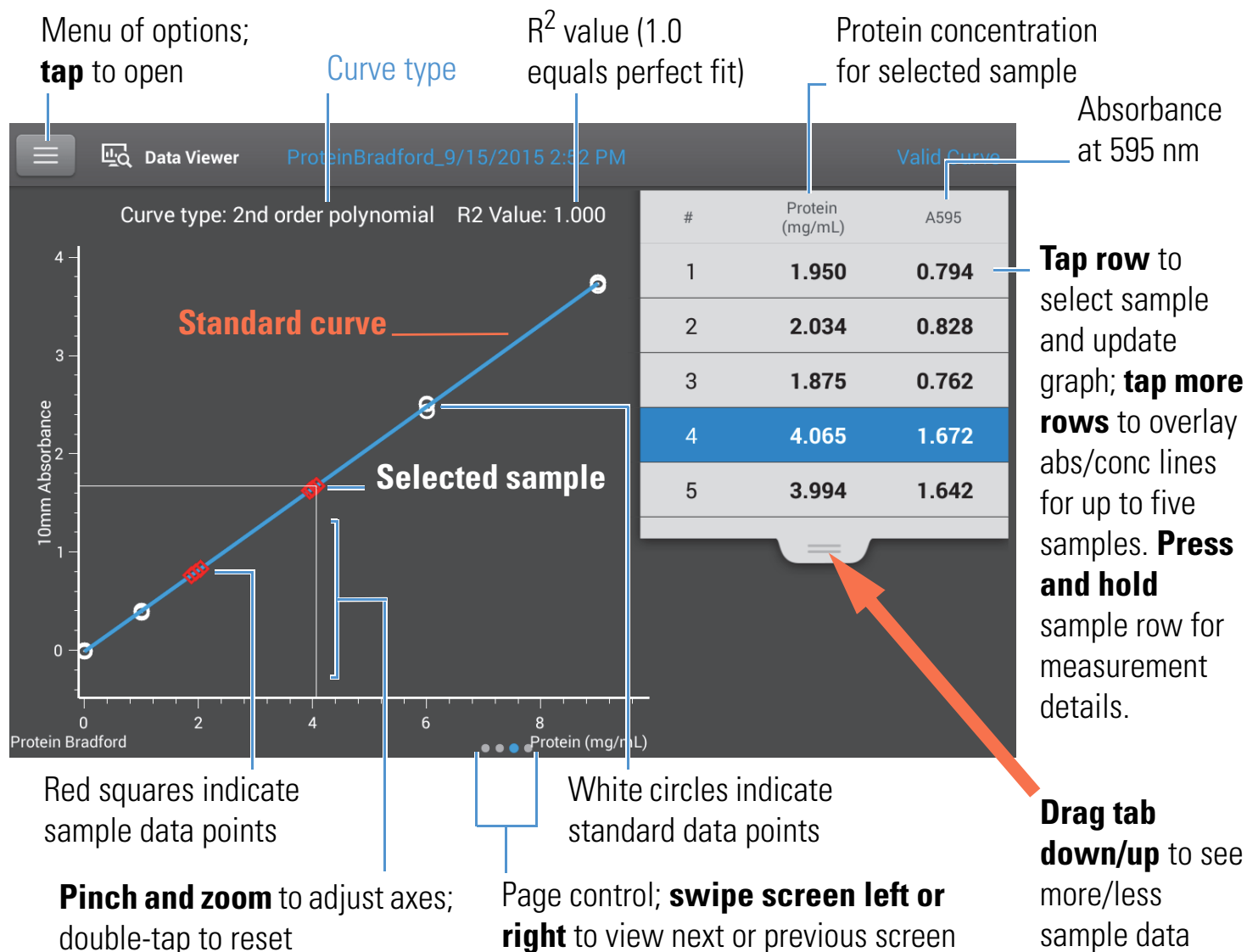
**Note**

- A baseline correction is performed at 750 nm (absorbance value at 750 nm is subtracted from absorbance values at all wavelengths in sample spectrum).
- Micro-volume absorbance measurements and measurements taken with nonstandard cuvettes are normalized to a 10.0 mm pathlength equivalent.

## Protein Bradford standard curve screen

The standard curve screen shows graphically the relationship between the measured standards, the calculated standard curve, and the measured absorbance and calculated concentration for a selected sample. A horizontal line connects the sample absorbance value on the Y-axis to the standard curve. A vertical line connects that point to the sample concentration value on the X-axis.

The  $R^2$  value indicates how well the standard curve fits the standard data points (1.0 is a perfect fit; that is, all points lie exactly on the curve).

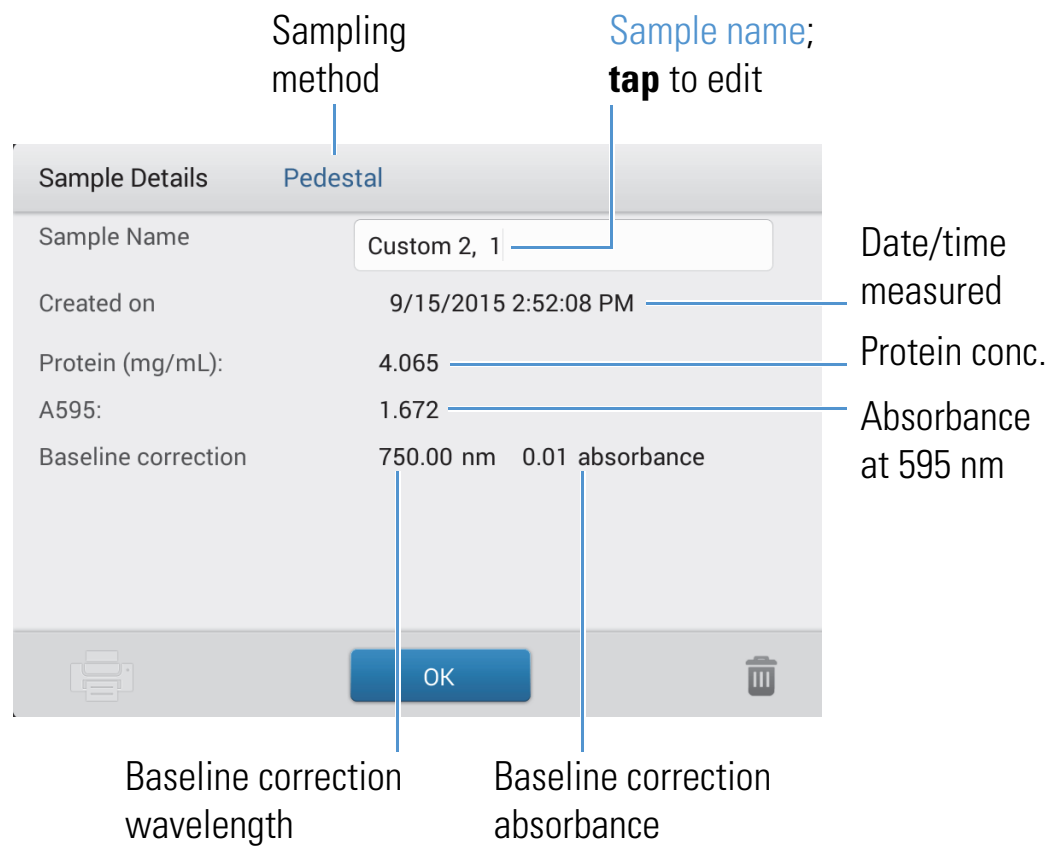


**Note**

- A baseline correction is performed at 750 nm (absorbance value at 750 nm is subtracted from absorbance values at all wavelengths in sample spectrum).
- Micro-volume absorbance measurements and measurements taken with nonstandard cuvettes are normalized to a 10.0 mm pathlength equivalent.

### Protein Bradford reported values


The initial screen that appears after each measurement and the standards screen (see previous image) show a summary of the reported values. To view all reported values, press and hold the sample row. Here is an example:



### Related Topics

- [Example standard curve](#)
- [Basic Instrument Operations](#)
- [Protein A280 Calculations](#)

## Settings for Protein Bradford Measurements

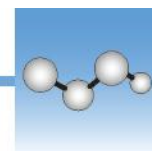
To show the Protein Bradford settings, from the Protein Bradford measurement screen, tap  > **Protein Bradford Setup**.

**Note** You can edit the Curve Type setting when measuring standards by changing the list box at the top of the application measurement screen. You can edit the concentration value for a standard from the application setup screen. After the first sample measurement, these settings cannot be changed.

Setting	Description
Curve Type	<p>Specify type of equation used to create standard curve from standard concentration values. Available options:</p> <ul style="list-style-type: none"> <li>– <b>Linear:</b> Draws the linear least squares line through all measured standards (requires reference measurement and at least one standard)</li> <li>– <b>Interpolation:</b> Draws a series of straight lines to connect all measured standards (requires reference measurement and at least one standard)</li> <li>– <b>2<sup>nd</sup> order polynomial:</b> Draws the 2<sup>nd</sup> order least squares polynomial using all measured standards (requires reference measurement and at least two standards)</li> <li>– <b>3<sup>rd</sup> order polynomial:</b> Draws the 3<sup>rd</sup> order least squares polynomial using all measured standards (requires reference measurement and at least three standards)</li> </ul>
Replicates	<p>Enter number of measurements of the reference or the same standard or sample that are averaged together to produce its associated concentration value.</p> <p><b>Note:</b> Replicates setting cannot be changed after the first standard has been measured.</p>
Standards	<p>Enter actual concentration value of each standard.</p> <p><b>Note:</b> Concentration values can be entered in any order but the standards must be measured in the order they were entered.</p>

### Related Topics

- [Instrument Settings](#)



## Measure Protein Lowry

Measures total protein concentration of unpurified protein samples using a Folin-Ciocalteu colorimetric detection reagent.

[Measure Total Protein](#)

[Reported Results](#)

[Settings](#)

[Detection Limits](#)



## Measure Total Protein Concentration

The Protein Lowry assay uses Folin-Ciocalteu as a colorimetric detection reagent to determine total protein concentration in unpurified protein samples. This application is an alternative to the other colorimetric applications for measuring dilute protein solutions or proteins in the presence of components that exhibit significant absorbance between 200 nm and 280 nm. This application measures absorbance at 650 nm and uses a standard curve to calculate protein concentration. See [Working with Standard Curves](#) for more information. A single-point baseline correction is applied.

### Theory of Protein Lowry assay

The Protein Lowry assay involves the reaction of protein with cupric sulfate in alkaline solution, resulting in the formation of tetradentate copper-protein complexes. The Folin-Ciocalteu reagent is effectively reduced in proportion to the chelated copper-complexes. The water-soluble blue reaction product is measured at 650 nm and baseline-corrected using the absorbance value at 405 nm. Pre-formulated kits of Folin-Ciocalteu reagent and  $\text{CuSO}_4$  are available from us or a local distributor.

## Protein assay kits and protocols

Follow the assay kit manufacturer's recommendations for all standards and samples (unknowns). Ensure each is subjected to the same timing and temperature throughout the assay.

### To measure Protein Lowry standards and samples

#### NOTICE

- Do not use a squirt or spray bottle on or near the instrument as liquids will flow into the instrument and may cause permanent damage.
- Do not use hydrofluoric acid (HF) on the pedestals. Fluoride ions will permanently damage the quartz fiber optic cables.

#### Before you begin...

Before taking pedestal measurements with the NanoDrop One instrument, lift the instrument arm and clean the upper and lower pedestals. At a minimum, wipe the pedestals with a new laboratory wipe. For more information, see [Cleaning the Pedestals](#).

#### ❖ To measure Protein Lowry standards and samples

1. From the Home screen, select the **Proteins** tab and tap **Protein Lowry**.
2. Specify a [curve type](#) and number of [replicates for each standard](#) and enter the [concentration of each standard](#).

**Tip:** For this assay, we recommend setting **Curve Type** to “2nd Order Polynomial.”

3. Measure blank:
  - pipette 2  $\mu\text{L}$  DI  $\text{H}_2\text{O}$  onto lower pedestal and lower arm, or insert DI  $\text{H}_2\text{O}$  blanking cuvette into cuvette holder

**Tip:** If using a cuvette, make sure to [align cuvette light path](#) with instrument light path.

- tap **Blank** and wait for measurement to complete
  - lift arm and clean both pedestals with new laboratory wipe, or remove cuvette
4. Measure reference standard:
- pipette 2  $\mu\text{L}$  reference solution onto pedestal, or insert reference cuvette (reference solution should contain none of the standard protein stock, see [Working With Standard Curves](#) for details)
  - lower arm to start measurement (or tap **Measure** if Auto-Measure is off)
  - lift arm and clean both pedestals with new wipe, or remove cuvette
  - if Replicates setting is greater than 1, repeat measurement
5. Measure remaining standards:
- pipette 2  $\mu\text{L}$  standard 1 onto pedestal, or insert standard 1 cuvette
  - lower arm to start measurement (or tap **Measure** if Auto-Measure is off)
  - lift arm and clean both pedestals with new wipe, or remove cuvette
  - if Replicates setting is greater than 1, repeat measurement
  - repeat substeps above for each additional standard (when specified number of standards and replicates have been measured, a message asks whether to load more standards or begin measuring samples)
  - if finished measuring standards, tap **Done** (swipe left to view standard curve)
6. Measure samples:
- pipette 2  $\mu\text{L}$  sample 1 onto pedestal, or insert sample 1 cuvette
  - lower arm to start measurement (or tap **Measure** if Auto-Measure is off)
  - lift arm and clean both pedestals with new wipe, or remove cuvette
  - if Replicates setting is greater than 1, repeat measurement
7. When you are finished measuring samples, tap **End Experiment**.
8. Lift the arm and clean both pedestals with a new wipe, or remove the sample cuvette.

### Related Topics

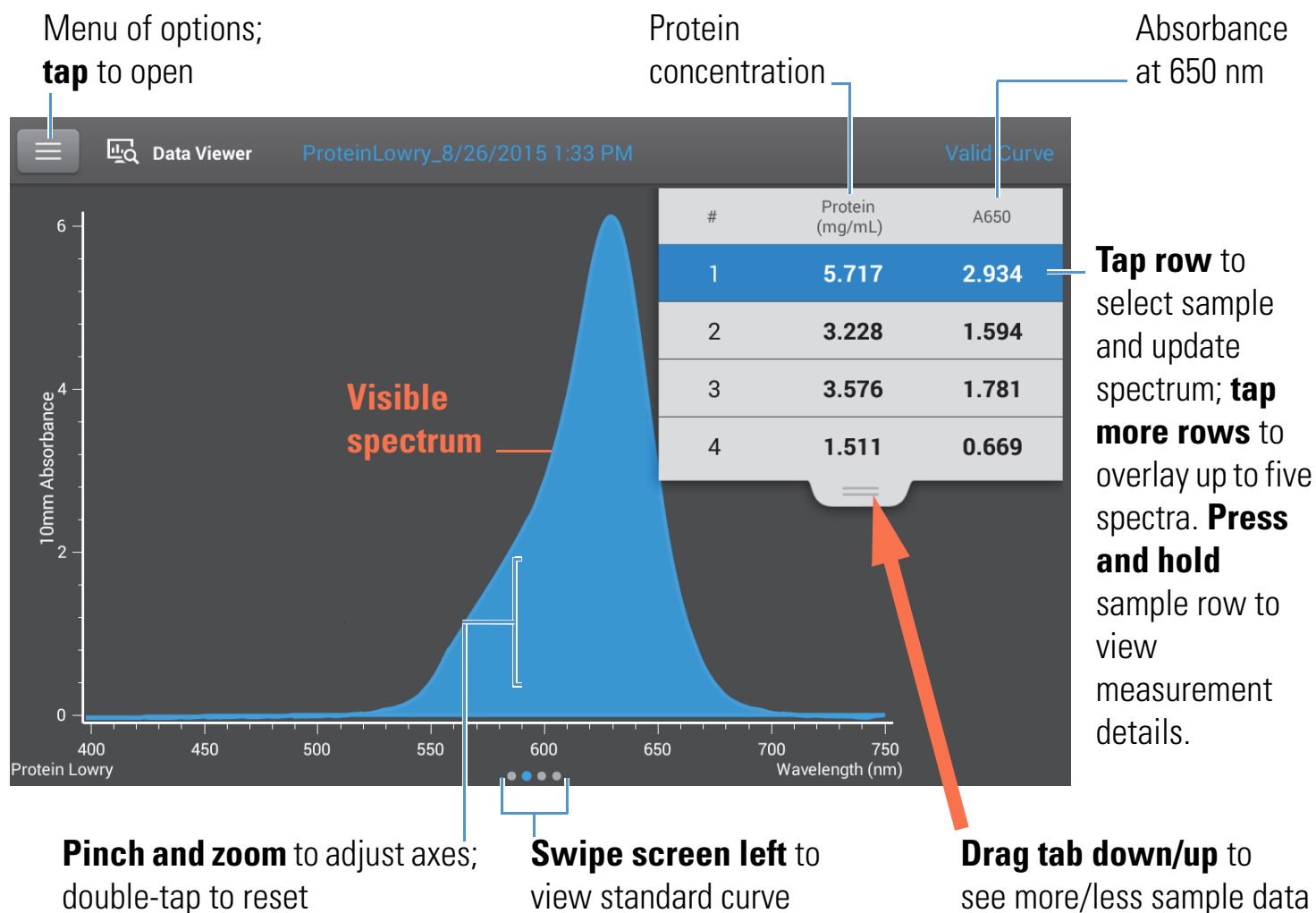
- [Working with standard curves](#)
- [Best practices for protein measurements](#)
- [Measure a Micro-Volume Sample](#)

- Measure a Sample Using a Cuvette
- Prepare Samples and Blanks
- Basic Instrument Operations

## Protein Lowry Reported Results

### Protein Lowry measurement screen (shown from Data Viewer)

For each measured sample and standard, this application shows the visible absorbance spectrum and a summary of the results. The standard curve is also available by swiping left from the measurement screen (or in the [Data Viewer](#) as shown below).





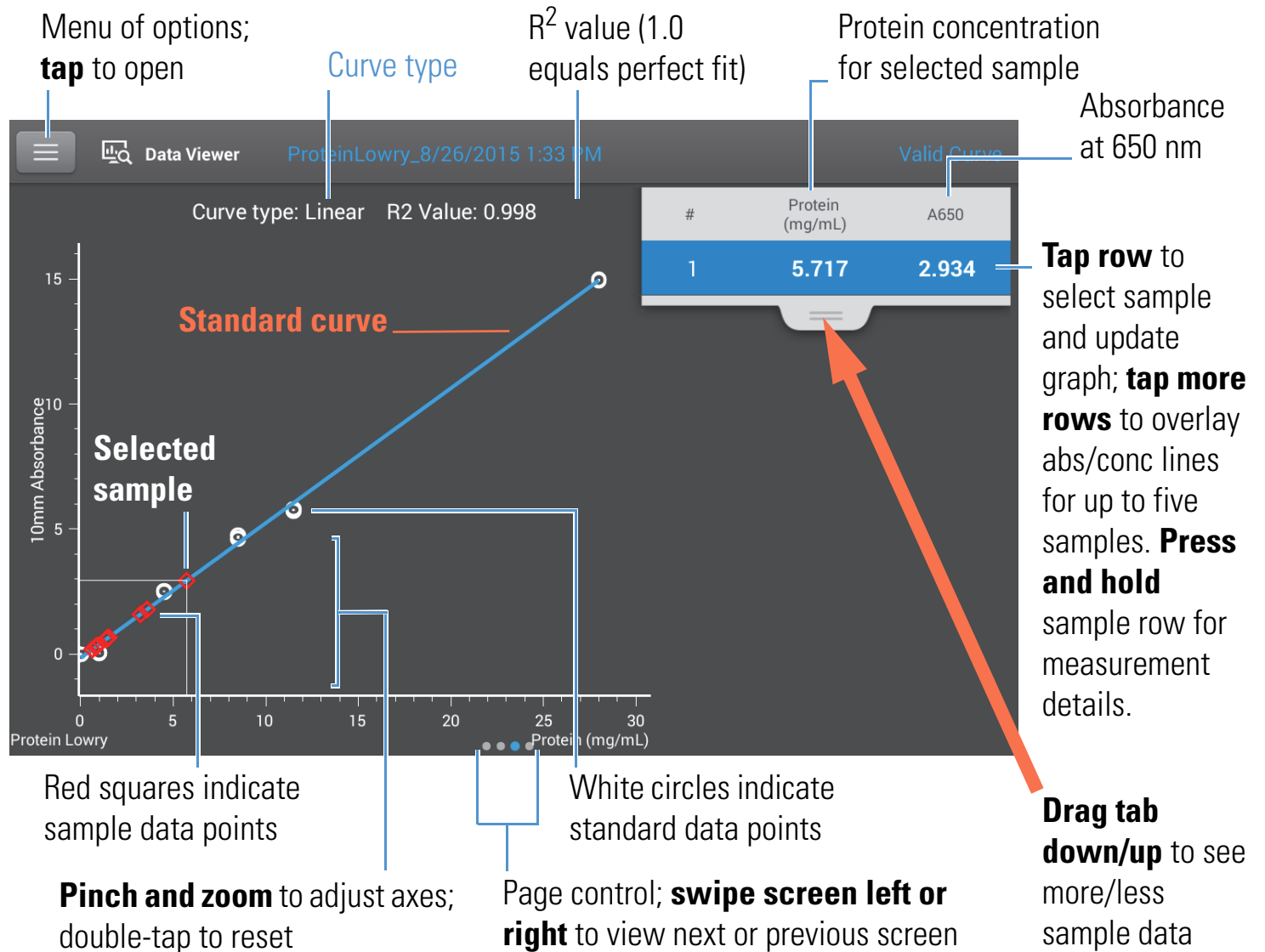
**Note**

- A baseline correction is performed at 405 nm (absorbance value at 405 nm is subtracted from absorbance values at all wavelengths in sample spectrum).
- Micro-volume absorbance measurements and measurements taken with nonstandard cuvettes are normalized to a 10.0 mm pathlength equivalent.

## Protein Lowry standard curve screen

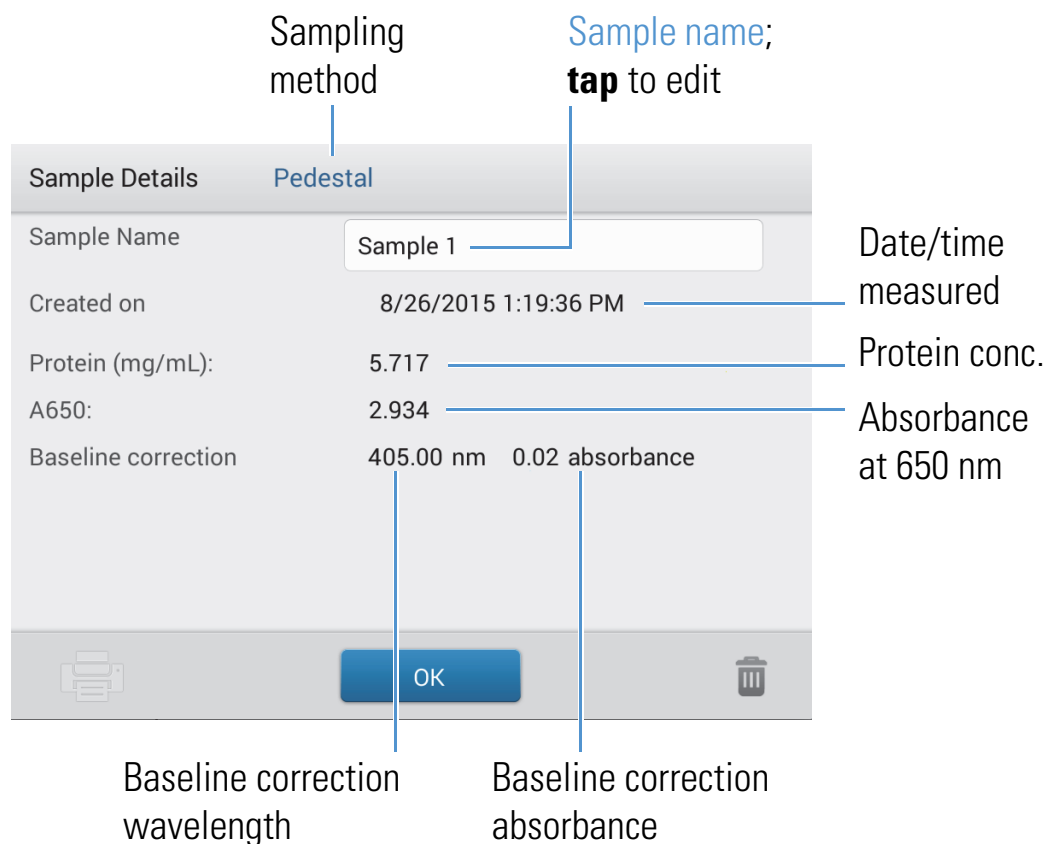
The standard curve screen shows graphically the relationship between the measured standards, the calculated standard curve, and the measured absorbance and calculated concentration for a selected sample. A horizontal line connects the sample absorbance value on the Y-axis to the standard curve. A vertical line connects that point to the sample concentration value on the X-axis.

The  $R^2$  value indicates how well the standard curve fits the standard data points (1.0 is a perfect fit; that is, all points lie exactly on the curve).



## Protein Lowry reported values

The initial screen that appears after each measurement and the standards screen (see previous image) show a summary of the reported values. To view all reported values, press and hold the sample row. Here is an example:



### Related Topics

- [Example standard curve](#)
- [Basic Instrument Operations](#)

## Settings for Protein Lowry Measurements

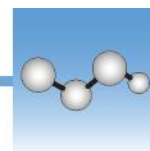
To show the Protein Lowry settings, from the Protein Lowry measurement screen, tap  > **Protein Lowry Setup**.

**Note** You can edit the Curve Type setting when measuring standards by changing the list box at the top of the application measurement screen. You can edit the concentration value for a standard from the application setup screen. After the first sample measurement, these settings cannot be changed.

Setting	Description
Curve Type	Specify type of equation used to create standard curve from standard concentration values. Available options: <ul style="list-style-type: none"> <li>– <b>Linear:</b> Draws the linear least squares line through all measured standards (requires reference measurement and at least one standard)</li> <li>– <b>Interpolation:</b> Draws a series of straight lines to connect all measured standards (requires reference measurement and at least one standard)</li> <li>– <b>2<sup>nd</sup> order polynomial:</b> Draws the 2<sup>nd</sup> order least squares polynomial using all measured standards (requires reference measurement and at least two standards)</li> <li>– <b>3<sup>rd</sup> order polynomial:</b> Draws the 3<sup>rd</sup> order least squares polynomial using all measured standards (requires reference measurement and at least three standards)</li> </ul>
Replicates	Enter number of measurements of the reference or the same standard or sample that are averaged together to produce its associated concentration value.  <b>Note:</b> Replicates setting cannot be changed after the first standard has been measured.
Standards	Enter actual concentration value of each standard.  <b>Note:</b> Concentration values can be entered in any order but the standards must be measured in the order they were entered.

### Related Topics

- [Instrument Settings](#)



## Measure Protein Pierce 660

Measures total protein concentration of unpurified protein samples using a proprietary colorimetric detection reagent.

[Measure Total Protein](#)

[Reported Results](#)

[Settings](#)

[Detection Limits](#)



## Measure Total Protein Concentration

The Protein Pierce 660 assay uses a proprietary protein binding material as a colorimetric detection reagent to determine total protein concentration in unpurified protein samples. This application is suitable for protein solutions that contain high concentrations of detergents, reducing agents and other commonly used reagents. The Pierce 660 application measures absorbance at 660 nm and uses a standard curve to calculate protein concentration (see [Working with Standard Curves](#) for more information). A single-point baseline correction is applied.

### Theory of Protein Pierce 660 assay

The Protein Pierce 660 assay is based on the binding of a proprietary dye-metal complex to protein in acidic conditions that causes a shift in the dye's absorption maximum, which is measured at 660 nm. The dye-metal complex is reddish-brown and changes to green upon protein binding. The color change is produced by deprotonation of the dye at low pH facilitated by interactions with positively charged amino acid groups in proteins. The dye interacts mainly with basic residues in proteins such as histidine, arginine and lysine and to a lesser extent tyrosine, tryptophan and phenylalanine. The reaction product is measured at 660 nm and baseline-corrected using the absorbance value at 750 nm.

The color produced in the assay is stable and increases in proportion to a broad range of increasing protein concentrations. An optional Ionic Detergent Compatibility Reagent (IDCR) may be added to the assay reagent to increase compatibility with high amounts of ionic detergents, including Laemmli SDS sample buffer with bromophenol blue. The IDCR dissolves completely by thorough mixing and has no effect on the assay. Pre-formulated kits of the protein binding material are available from us or a local distributor. For information about IDCR, refer to the kit manufacturer.

## Protein assay kits and protocols

Please refer to the NanoDrop website for up-to-date kits and protocols for the NanoDrop One instruments. Follow the assay kit manufacturer's recommendations for all standards and samples (unknowns). Ensure each is subjected to the same timing and temperature throughout the assay.

Protein standards for generating a standard curve may also be provided by the kit manufacturer. Since the NanoDrop One pedestals can measure higher protein concentrations than traditional cuvette-based spectrophotometers, you may need to supply your own protein standards at higher concentrations than provided by the manufacturer. For example, additional standards may be required to ensure the standard curve covers the dynamic range of the assay and the expected range of the unknown samples.

## To measure Protein Pierce 660 standards and samples

### NOTICE

- Do not use a squirt or spray bottle on or near the instrument as liquids will flow into the instrument and may cause permanent damage.
- Do not use hydrofluoric acid (HF) on the pedestals. Fluoride ions will permanently damage the quartz fiber optic cables.

### Before you begin...

Before taking pedestal measurements with the NanoDrop One instrument, lift the instrument arm and clean the upper and lower pedestals. At a minimum, wipe the pedestals with a new laboratory wipe. For more information, see [Cleaning the Pedestals](#).

❖ **To measure Protein Pierce 660 standards and samples**

1. From the Home screen, select the **Proteins** tab and then tap **Protein Pierce 660**.
2. Specify a [curve type](#) and number of [replicates for each standard](#) and enter the [concentration of each standard](#).

**Tip:** For this assay, we recommend setting **Curve Type** to “Linear”.

3. Measure blank:
  - Pipette 2  $\mu$ L reference solution onto lower pedestal and lower arm, or insert reference solution blanking cuvette into cuvette holder (reference solution should contain none of the standard protein stock; see [Working With Standard Curves](#) for details)

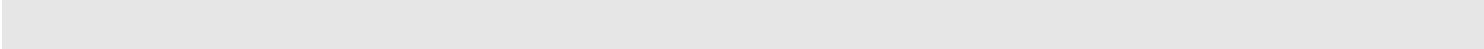
**Tip:** If using a cuvette, make sure to [align cuvette light path](#) with instrument light path.

- tap **Blank** and wait for measurement to complete
  - lift arm and clean both pedestals with new laboratory wipe, or remove cuvette
4. Measure reference standard:
- pipette 2  $\mu\text{L}$  reference solution onto pedestal, or insert reference cuvette (reference solution should contain none of the standard protein stock, see [Working With Standard Curves](#) for details)
  - lower arm to start measurement (or tap **Measure** if Auto-Measure is off)
  - lift arm and clean both pedestals with new wipe, or remove cuvette
  - if Replicates setting is greater than 1, repeat measurement
5. Measure remaining standards:
- pipette 2  $\mu\text{L}$  standard 1 onto pedestal, or insert standard 1 cuvette
  - lower arm to start measurement (or tap **Measure** if Auto-Measure is off)
  - lift arm and clean both pedestals with new wipe, or remove cuvette
  - if Replicates setting is greater than 1, repeat measurement
  - repeat substeps above for each additional standard (when specified number of standards and replicates have been measured, a message asks whether to load more standards or begin measuring samples)
  - if finished measuring standards, tap **Done** (swipe left to view standard curve)
6. Measure samples:
- pipette 2  $\mu\text{L}$  sample 1 onto pedestal, or insert sample 1 cuvette
  - lower arm to start measurement (or tap **Measure** if Auto-Measure is off)
  - lift arm and clean both pedestals with new wipe, or remove cuvette
  - if Replicates setting is greater than 1, repeat measurement
7. When you are finished measuring samples, tap **End Experiment**.
8. Lift the arm and clean both pedestals with a new wipe, or remove the sample cuvette.

### Related Topics

- [Working with standard curves](#)
- [Best practices for protein measurements](#)
- [Measure a Micro-Volume Sample](#)

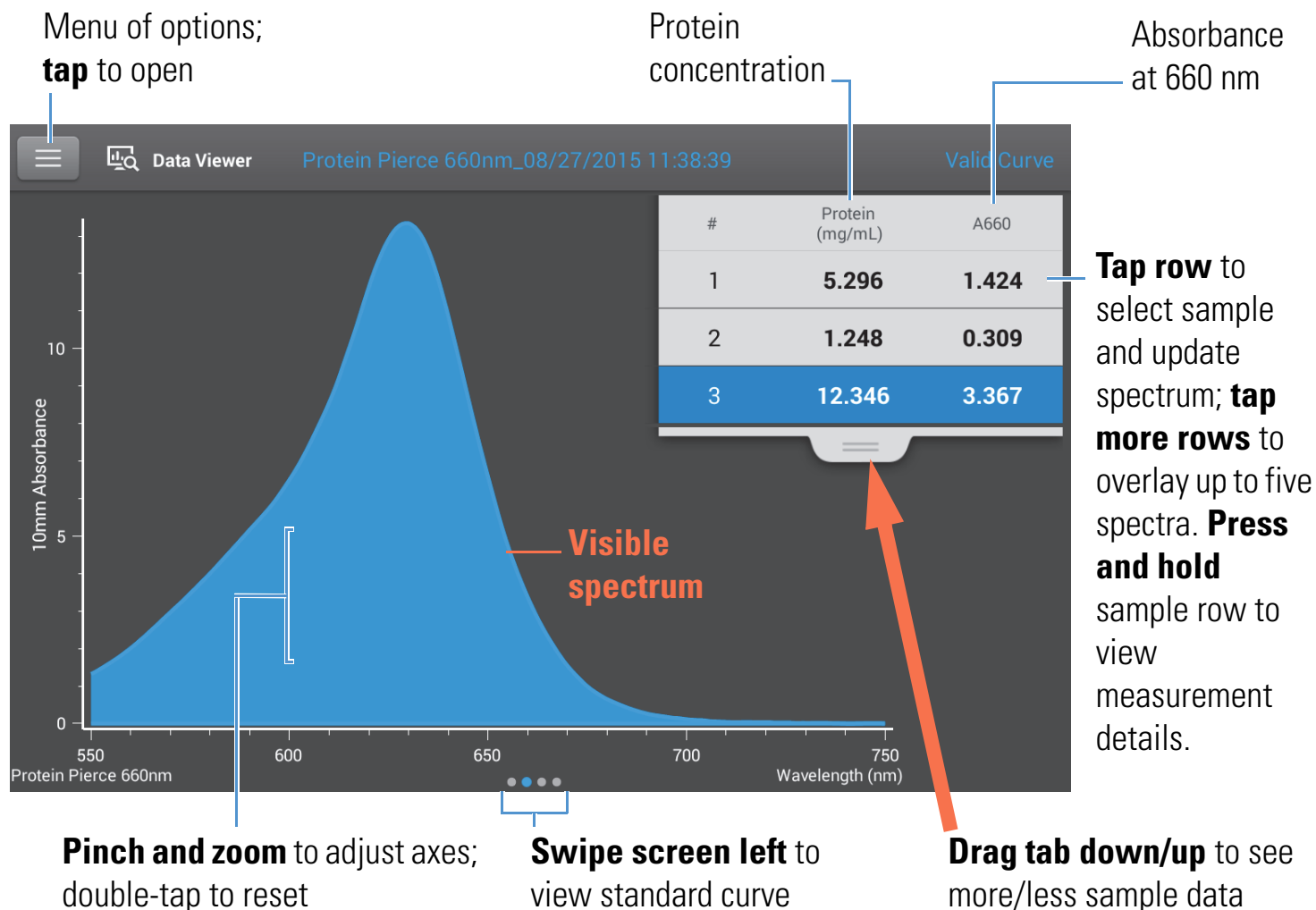


- Measure a Sample Using a Cuvette
  - Prepare Samples and Blanks
  - Basic Instrument Operations
- 

## Protein Pierce 660 Reported Results

### Protein Pierce 660 measurement screen (shown from Data Viewer)

For each measured sample and standard, this application shows the visible absorbance spectrum and a summary of the results. The standard curve is also available by swiping left from the measurement screen (or in the [Data Viewer](#) as shown below).



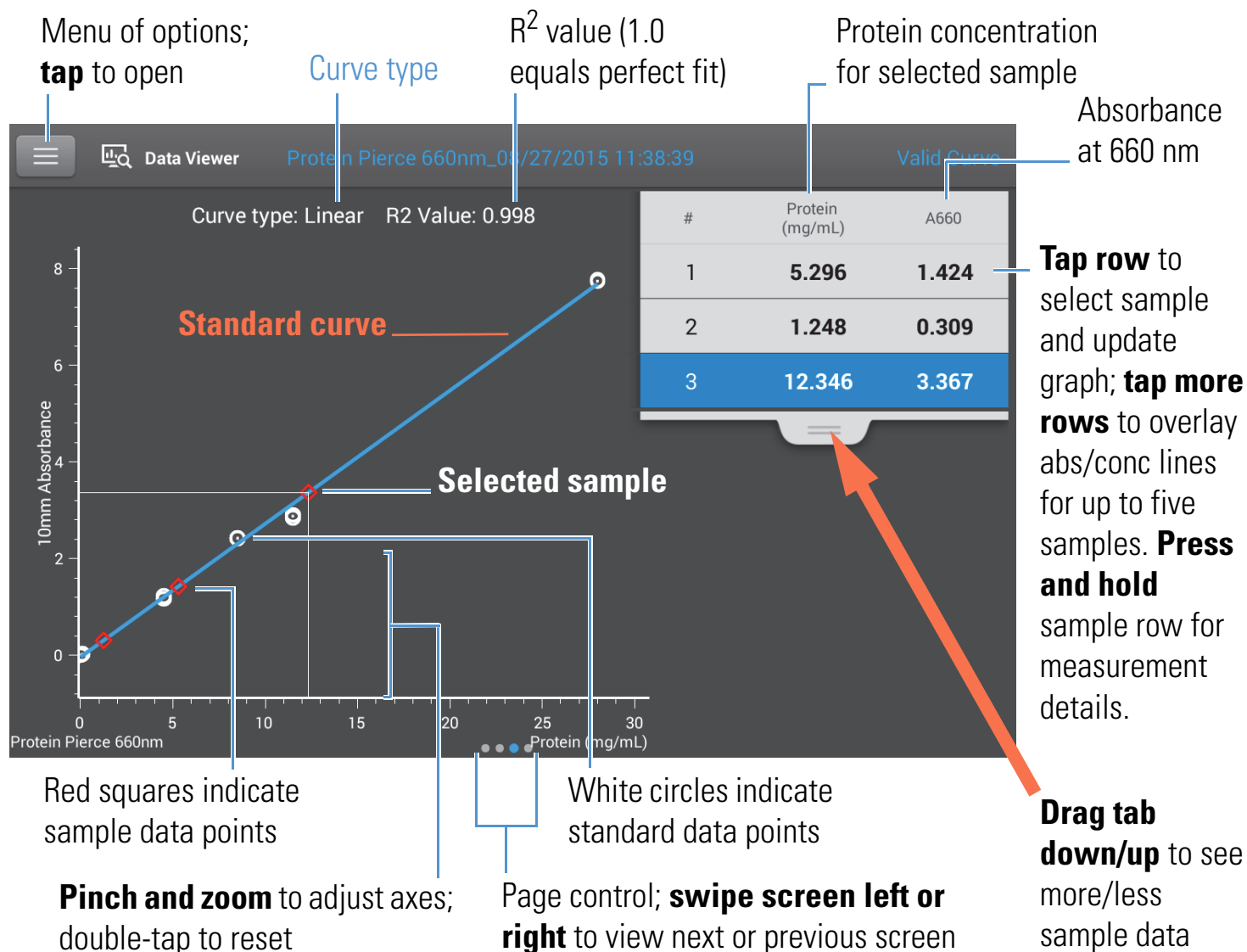
#### Note

- A baseline correction is performed at 750 nm (absorbance value at 750 nm is subtracted from absorbance values at all wavelengths in sample spectrum).
- Micro-volume absorbance measurements and measurements taken with nonstandard cuvettes are normalized to a 10.0 mm pathlength equivalent.

## Protein Pierce 660 standard curve screen

The standard curve screen shows graphically the relationship between the measured standards, the calculated standard curve, and the measured absorbance and calculated concentration for a selected sample. A horizontal line connects the sample absorbance value on the Y-axis to the standard curve. A vertical line connects that point to the sample concentration value on the X-axis.

The  $R^2$  value indicates how well the standard curve fits the standard data points (1.0 is a perfect fit; that is, all points lie exactly on the curve).



## Protein Pierce 660 reported values

The initial screen that appears after each measurement and the standards screen (see previous image) show a summary of the reported values. To view all reported values, press and hold the sample row. Here is an example:

The screenshot shows a mobile application interface for reporting protein measurement data. The screen is titled "Sample Details" and "Pedestal". It displays the following information:


- Sample Name:** Sample 3 (with a note: "Sample name; tap to edit")
- Created on:** 8/27/2015 11:38:45 AM (with a note: "Date/time measured")
- Protein (mg/mL):** 12.346 (with a note: "Protein conc.")
- A660:** 3.367 (with a note: "Absorbance at 660 nm")
- Baseline correction:** 750.00 nm (with a note: "Baseline correction wavelength") and 0.01 absorbance (with a note: "Baseline correction absorbance")

At the bottom of the screen, there is a printer icon, an "OK" button, and a trash icon.

### Related Topics

- [Example standard curve](#)
- [Basic Instrument Operations](#)

## Settings for Protein Pierce 660 Measurements

To show the Protein Pierce 660 settings, from the Protein Pierce 660 measurement screen, tap  > **Protein Pierce 660 Setup**.

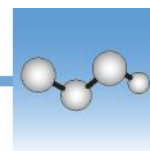
**Note** You can edit the Curve Type setting when measuring standards by changing the list box at the top of the application measurement screen. You can edit the concentration value for a standard from the application setup screen. After the first sample measurement, these settings cannot be changed.

Setting	Description
Curve Type	Specify type of equation used to create standard curve from standard concentration values. Available options: <ul style="list-style-type: none"> <li>– <b>Linear:</b> Draws the linear least squares line through all measured standards (requires reference measurement and at least one standard)</li> <li>– <b>Interpolation:</b> Draws a series of straight lines to connect all measured standards (requires reference measurement and at least one standard)</li> <li>– <b>2<sup>nd</sup> order polynomial:</b> Draws the 2<sup>nd</sup> order least squares polynomial using all measured standards (requires reference measurement and at least two standards)</li> <li>– <b>3<sup>rd</sup> order polynomial:</b> Draws the 3<sup>rd</sup> order least squares polynomial using all measured standards (requires reference measurement and at least three standards)</li> </ul>
Replicates	Enter number of measurements of the reference or the same standard or sample that are averaged together to produce its associated concentration value.  <b>Note:</b> Replicates setting cannot be changed after the first standard has been measured.
Standards	Enter actual concentration value of each standard.  <b>Note:</b> Concentration values can be entered in any order but the standards must be measured in the order in which they were entered.  If you also want to enter previously measured absorbance values for the standards, select this check box: <div style="border: 1px solid #ccc; background-color: #f0f0f0; padding: 5px; margin-top: 10px;"> <input checked="" type="checkbox"/> Absorbance data for standards can be either measured or entered manually. Uncheck this box to measure absorbance data. Check the box to manually enter the absorbance values.           </div> and then enter absorbance values for all the standards.

### Related Topics

- [Instrument Settings](#)





## Measure OD600

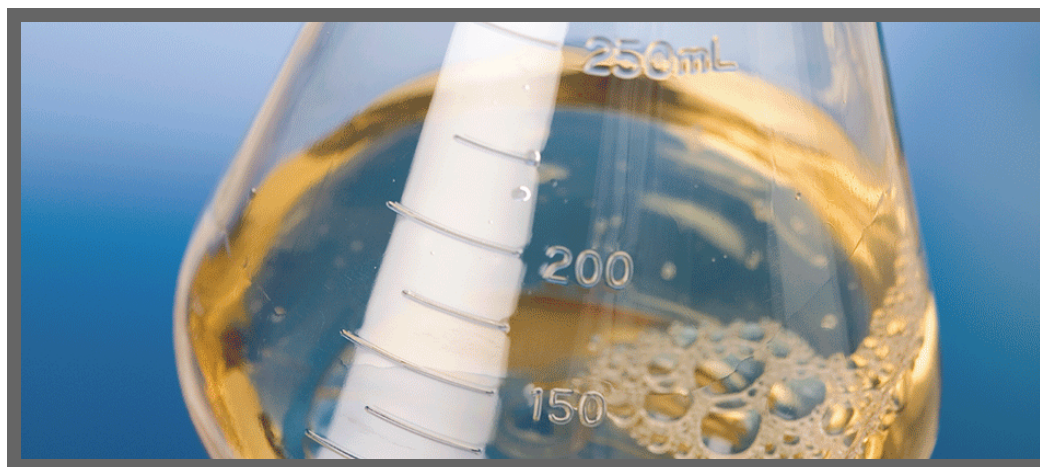
Measures the concentration of microbial cell cultures in solution by measuring scattered light at 600 nm.

[Measure OD600](#)

[Reported Results](#)

[Settings](#)

[Calculations](#)



## Measure OD600

Use the OD600 application to monitor the growth rate of bacterial or other microbial cell cultures by measuring the optical density (absorbance) of the culture in growth media at 600 nm. The Beer-Lambert equation and a user-entered conversion factor are used to correlate absorbance with concentration. Reported concentration values can be used to identify the phase of cultured cell populations, e.g., log or exponential and stationary.

The OD600 application reports cell concentration in cells/mL. A single-point absorbance correction can be used. This application does not require a standard curve.

**Note** Due to the amount of scattered light present in this assay, absorbance readings are typically very low.

### Theory of OD600 application

The OD600 application measures light transmission and uses that value to calculate absorbance. In spectroscopy, transmitted light is defined as any light that is not absorbed by, reflected from and scattered off a sample.

In the case of living cells, most of the incident light is transmitted through the sample rather than scattered, reflected or absorbed. The amount of scattered light is low and can vary from instrument to instrument. As a result, calculated absorbance readings are typically very low.

The calculated absorbance values are used to determine the density of cells in solution in cells/mL. The physical concepts and formulas that relate optical properties of living cells to concentration include:

- Cells, which have a different index of refraction from the surrounding medium, randomly reflect and scatter light out of the incident light path. The amount of scattering is proportional to the density of cells in the sample.
- The Beer's Law equation is used to relate absorbance to concentration. See [Calculations for OD600 Measurements](#) for details.
- For cuvette reading with the NanoDrop One instrument, accurate absorbance readings are typically in the range between 0.04 A and 1.5 A. Serial dilutions of the sample are usually needed to bring the absorbance readings within this range.
- All measurements should be made on the same type of spectrophotometer and method (i.e., pedestal vs. cuvette) as the amount of scattered light captured varies based on the optical configuration. When using a different spectrophotometer or method, calculate and apply a conversion factor to the reported results. For example, to compare OD readings using the pedestal vs. a cuvette, a conversion factor can be calculated as follows:

$$\text{Conversion factor} = \text{Cuvette OD} / \text{Pedestal OD}$$

## Best practices for OD600 measurements

- Ensure the sample is within the instrument's [absorbance detection limits](#).
- Blank with the growth or culture media the cells of interest are suspended in.
- Run a [blanking cycle](#) to assess the absorbance contribution of your media solution. If the media solution exhibits strong absorbance at or near the analysis wavelength (600 nm), you may need to choose a different media solution or application. See [Choosing and Measuring a Blank](#) for more information.
- Make dilutions as necessary to ensure sample cultures do not exceed the linear dynamic range of the assay before the culture reaches the stationary phase. The linear range depends largely on optical configuration and, therefore, differs for pedestal and cuvette measurements. To determine the linear range:
  - Measure a series of dilutions using a young overnight culture (~16 hrs) of the microbial strain
  - Graph the OD600 measurements against the dilution factor



The upper detection limit is the measured OD600 value at which there ceases to be a linear correlation between dilution factors and OD600 readings.

- Mix samples gently but thoroughly immediately before taking an aliquot for measurement.
- For micro-volume measurements:
  - Ensure pedestal surfaces are properly [cleaned](#) and [conditioned](#).
  - Avoid introducing bubbles when mixing and pipetting.
  - Start the measurement promptly to avoid settling or evaporation.
  - Follow [best practices for micro-volume measurements](#).
  - Use 2  $\mu$ L sample volume. See [Recommended Sample Volumes](#) for more information.
  - For dilute samples that exhibit low absorbance at 600 nm, use an alternative wavelength such as 400 nm to measure absorbance, or use cuvettes instead of micro-volume measurements.
- For cuvette measurements (NanoDrop One<sup>C</sup> instruments only):
  - Use clean plastic, glass or quartz cuvettes.
  - Follow [best practices for cuvette measurements](#).
  - Do not use the automatic [stirring](#) feature for this assay.

## To measure OD600 samples

### NOTICE

- Do not use a squirt or spray bottle on or near the instrument as liquids will flow into the instrument and may cause permanent damage.
- Do not use hydrofluoric acid (HF) on the pedestals. Fluoride ions will permanently damage the quartz fiber optic cables.

### Before you begin...

Before taking pedestal measurements with the NanoDrop One instrument, lift the instrument arm and clean the upper and lower pedestals. At a minimum, wipe the pedestals with a new laboratory wipe. For more information, see [Cleaning the Pedestals](#).

**❖ To measure an OD600 sample**

1. From the Home screen, select the **OD600** tab and tap **OD600**.
2. Specify the [cell number conversion factor](#) and a [second monitored wavelength](#) or [absorbance correction](#) if desired.
3. Pipette 2  $\mu$ L blanking solution (i.e., the media solution the cells of interest are suspended in) onto the lower pedestal and lower the arm, or insert the blanking cuvette into the cuvette holder.

**Tip:** If using a cuvette, make sure to [align the cuvette light path](#) with the instrument light path.

4. Tap **Blank** and wait for the measurement to complete.

**Tip:** If [Auto-Blank](#) is On, the blank measurement starts automatically after you lower the arm. (This option is not available for cuvette measurements.)

5. Lift the arm and clean both pedestals with a new laboratory wipe, or remove the blanking cuvette.
6. Pipette 2  $\mu$ L sample solution onto the pedestal and lower the arm, or insert the sample cuvette into the cuvette holder.
7. Start the sample measurement:
  - Pedestal: If [Auto-Measure](#) is On, lower arm; if Auto-Measure is off, lower arm and tap **Measure**.
  - Cuvette: Tap **Measure**

When the sample measurement is completed, the spectrum and reported values are displayed (see the next section).

8. When you are finished measuring samples, tap **End Experiment**.
9. Lift the arm and clean both pedestals with a new wipe, or remove the sample cuvette.

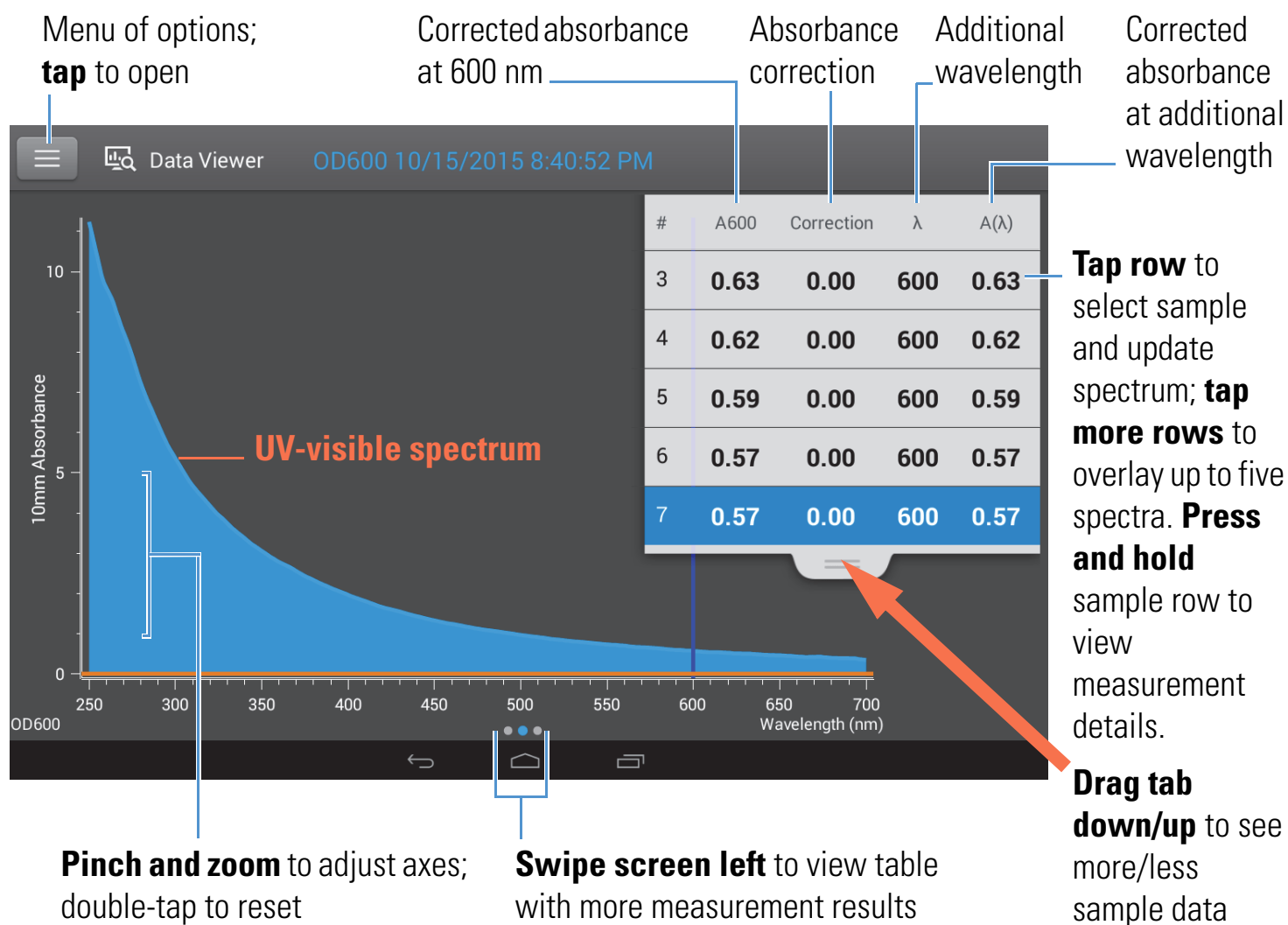
**Related Topics**

- [Measure a Micro-Volume Sample](#)
- [Measure a Sample Using a Cuvette](#)
- [Prepare Samples and Blanks](#)
- [Basic Instrument Operations](#)

## OD600 Reported Results

### OD600 measurement screen (shown from Data Viewer)

For each measured sample, this application shows the absorbance spectrum and a summary of the results. Here is an example:



**Note** Micro-volume absorbance measurements and measurements taken with nonstandard cuvettes are normalized to a 10.0 mm pathlength equivalent.

## OD600 reported values

The initial screen that appears after each measurement (see previous image) shows a summary of the reported values. To view all reported values, press and hold the sample row. Here is an example:

The screenshot shows the 'Sample Details' screen for an OD600 measurement. The fields and their values are as follows:

Field	Value
Application	OD600
Sampling method	Pedestal
Sample Name	Sample 7
Created on	10/15/2015 8:43:59 PM
A600:	0.57
Absorbance correction	0.00
Additional monitored wavelength (λ)	600 nm
Abs(Wavelength)	0.57
Factor (10 <sup>8</sup> )	1.00
Cells/mL (10 <sup>8</sup> )	0.57


Callouts from the image:

- Application:** OD600
- Sampling method:** Pedestal
- Sample name; tap to edit:** Sample 7
- Date/time measured:** 10/15/2015 8:43:59 PM
- Corrected abs. at 600 nm:** 0.57
- Absorbance correction:** 0.00
- Absorbance correction:** 600 nm
- Additional wavelength:** 600 nm
- Additional wavelength:** 0.57
- Factor:** 1.00
- Factor:** 0.57
- Cell culture concentration (A600 \* Factor):** 0.57
- Corrected absorbance at additional wavelength:** 0.57

### Related Topics

- [Basic Instrument Operations](#)
- [OD600 Calculations](#)

## Settings for OD600 Measurements

To show the OD600 settings, from the OD600 measurement screen, tap  > **OD600 Setup**.

Setting	Available Options	Description
Absorbance correction	Absorbance value between 0 and 300 A	<p>User-defined absorbance correction. Enter absorbance correction for displayed spectrum. This can be useful, for example, to correct baseline offset caused by any difference between the media solution used to blank the instrument and media used to suspend the cell culture sample, and because scattered light generally produces an offset.</p> <p>Absorbance correction value is subtracted from absorbance values at all wavelengths in sample spectrum. (All displayed absorbance values are corrected values.)</p>

---

Setting	Available Options	Description
Additional monitored wavelength ( $\lambda$ )	Any wavelength between 250 nm and 700 nm	<p>User-defined wavelength. Enter an additional wavelength to measure if desired (useful for dilute samples that exhibit low absorbance at 600 nm).</p> <p>If an alternative wavelength is specified, use this equation to calculate cell concentration:</p> $c = A(\lambda) * \text{factor}(\lambda)$ <p>where:</p> <p><math>c</math> = analyte concentration in cells/mL</p> <p><math>A(\lambda)</math> = UV-visible absorbance at specified wavelength in absorbance units (A)</p> <p><math>\text{factor}(\lambda) = 1/(\epsilon(\lambda) * b)</math> in mL/cell-cm</p> <p>where:</p> <p><math>\epsilon(\lambda)</math> = molar absorption coefficient (or extinction coefficient) at specified wavelength</p> <p><math>b</math> = pathlength in cm (1.0 cm for the NanoDrop One instruments)</p>
Cell number conversion factor ( $10^8$ )	Any number	<p>User-defined factor. Generally accepted factor for measured cell type, or one derived empirically using a solution of study cells at known concentration using the same media.</p> <p>Default value is <math>1 \times 10^8</math> which is the generally accepted factor for most bacterial cell suspensions such as E. coli.</p> <p><b>Tip:</b> The factor is wavelength specific for each cell type and can be affected by the type of media used for the measurements. Ideally, the factor should be determined empirically using a solution of the study cells at a known concentration using the same media.</p>

### Related Topics

- [Instrument Settings](#)

## Calculations for OD600 Measurements

Similar to the nucleic acid applications, the OD600 application uses a [modification of the Beer-Lambert equation](#) to calculate sample concentration where the extinction coefficient and pathlength are combined and referred to as a “factor.”

The OD600 application offers a user-specified factor, to be used in conjunction with Beer’s Law to calculate sample concentration. If the factor is known, enter the factor. Otherwise, use  $1 \times 10^8$ , which is the generally accepted factor for most bacterial cell suspensions such as E. coli.

Calculated cell concentrations are based on the absorbance value at 600 nm, the entered factor and the sample pathlength. A single-point absorbance correction may be applied.

### Measured Values

#### A600 absorbance

**Note:** For micro-volume absorbance measurements and measurements taken with nonstandard (other than 10 mm) cuvettes, the spectra are normalized to a 10 mm pathlength equivalent.

- Cell culture absorbance values are measured at 600 nm using the normalized spectrum. If no Absorbance Correction is specified, this is the reported A600 value and the value used to calculate cell concentration.
- If an [Absorbance Correction](#) is specified, the normalized and (absorbance) corrected absorbance value at 600 nm is reported and used to calculate cell concentration.

#### $A(\lambda)$ absorbance

- Normalized and (absorbance) corrected (if used) absorbance value at any specified [Additional Monitored Wavelength](#) ( $\lambda$ ) is also reported.

#### Sample Pathlength

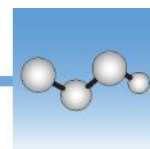
- For micro-volume measurements, the software selects the optimal pathlength (between 1.0 mm and 0.03 mm) based on sample absorbance at the analysis wavelength.
- For cuvette measurements, pathlength is determined by the cuvette Pathlength setting in the software (see [General Settings](#)).
- Displayed spectra and absorbance values are normalized to a 10 mm pathlength equivalent.
- 

### Reported Values

**Cell concentration.** Reported in cells/mL. Calculations are based on Beer-Lambert equation using corrected A600 absorbance value.







## Measure Custom

Runs a custom measurement method created using NanoDrop One Viewer software.

[Measure Custom Method](#)

[Delete Custom Method](#)

[Reported Results](#)



## Measure using a Custom Method

Use the Custom application to run a user-defined method created using the NanoDrop One Viewer software running on a personal computer. For more information, see [Create Custom Method](#).

### To load a custom method

Custom methods can only be created on a personal computer running the NanoDrop One Viewer software. If you want to run a custom method and store the measurement results on the instrument, the method must also reside on the instrument. (This is the only way to run a custom method if your instrument is not connected to the computer with an Ethernet cable or through a wireless network.)

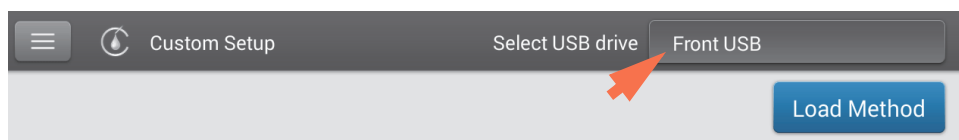
**Note** If the computer is connected to the instrument with an Ethernet cable or through a wireless network, custom methods can reside on the computer and the measurement results will be stored in that computer's database. For more information, see "Set Up Ethernet Connection" or "Set Up Wi-Fi Connections" in [Set Up the Instrument](#).

### Load custom methods onto the instrument

1. **Export the method** from the personal computer and copy the method file to the root of a portable USB device such as a memory stick.

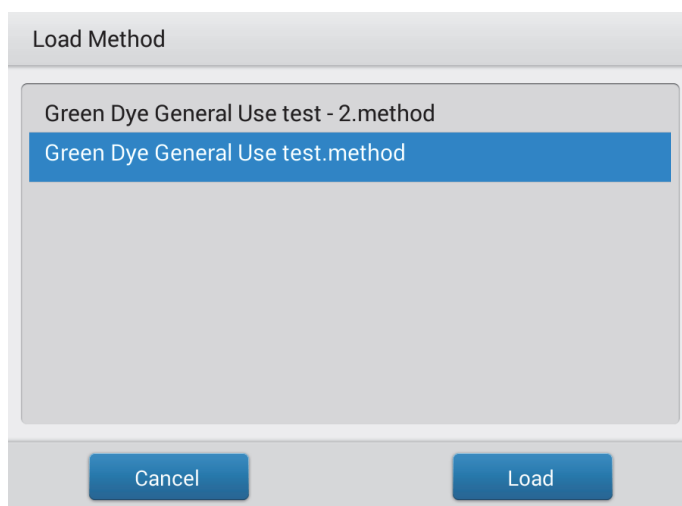
Method files have a “.method” filename extension.

2. Connect the USB device to one of the **USB ports** on the instrument.
3. From the Home screen, select the **Custom** tab and tap **Custom**.
4. Use the list box at the top of the screen to indicate the USB port used.



5. Tap **Load Method**.

A message box shows the NanoDrop One methods available on the selected USB device.



6. Tap one or more method names in the Load Method box to select the methods to load.
7. Tap **Load**.

## To measure using a custom method

### NOTICE

- Do not use a squirt or spray bottle on or near the instrument as liquids will flow into the instrument and may cause permanent damage.
- Do not use hydrofluoric acid (HF) on the pedestals. Fluoride ions will permanently damage the quartz fiber optic cables.

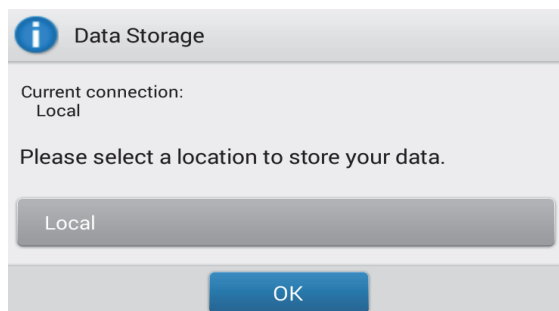
### Before you begin...

Before taking pedestal measurements with the NanoDrop One instrument, lift the instrument arm and clean the upper and lower pedestals. At a minimum, wipe the pedestals with a new laboratory wipe. For more information, see [Cleaning the Pedestals](#).

### ❖ To measure a sample using a custom method

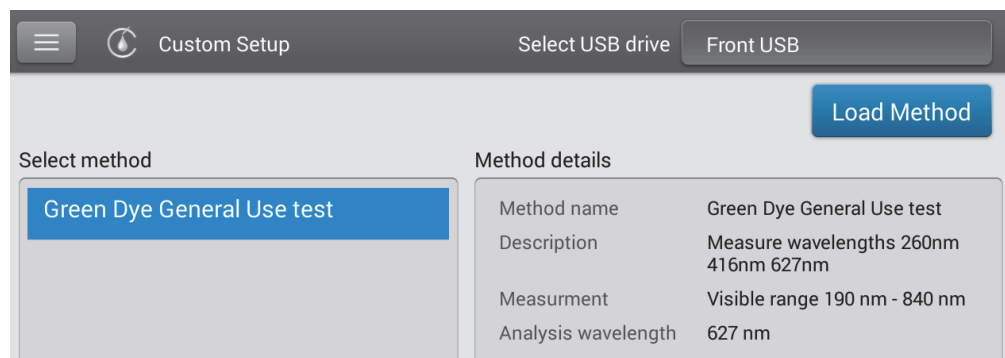
1. Make sure the method resides in same location as the database where you want to store the measurement results (see [To Load a Custom Method](#) for details).
2. From the Home screen, select the **Custom** tab and tap **Custom**.

If the instrument has a working Ethernet or wireless connection to a remote personal computer (PC), the Data Storage message box appears.



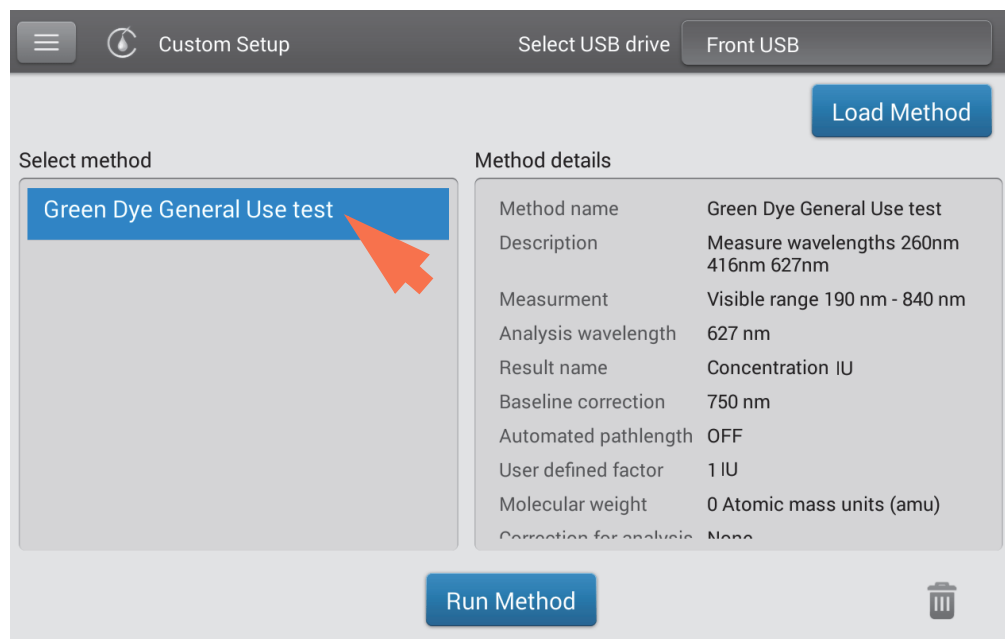
- To run a custom method that is loaded on the instrument and store all subsequently acquired measurement results in the database on the instrument, set Data Storage to **Local** (see example above).
- To run a custom method that resides on a personal computer connected to the instrument with an Ethernet cable and store all subsequently acquired measurement results in the database on that computer, set Data Storage to **Direct-Connect PC** (see “Set Up Ethernet Connection” in [Set Up the Instrument](#) for more information).
- To run a custom method that resides on a personal computer connected to the instrument through a wireless network and store all subsequently acquired measurement results in the database on that computer, set Data Storage to the **computer’s assigned name** (see “Set Up Wi-Fi Connections” in [Set Up the Instrument](#) for more information).

After you tap **OK**, the Custom Setup box (local or remote) is displayed.



- If Data Storage is set to **Local** (see the previous step), Custom Setup shows only custom methods that reside on the instrument (see [To Load a Custom Method](#) for more information).
- If Data Storage is set to **Direct-Connect PC** (Ethernet) or a specific **computer name** (wireless), Custom Setup shows only custom methods that reside on the wired (Ethernet) or specified (wireless) computer (see [Create Custom Method](#) for more information).

3. In the Select Method box, tap to select the method to run.



Information about the selected method appears in the Method Details box.


4. Tap **Run Method**.
5. Follow the on-screen instructions to measure a sample.

### Related Topics

- [Measure a Micro-Volume Sample](#)
- [Measure a Sample Using a Cuvette](#)
- [Create Custom Method](#)
- [Set Up the Instrument](#)
- [Export Custom Method](#)

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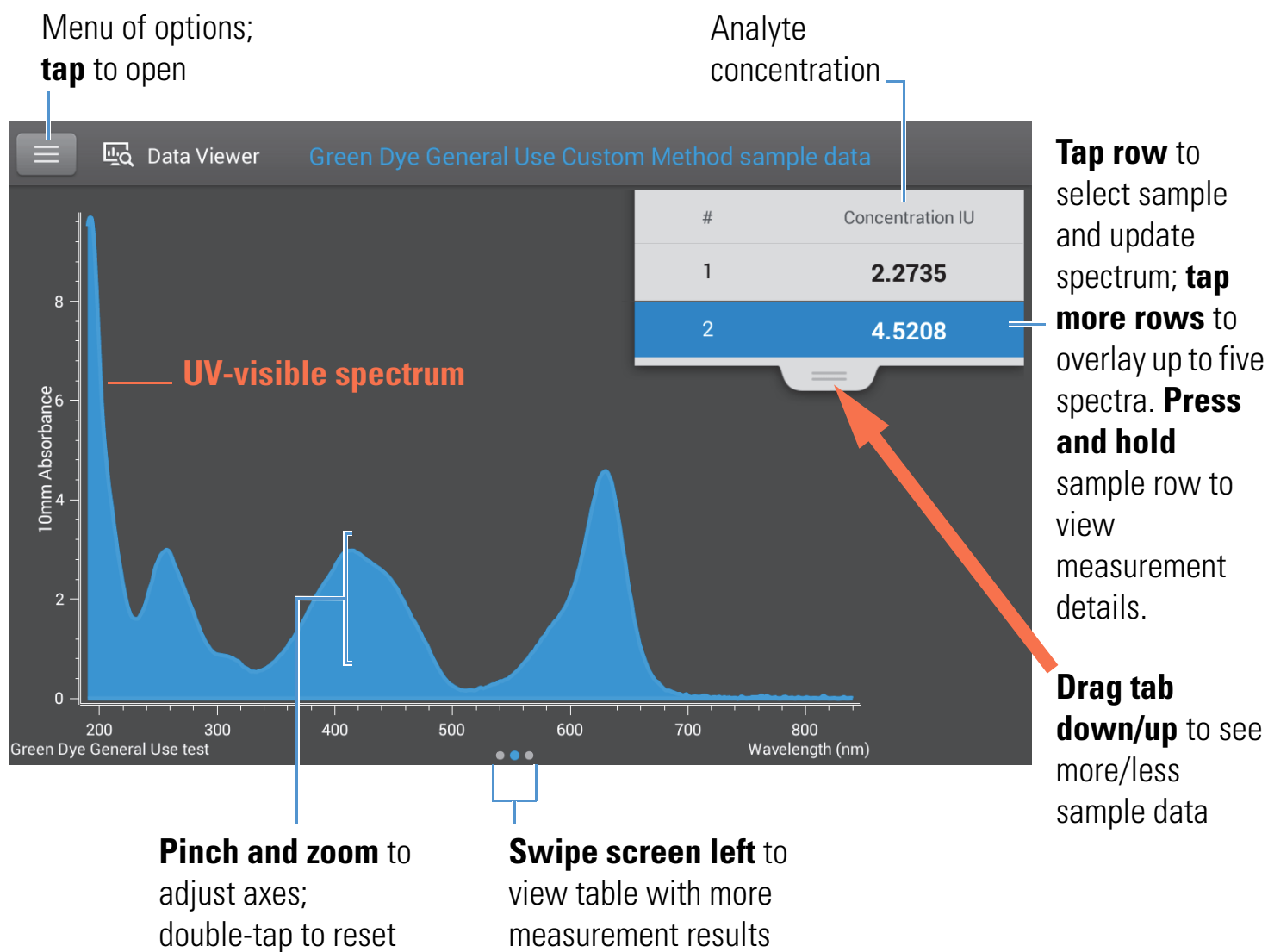
## Delete Custom Method

- From Home screen, select **Custom** tab and tap **Custom**.
- In Select Method box, tap to select method to delete
- tap 

## Custom Method Reported Results

### Custom method measurement screen (shown from Data Viewer)

For each measured sample, this application shows the absorbance spectrum and a summary of the results. Here is an example:



**Note** Micro-volume absorbance measurements and measurements taken with nonstandard cuvettes are normalized to a 10.0 mm pathlength equivalent.

## Custom method reported values

The initial screen that appears after each measurement (see previous image) shows a summary of the reported values. To view all reported values, press and hold the sample row. Here is an example:

The screenshot displays the 'Sample Details' screen for a measurement. The title bar shows 'Sample Details', 'Green Dye General Use test', and 'Pedestal'. The main content area lists various parameters and their values:

Parameter	Value
Sample Name	Sample 2
Created on	9/22/2015 6:41:24 PM
Concentration	4.5208 IU
Analysis wavelength	627 nm
Factor	1 IU
Baseline correction	750 nm 0.00 absorbance
Formula results	A627 4.521 OD A260 2.927 OD A416 2.977 OD Date: (09/22/2015) 06:41:24

Annotations on the right side of the screen point to specific fields:

- Method name**: Points to 'Green Dye General Use test' in the title bar.
- Sampling method**: Points to 'Pedestal' in the title bar.
- Sample name; tap to edit**: Points to the 'Sample Name' field.
- Date/time measured**: Points to the 'Created on' field.
- Analyte concentration**: Points to the 'Concentration' field.
- Method details**: Points to the 'Formula results' field.

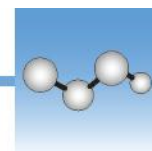
At the bottom of the screen, there is a printer icon, an 'OK' button, and a trash icon.

### Related Topics

- [Basic Instrument Operations](#)







## Measure UV-Vis

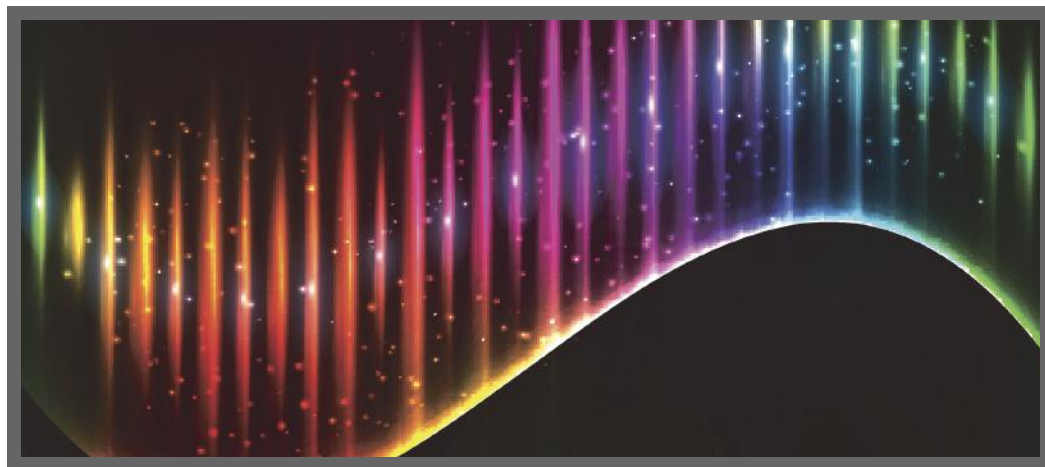
Measures the absorbance of any sample at up to 40 wavelengths across the ultra-violet (UV) and visible regions of the spectrum.

[Measure UV-Vis](#)

[Reported Results](#)

[Settings](#)

[Detection Limits](#)



## Measure UV-Vis

The UV-Vis application allows the instrument to function as a conventional spectrophotometer. Sample absorbance is displayed on the screen from 190 nm to 850 nm. Up to 40 wavelengths can be designated for absorbance monitoring and inclusion in the report. Automatic pathlength adjustment and a single-point baseline correction can also be used.

## To make UV-Vis measurements

### NOTICE

- Do not use a squirt or spray bottle on or near the instrument as liquids will flow into the instrument and may cause permanent damage.
- Do not use hydrofluoric acid (HF) on the pedestals. Fluoride ions will permanently damage the quartz fiber optic cables.

**Before you begin...**

Before taking pedestal measurements with the NanoDrop One instrument, lift the instrument arm and clean the upper and lower pedestals. At a minimum, wipe the pedestals with a new laboratory wipe. For more information, see [Cleaning the Pedestals](#).

**❖ To measure a sample using the UV-Vis application**

1. From the Home screen, select the **Custom** tab and tap **UV-Vis**.
2. Specify up to [40 wavelengths to monitor](#) (or you can specify them later if desired) and whether automated pathlength adjustment and baseline correction will be used.
3. Pipette 1–2  $\mu\text{L}$  blanking solution onto the lower pedestal and lower the arm, or insert the blanking cuvette into the cuvette holder.

**Tip:** If using a cuvette, make sure to [align the cuvette light path](#) with the instrument light path.

4. Tap **Blank** and wait for the measurement to complete.

**Tip:** If [Auto-Blank](#) is On, the blank measurement starts automatically after you lower the arm. (This option is not available for cuvette measurements.)

5. Lift the arm and clean both pedestals with a new laboratory wipe, or remove the blanking cuvette.
6. Pipette 1-2  $\mu\text{L}$  sample solution onto the pedestal and lower the arm, or insert the sample cuvette into the cuvette holder.
7. Start the sample measurement:
  - Pedestal: If [Auto-Measure](#) is On, lower arm; if Auto-Measure is off, lower arm and tap **Measure**.
  - Cuvette: Tap **Measure**.

When the sample measurement is completed, the spectrum and reported values are displayed (see the next section).

8. When you are finished measuring samples, tap **End Experiment**.
9. Lift the arm and clean both pedestals with a new wipe, or remove the sample cuvette.

## Best practices for UV-Vis measurements

- Ensure the sample absorbance is within the instrument's [absorbance detection limits](#).
- Blank with the same buffer solution used to resuspend the analyte of interest. The blanking solution should be a similar pH and ionic strength as the analyte solution.
- Run a [blanking cycle](#) to assess the absorbance contribution of your buffer solution. If the buffer exhibits strong absorbance at or near an analysis wavelength, you may need to choose a different buffer or application. See [Choosing and Measuring a Blank](#) for more information.
- For micro-volume measurements:
  - Ensure pedestal surfaces are properly [cleaned](#) and [conditioned](#).
  - Ensure samples are homogeneous before taking a measurement. Avoid introducing bubbles when mixing and pipetting.
  - Follow [best practices for micro-volume measurements](#).
  - Use a 1-2  $\mu\text{L}$  sample volume. See [Recommended Sample Volumes](#) for more information.
- For cuvette measurements (NanoDrop One<sup>C</sup> instruments only), use compatible cuvettes and follow [best practices for cuvette measurements](#).

### Related Topics

- [Measure a Micro-Volume Sample](#)
- [Measure a Sample Using a Cuvette](#)
- [Best Practices for Micro-Volume Measurements](#)
- [Best Practices for Cuvette Measurements](#)
- [Prepare Samples and Blanks](#)
- [Basic Instrument Operations](#)

## UV-Vis Reported Results

### UV-Vis measurement screen

For each measured sample, this application shows the absorbance spectrum and a summary of the results. Here is an example:

The screenshot shows the UV-Vis measurement screen. At the top, there is a menu icon (three horizontal lines) on the left, labeled 'Menu of options; tap to open'. Next to it is the text 'Sample 2' with a small edit icon, labeled 'Sample name; tap to edit'. To the right is 'Load #2'. Further right are two wavelength selection fields: '450' with a dropdown arrow, labeled 'Absorbance at user-defined wavelength 1 (450 nm)', and '623' with a dropdown arrow, labeled 'Absorbance at user-defined wavelength 2 (623 nm)'. Below these is a table with two columns: '#', 'λ'. The first row contains '1', '3.01', and '6.45'. A small menu icon is visible below the table, labeled 'Tap to edit' and 'Tap to add'. Below the table is a large orange arrow pointing to the table, labeled 'Tap row to select sample and update spectrum; tap more rows to overlay up to five spectra. Press and hold sample row to view measurement details.' At the bottom right, there is a tab with a menu icon, labeled 'Drag tab down/up to see more/less sample data'. The main area is a graph titled 'UV-Vis spectrum' showing '10mm Absorbance' on the y-axis (0 to 10) and 'Wavelength (nm)' on the x-axis (200 to 800). The graph shows a blue curve with several peaks. At the bottom, there are three buttons: 'Blank', 'Measure' (with a right arrow), and 'End Experiment'. The 'Measure' button has a small 'OFF' indicator next to it, labeled 'Pinch and zoom to adjust axes; double-tap to reset'. Below the 'Measure' button is a label 'Swipe screen left to view table with more measurement results'. Below the 'End Experiment' button is a label 'Tap to end experiment and export data'.

**Note** Micro-volume absorbance measurements and measurements taken with nonstandard cuvettes are normalized to a 10.0 mm pathlength equivalent.

## UV-Vis reported values

The initial screen that appears after each measurement (see previous image) shows a summary of the reported values. To view all reported values, press and hold the sample row. Here is an example:

The screenshot shows the 'Sample Details' screen for a UV-Vis measurement. The interface includes a header with 'Sample Details', 'UV-Vis', and 'Pedestal'. Below the header, there are several fields: 'Sample Name' (Sample 1), 'Created on' (11/22/2015 7:05:23 PM), 'Automated pathlength' (ON), and 'Baseline correction' (750 nm 0.00 absorbance). A table of 'Wavelength #1', 'Wavelength #2', and 'Wavelength #3' shows absorbance values at 450 nm (3.01), 623 nm (6.45), and 635 nm (6.49). At the bottom, there is a printer icon, an 'OK' button, and a trash icon.

Callouts in the image identify the following elements:


- Application:** UV-Vis
- Sampling method:** Pedestal
- Sample name; tap to edit:** Sample 1
- Date/time measured:** 11/22/2015 7:05:23 PM
- Automated pathlength setting:** ON
- Baseline correction absorbance:** 750 nm 0.00 absorbance
- Absorbance at 450 nm:** 450 nm 3.01 absorbance
- Absorbance at 623 nm:** 623 nm 6.45 absorbance
- Absorbance at 635 nm:** 635 nm 6.49 absorbance
- User-defined wavelengths:** Wavelength #1, Wavelength #2, Wavelength #3
- Baseline correction wavelength:** 750 nm

**Note** Scroll up to display absorbance values for any additional user-defined wavelengths.

### Related Topics

- [Basic Instrument Operations](#)

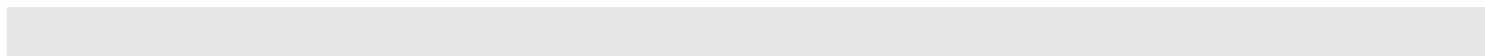
## Settings for UV-Vis Measurements

To show the UV-Vis settings, from the UV-Vis measurement screen, tap  > **UV-Vis Setup**.

Setting	Available Options	Description
Monitored wavelengths	Enter up to 40 wavelengths between 190 nm and 850 nm	<p><b>User-defined wavelengths to be measured and reported at run time.</b> Absorbance values for the first three entered wavelengths are displayed in the <a href="#">measurement</a> screen. To see absorbance values for 8 monitored wavelengths, swipe left in the measurement screen to show the <a href="#">Data table</a>. To see all monitored wavelengths, press and hold a sample row to show the <a href="#">Sample Details</a> screen (scroll up to display absorbance values for any additional user-defined wavelengths).</p> <p><b>Note:</b> If Baseline Correction is selected, all displayed absorbance values are the corrected values.</p>
Automated Pathlength	On or Off (affects pedestal measurements only)	<p><b>Optional automated pathlength selection.</b> Allows the software to use the optimal (shorter) pedestal pathlength for high concentration samples to help prevent detector saturation (see <a href="#">Detection Limits</a> for details).</p> <ul style="list-style-type: none"> <li>When selected, the shorter pathlength is used when any wavelength between 220 nm and 850 nm has 10 mm equivalent absorbance value of 12.5 or higher. For wavelengths between 190 nm and 219 nm the change to the shorter pathlength occurs when any wavelength in this range has a 10 mm equivalent absorbance value of 10 or higher.</li> <li>When deselected, the pedestal pathlength is restricted to 10 mm across all wavelengths.</li> </ul> <p><b>Note:</b> In either case, displayed absorbance values have been normalized to a 10 mm pathlength equivalent.</p>
Baseline Correction	On or off  Enter baseline correction wavelength in nm or use default value (750 nm)	<p><b>Optional user-defined baseline correction.</b> Can be used to correct for any offset caused by light scattering particulates by subtracting measured absorbance at specified baseline correction wavelength from absorbance values at all wavelengths in sample spectrum. As a result, absorbance of sample spectrum is zero at specified baseline correction wavelength.</p>

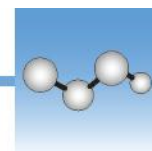
### Related Topics

- [Instrument Settings](#)



Measure UV-Vis





## Measure Kinetics

Make time-based kinetic measurements using the cuvette holder (NanoDrop One<sup>C</sup> model instruments only).

[Measure Kinetics](#)

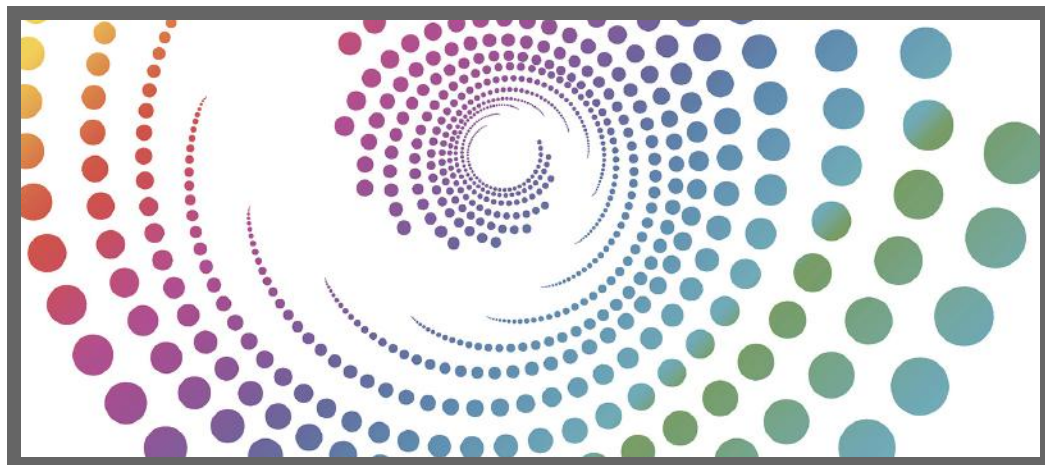
[Create Kinetics Method](#)

[Edit Kinetics Method](#)

[Reported Results](#)

[Settings](#)

[Detection Limits](#)



## Measure Kinetics

The NanoDrop One<sup>C</sup> model instrument can be used to make time-based kinetic measurements on samples in cuvettes. Up to 3 wavelengths between 190 nm and 850 nm can be designated for continuous absorbance monitoring at user-defined intervals in up to 5 stages. Cuvette measurements offer an extended lower [detection limit](#) and an optional 37 °C heater and micro-stirrer.

**Note** The instrument arm can be up during cuvette measurements, which allows you to add reagents to the sample solution if desired.

## To make kinetic measurements

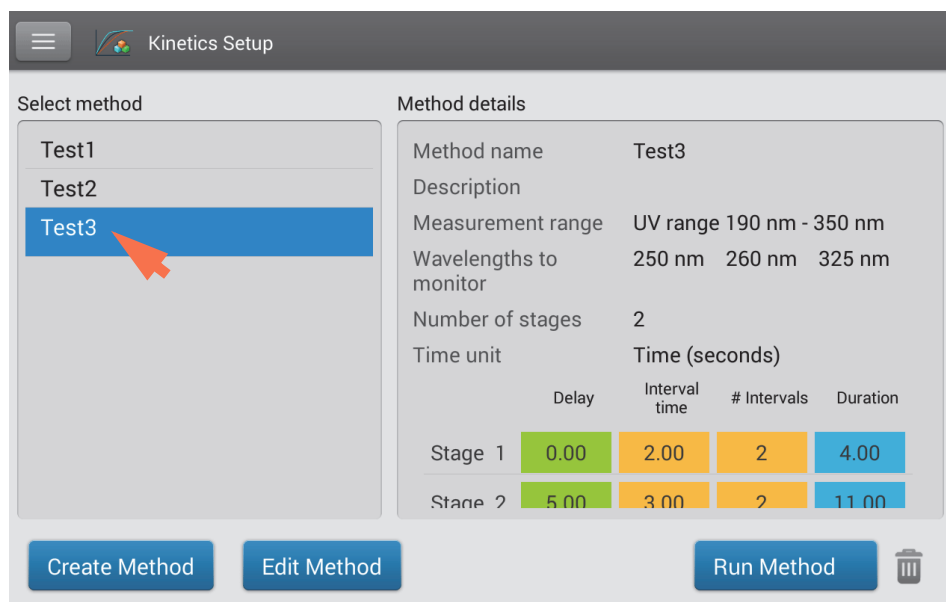
### NOTICE


- To prevent damage from spills, keep containers of liquids away from the instrument.
- Do not use a squirt or spray bottle on or near the instrument as liquids will flow into the instrument and may cause permanent damage.

### ❖ To measure a sample using the Kinetics application

1. From the instrument Home screen, select the **Kinetics** tab and tap the **Kinetics** icon.

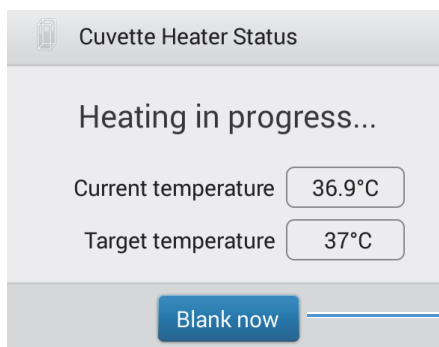
The Kinetics Setup screen is displayed. If one or more kinetic methods exist in the currently selected Data Storage Location, they will be listed in the Select Method box. A description of the selected method appears in the Method Details box.



2. Select a method:
  - select an existing method by tapping the **method name** in the Select Method box
  - [create a new method](#) by tapping **Create Method**, specifying the [method settings](#) and choosing **Save Method**
  - [edit an existing method](#) by tapping the **method name** and choosing **Edit Method**
3. Specify any cuvette options such as heating or stirring by tapping  > **Settings** (see [General settings](#) for details).
 

**Note:** If your cuvette pathlength is not 10 mm, specify the correct pathlength in General Settings.
4. Tap **Run Method**.
5. Measure a blank:
  - Fill clean, dry cuvette with enough blanking solution to cover [instrument optical path](#)
  - Lift instrument arm and insert blanking cuvette into cuvette holder, making sure to align light path of cuvette with light path of instrument
  - Tap **Blank**

If **Heat Cuvette to 37 °C** is selected in [General Settings](#), a message tells you the current temperature and waits for the heater to reach the target temperature before starting the measurements:



To override the wait and start the blank measurement immediately, tap **Blank Now.**

- Wait for blank measurement to complete and then remove cuvette

**Note:** The heater target temperature is not adjustable.

#### 6. Measure a sample:

- Fill clean, dry cuvette with enough sample solution to cover [optical path](#)
- Insert sample cuvette into cuvette holder, making sure to align light paths
- Tap **Measure**

If **Heat Cuvette to 37 °C** is selected in [General Settings](#), a message tells you the current temperature and waits for the heater to reach the target temperature before starting the measurements:

**Note:** You may add reagents to the sample solution at any time during the measurement

Use the **Pause** button at the bottom of the measurement screen to pause the experiment (if you need to end the experiment early, tap **Stop**)



- Wait for all measurement stages to complete
- Remove cuvette and clean it according to manufacturer specifications

Results for each measurement in each interval are displayed in real time. When all stages are completed, the [spectra and reported values](#) for the entire experiment are displayed.

7. When you are finished reviewing the data, tap **End Experiment**. Each saved experiment contains one complete set of kinetic measurements based on the selected method.

## Related Topics

- [Measure a Sample Using a Cuvette](#)

- [Best Practices for Cuvette Measurements](#)
- [Prepare Samples and Blanks](#)
- [Basic Instrument Operations](#)

## Create Kinetics Method

Kinetics methods can be created and run only on the NanoDrop One instrument. However, once the method is created, it can be saved in the NanoDrop One database on the local instrument, or in the NanoDrop Viewer database on a connected PC. To create a new kinetics method:

- from Home screen, tap **Kinetics** tab > **Kinetics** application
- tap **Create Method** (the method settings are displayed with [Name and Range](#) tab selected)

The screenshot shows the 'Kinetics Setup' application interface. At the top, there is a menu icon and the title 'Kinetics Setup'. Below this, there are two tabs: 'Name and Range' (selected) and 'Stages and Intervals'. The 'Name and Range' tab contains the following fields and options:

- Method name:** A text input field containing 'Test'.
- Description:** An empty text input field.
- Measurement range:** A section with four radio button options:
  - UV range (190 nm - 350 nm)
  - Visible range (350 nm - 840 nm)
  - UV-Vis range (190 nm - 840 nm)
  - Custom range: 190 nm to 350 nm
- Wavelengths to monitor:** A table with three rows:

Item	Wavelength (nm)
1	250
2	260
3	325

At the bottom of the screen, there are two buttons: 'Save Method' and 'Run Method'.

- enter **Method Name** and **Description** (if desired), select **Measurement range** and specify up to three **Wavelengths to monitor**

- tap **Stages and Intervals** tab (the stages and intervals settings are displayed)

	Delay	Interval time	# Intervals	Duration
Stage 1	0	3	3	9
Stage 2	0	2	3	6
Stage 3	5	5	2	15

- select **Number of stages** and **Time unit** (minutes or seconds)
- for each stage, specify **# intervals**, **Interval times** and any **Delays** between stages

The colored rows and boxes at the right visually represent the specified stages. The colored **rows** show the start and end times for each stage; the colored **boxes** correspond with the specified delay and number of intervals for each stage.

- to save the method and return to the Kinetics menu, tap **Save Method**

**Note** The method is saved in the currently selected Data Storage Location (local instrument or a connected PC).

- to run the method, tap **Run Method**

## Related Topics

- [Edit Kinetics Method](#)

## Edit Kinetics Method

Kinetics methods can be edited only on the NanoDrop One instrument. To edit an existing kinetics method:

- if the instrument has a connected PC (Ethernet or Wi-Fi), make sure Data Storage is set to the correct location for the kinetics method you want to edit

- from Home screen, tap **Kinetics** tab > **Kinetics** application
- select a method by tapping the method name in the Select Method box
- tap **Edit Method**
- edit [method settings](#) as desired
- tap **Save Method** to save your changes
- tap **Run Method** to run the updated method

### Related Topics

- [Create Kinetic Method](#)

## Kinetics Reported Results

### Absorbance measurement screen

The absorbance measurement screen appears immediately after you tap Measure in the kinetics experiment. This screen shows the absorbance spectrum for each measurement, with wavelength on the X-axis and absorbance on the Y-axis. Vertical lines indicate the specified wavelengths to monitor. The list at the right shows the time each measurement was taken in each specified stage (drag the tab down to see more entries). Each item in the list at the right has a corresponding absorbance spectrum at the left. The image below highlights the available features.

Menu of options; **tap** to open

Method name

User-defined wavelengths (i.e., 260 nm, 340 nm, 660 nm)

**Tap row** to select measurement and update spectrum; **tap more rows** to overlay up to five spectra. **Press and hold** row to view measurement details.

**Drag tab down/up** to see more/less sample data

**Pinch and zoom** to adjust axes; double-tap to reset

**Swipe screen left** to view Rate measurement screen

**Tap** to end experiment and export data

Stage	Time (seconds)
1	560.01
1	570.00
1	580.01
1	590.01
1	600.01

**Note** For measurements taken with nonstandard (other than 10 mm) cuvettes, the spectra are normalized to a 10 mm pathlength equivalent.

## Rate measurement screen

To see the Rate measurement screen, swipe the absorbance measurement screen (see above) to the left. The Rate measurement screen shows a sample's absorbance measured at each user-defined wavelength over time, with time on the X-axis and absorbance on the Y-axis. Measurements taken at each specified wavelength are presented in a unique color. A key showing the monitored wavelengths and their assigned colors appears in the upper left corner of the screen.

User-defined wavelengths



**Tap** to update plot to show change in measured absorbance over time (see example below)

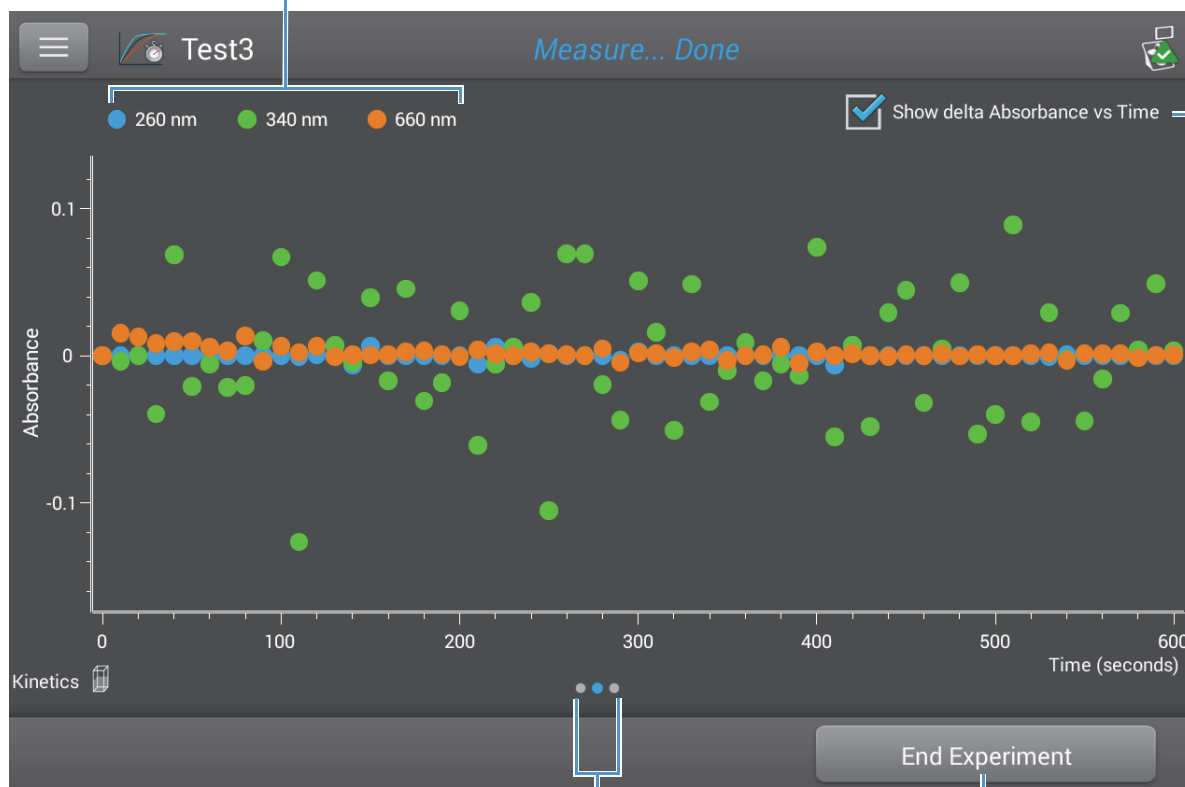
**Swipe screen left** to view data table; **swipe right** to return to absorbance measurement screen

**Tap** to end experiment and export data



Tap **Show Delta Absorbance Vs Time** to show the change in measured absorbance over time, where each data point is the difference in absorbance from the previous measurement.

User-defined wavelengths



**Tap** to update plot to show measured absorbance over time (see example above)

**Swipe screen left** to view data table; **swipe right** to return to absorbance measurement screen

**Tap** to end experiment and export data

## Data Table

To see the data table, swipe the rate measurement screen (see above) to the left. Each row in the table shows the absorbance values at all user-defined wavelengths at a given stage and time. Scroll down to see measurement information that is out of view. The image below highlights the available features.

Measurement number	Stage	Measurement time (seconds)	Absorbance values for each user-defined wavelength		
#	Stage	Time (seconds)	A260	A340	A660
10	1	90.01	0.032	-0.008	0.282
11	1	100.01	0.032	0.059	0.288
12	1	110.01	0.031	-0.067	0.290
13	1	120.01	0.032	-0.016	0.297
14	1	130.00	0.032	-0.009	0.296
15	1	140.00	0.026	-0.014	0.297
16	1	150.01	0.032	0.026	0.297

**Press and hold** row to view measurement details

**Swipe screen right** to return to Rate measurement screen

**Tap** to end experiment and export data

## Measurement Details

To view details for a measurement, from the absorbance measurement screen or data table, press and hold the measurement row. Here is an example:


The screenshot shows the 'Measurement Details' screen for a measurement labeled '#1'. The screen is divided into several sections with callouts explaining their functions:

- Application used:** Kinetics
- Sampling method:** Cuvette
- Measurement number:** #1
- Date/time measured:** 1/11/2016 7:37:17 PM
- Meas stage:** 1
- Meas time:** 0.00
- Absorbance at 260 nm:** 0.0323
- Absorbance at 340 nm:** 0.0263
- Absorbance at 660 nm:** 0.2073
- Cuvette pathlength:** 10 mm
- Print this screen:** Represented by a printer icon.
- Return to previous screen:** Represented by an 'OK' button.
- Delete this measurement:** Represented by a trash can icon.
- User-defined wavelengths:** A260, A340, and A660.
- Method details (scroll up to view more):** A note indicating that scrolling up reveals more information about the measurement method.

### Related Topics

- [Basic Instrument Operations](#)

## Settings for Kinetic Measurements

To show the Kinetics settings, from the instrument Home screen, tap **Kinetics** (tab) > **Kinetics** (Method), and either tap **Create Method** or select a method and tap **Edit Method**. You can also display the settings from any Kinetics measurement screen, by tapping  > **Kinetics Setup**.

**Note** If the instrument has a connected PC (Ethernet or Wi-Fi), kinetics methods can be located in the NanoDrop One database on the local instrument, or in the NanoDrop Viewer database on a connected PC. Use the Data Storage box to select which database is active and then follow the steps to display the Kinetics methods that are stored in that location and their associated settings.

The settings appear on two tabs: “Name and Range” and “Stages and Intervals.” See the table below for details.

Tab	Setting	Description
Name and Range	Method name	<b>Enter a name</b> for this method (this name appears in the <a href="#">Kinetics Setup</a> box after the method has been saved).
	Description	Enter a detailed <b>description</b> for this method, if desired, such as the type of samples, added reagents, etc.
	Measurement range	<b>Select the spectral range</b> in which this method will acquire data. Available options: <ul style="list-style-type: none"> <li>• Ultra-violet only (190 nm - 350 nm)</li> <li>• Visible only (350 nm - 850 nm)</li> <li>• Ultra-violet and visible (190 nm - 850 nm)</li> <li>• Custom (specify starting and ending point in nanometers)</li> </ul> <b>Note:</b> For measurements taken with nonstandard (other than 10 mm) cuvettes, the spectra are normalized to a 10 mm pathlength equivalent.
	Monitored wavelengths	<b>Enter up to 3 wavelengths</b> to be measured and reported at run time. <p><b>Note:</b> All specified wavelengths must fall within the selected <a href="#">measurement range</a>.</p>
Stages and Intervals	Number of Stages	<b>Specify up to 5 stages</b> for kinetic measurements. Each stage can have unique Delay, Interval Time and # Intervals settings. <p><b>Note:</b> Many kinetic measurements include only one stage. Additional stages are necessary only when a variation in stage interval or duration is needed.</p>

Tab	Setting	Description
	Time Unit	Select the <b>unit</b> for time-based measurements (seconds or minutes).
	Stage 1, 2, etc.	<p>Specify the available settings for each stage:</p> <ul style="list-style-type: none"> <li>• <b>Delay.</b> Specify a delay before a stage starts.</li> <li>• <b>Interval Time.</b> Specify the length of time between measurements taken during this stage (minimum is 2 seconds). The first measurement occurs when the stage starts (or after the delay is completed if a Delay is specified).</li> </ul> <p><b>Note:</b> If two or more stages are specified with Delay set to zero, two measurements occur at the same time (the measurement at the beginning of the new stage directly overlaps the one at the end of the previous stage).</p> <ul style="list-style-type: none"> <li>• <b># Intervals.</b> Specify the number of absorbance measurements to take in this stage.</li> </ul> <p><b>Note:</b> Since the first measurement is taken when the stage starts, the number of measurements reported for each stage will be the # <b>Intervals</b> setting plus 1.</p> <ul style="list-style-type: none"> <li>• <b>Duration.</b> Readout shows the total time required for this stage, including any delay and all specified intervals.</li> </ul>

The colored **rows** at the right (see image below) show the start and end times for each stage; the colored **boxes** at the right correspond with the specified delay and number of intervals for each stage.



If no delay is specified, absorbance measurements are taken at the start and end of each stage and after each specified interval. If a delay is specified, as in stage 3 above, the first measurement occurs at the start of the first interval. If the unit is seconds in the example above, a total of 11 measurements are taken at the following times over a period of 32 seconds:

Tab	Setting	Description
		<ul style="list-style-type: none"><li>• Stage 1: 0, 3, 6 and 9 seconds</li><li>• Stage 2: 9, 11, 13, 15 and 17 seconds</li><li>• Stage 3: 22, 27 and 32 seconds</li></ul> <p><b>Note:</b> Kinetic experiments are limited to 1000 measurements. This means the total number of measurements from all intervals in all stages must be less than 1000. Consider available instrument or computer disc space for lengthy experiments.</p>

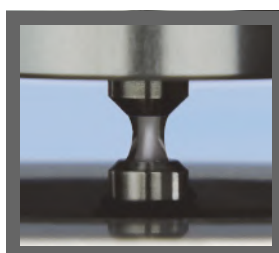
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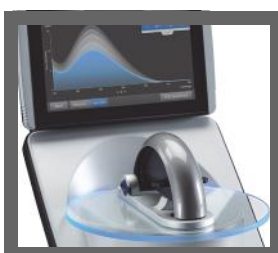
### Related Topics

- [Instrument Settings](#)

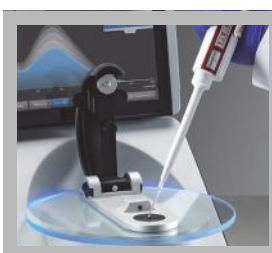
## Learning Center



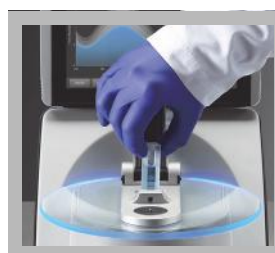
**How the Instrument Works**



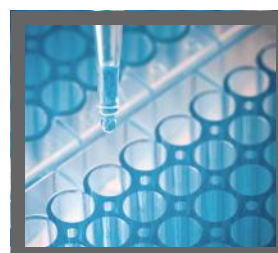
**Set Up the Instrument**



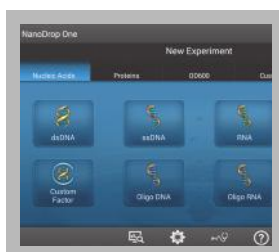
**Measure a Micro-Volume Sample**



**Measure using a Cuvette**



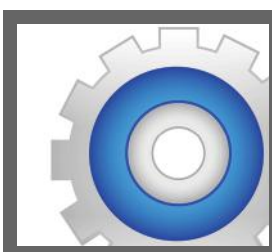
**Prepare Samples and Blanks**



**Basic Instrument Operations**



**Acclaro Sample Intelligence**



**Instrument Settings**



**NanoDrop One Viewer**



**Multimedia**

## Micro-Volume Sampling—How it Works

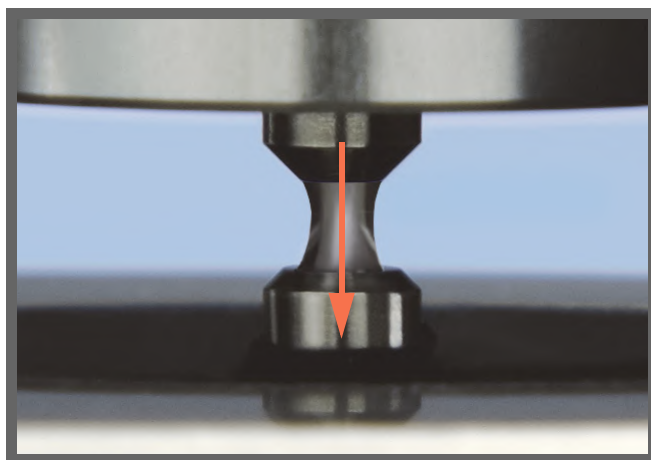
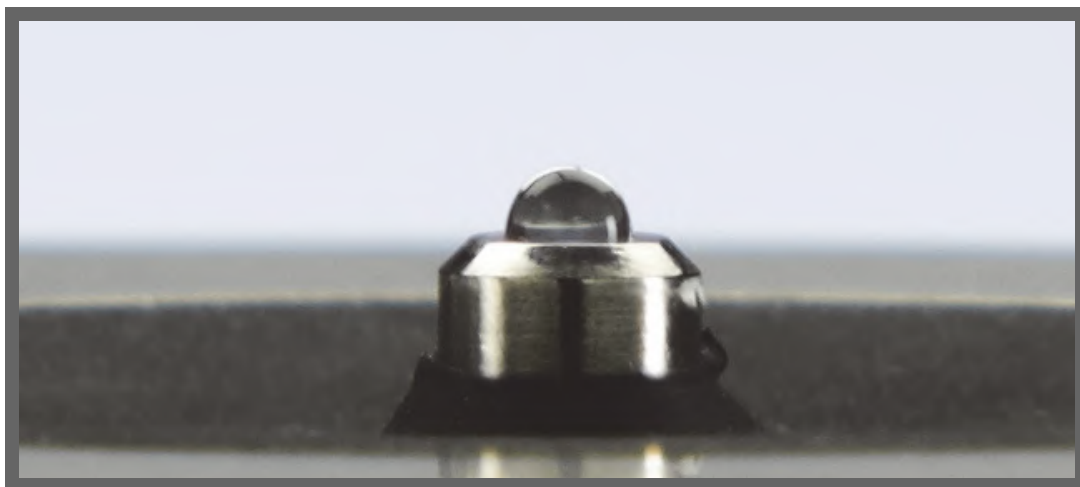
Surface Tension

Absorbance Spectrum

Sample Absorbance

Sample Concentration

Baseline Correction

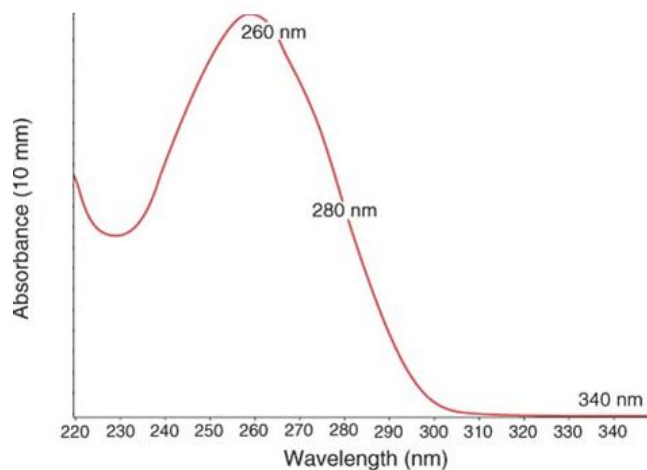


### Surface Tension

The NanoDrop One spectrophotometer uses surface tension to hold a small volume of sample between two pedestals. The patented sample retention system enables the measurement of highly concentrated samples without the need for dilutions.

A fiber optic cable embedded in the upper pedestal leads to a xenon light source. A second cable embedded in the lower pedestal leads to a detector. When the instrument arm is down, the sample forms a liquid column, essentially bridging the gap between the two fiber optic cables.





$$\text{Absorbance} = -\log \left[ \frac{\text{intensity}_{\text{sample}}}{\text{intensity}_{\text{blank}}} \right]$$

### Beer-Lambert equation

$$A = \epsilon \cdot b \cdot c$$

where:

**A** = absorbance in absorbance units (A)

**ε** = wavelength-dependent molar absorptivity coefficient (or extinction coefficient) in liter/mol-cm

**b** = pathlength in cm

**c** = analyte concentration in moles/liter or molarity (M)

## Absorbance Spectrum

The light passes through the liquid column to the detector, which generates a spectrum of absorbance versus wavelength. The spectrum shows the amount of light absorbed by the molecules of the sample at each measured wavelength.

**Note:** To prevent evaporation, which affects measurement accuracy, close the arm quickly after you finish loading a sample or blank.

The example at the left shows a typical absorbance spectrum taken of a nucleic acid sample. The spectrum is measured from 190 nm to 850 nm. The displayed range may vary for each application.

## Sample Absorbance

When the instrument is blanked, a reference spectrum is taken of the blanking solution and stored in memory. For each sample measurement, the sample intensities along with the blank intensities are used to calculate the total absorbance of the sample according to the equation at the left.

## Sample Concentration

The Beer-Lambert equation (Beer's law) shown at the left is used to correlate sample absorbance with concentration.

The pathlength is the distance between the two pedestals, which varies in real time during each measurement. This auto-ranging pathlength technique produces accurate concentration results over a wide dynamic range.

## Baseline Correction

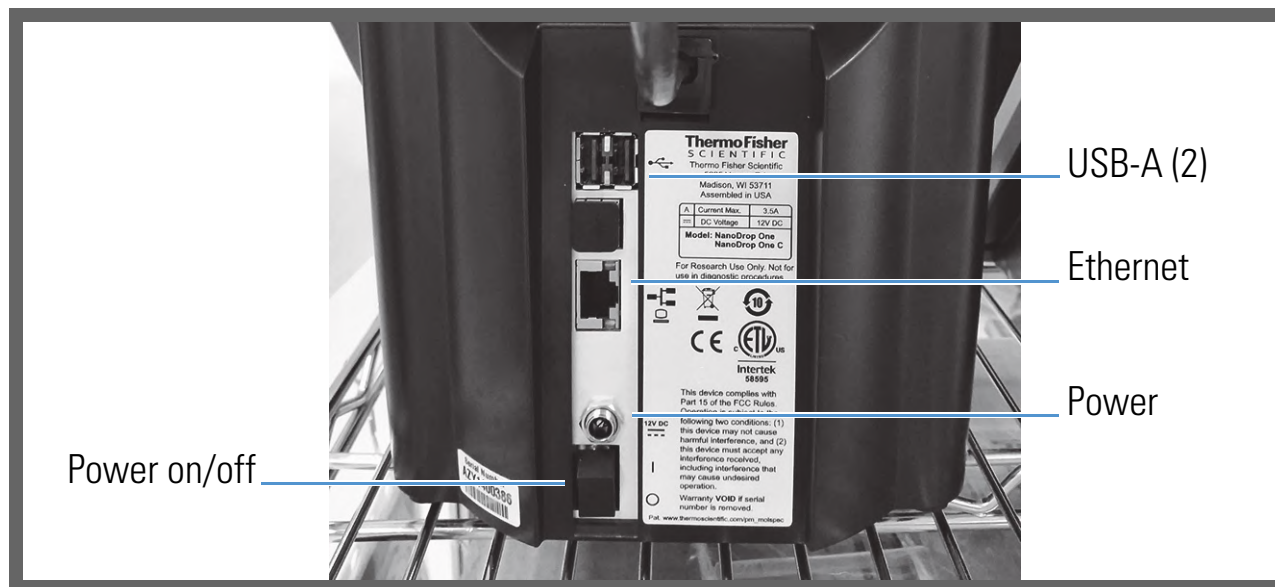
For some applications, the instrument can be set up to apply a baseline correction to each measurement to minimize any offset caused by light scattering particulates in the sample spectra. The correction subtracts the absorbance value at a reference wavelength that is close to zero from the absorbance value at each wavelength across the spectrum, essentially “anchoring” the spectrum to zero absorbance units at the reference wavelength.

### Related Topics

- [Instrument Models and Features](#)
- [Measure a Micro-Volume Sample](#)

- [Calculations for Nucleic Acid Measurements](#)
- [Calculations for Protein A280 Measurements](#)

## Set Up the Instrument



### Connect Power



**CAUTION** Avoid shock hazard. Each wall outlet used must be equipped with a ground. The ground must be a noncurrent-carrying wire connected to earth ground at the main distribution box.

Connect the provided power cord to a grounded wall outlet. [Tap here](#) for more information.

### Connect an Accessory


To connect a compatible printer or other compatible accessory such as a USB keyboard and/or mouse to the instrument, use any USB port on the instrument (front, back-left or back-right). See [Accessories](#) for information about accessories compatible with the NanoDrop One instruments.

## Set Up Bluetooth Connections

Use Bluetooth™ to connect the instrument to one or more Bluetooth (wireless) input devices such as a Bluetooth keyboard, mouse or barcode scanner.

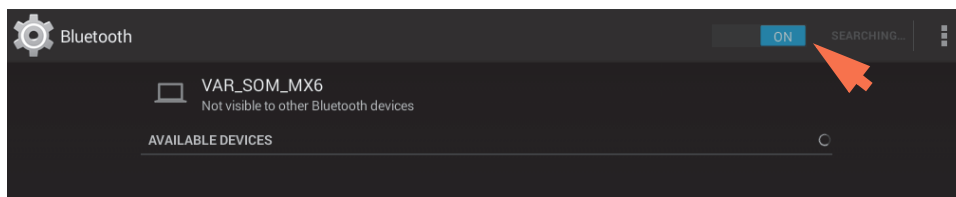
**Note** Make sure the device is labeled “Bluetooth” and not just “wireless.” All Bluetooth devices are wireless but not all wireless devices will run with Bluetooth.

### Set up Bluetooth connections on the instrument

- from instrument Home screen, tap  (**Settings**)
- tap **System** tab
- tap **Bluetooth** (if Bluetooth is disabled, button in upper right is set to “Off” and no Bluetooth input devices are listed)

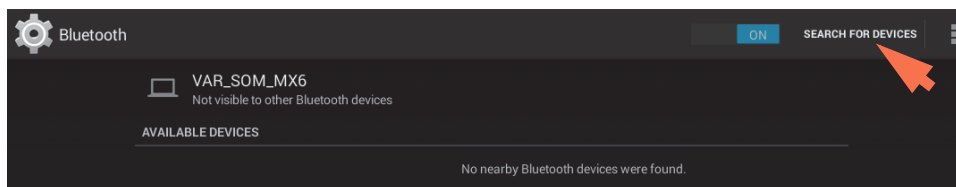


- tap **Off** button to enable Bluetooth connectivity (button turns blue, changes to “On” and software automatically searches for any available Bluetooth input devices)

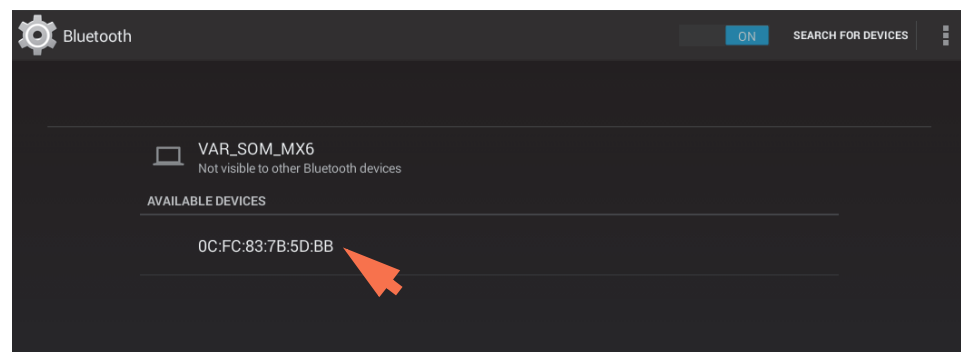


If no Bluetooth devices are found, after a few seconds the message “No nearby Bluetooth devices were found” is displayed

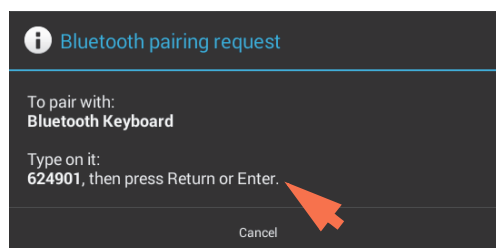
- to **add a Bluetooth device**, follow manufacturer instructions to pair the device (for example, you may need to hold down a button) and tap **Search For Devices** on instrument)



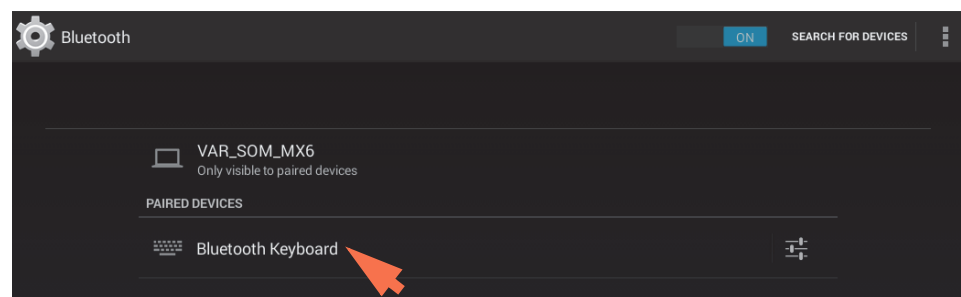
device name should appear in Available Devices list



- to pair device, **tap its name** in Available Devices list (a pairing request similar to the following may be displayed)

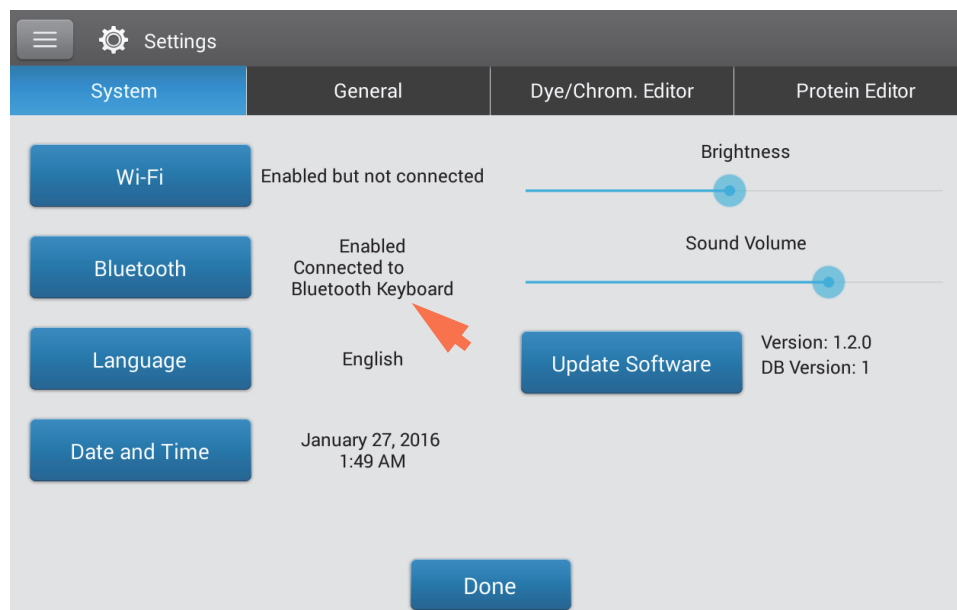


- **complete any instructions** to pair the device



**Note** If your Bluetooth device does not pair, restart the device and then repeat the steps above to pair it with the instrument (you may also try turning Bluetooth off and back on). After a device is paired, it remains paired even after the instrument is restarted.



- tap **Back** (Bluetooth status is displayed at right of Bluetooth button)

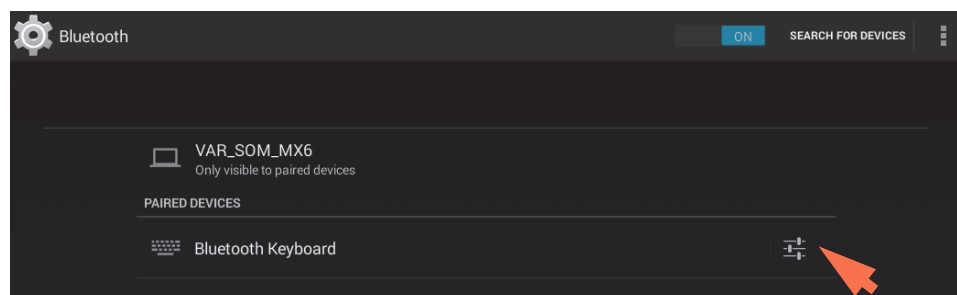


- repeat steps above to add another Bluetooth device or tap **Done** to close Settings

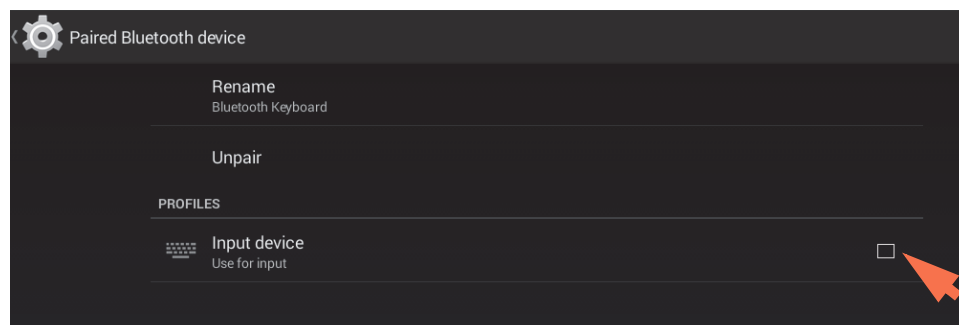
### Deselect Bluetooth input device

You may want to stop using a Bluetooth device for input without disconnecting or unpairing it. This allows others to easily reselect and use the device for input. For example, if there are multiple connected and paired Bluetooth input devices such as a keyboard and a barcode scanner, follow these steps to select the devices to use or to deselect devices you don't want to use:

- from instrument Home screen, tap 
- tap **System** tab
- tap **Bluetooth**
- to deselect a paired Bluetooth device such as a keyboard for input, tap its **Profiles** button 



- deselect **Use For Input** by clearing it's associated checkbox





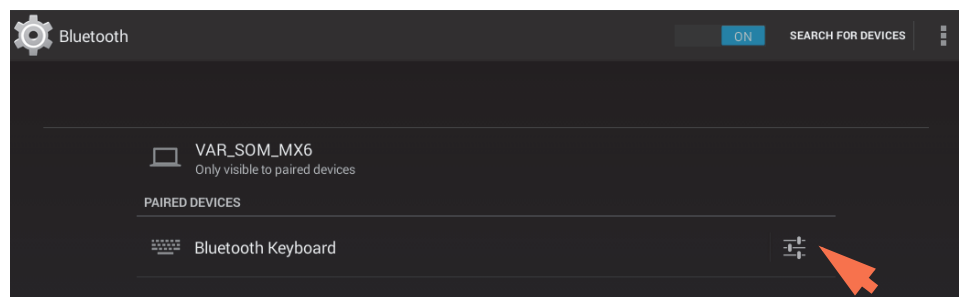
- tap **Paired Bluetooth Device** in upper left to return to previous screen
- tap **Back** to return to System settings
- tap **Done** to close Settings

**Note**

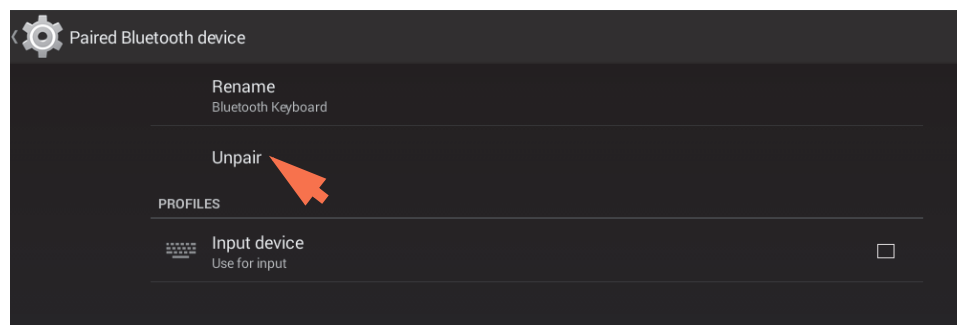
- If no Bluetooth device is selected for input, the instrument relies on the integrated touchscreen keyboard for input.
- To select the device again, follow the steps above and select the device's Use for Input checkbox.

**Disconnect Bluetooth device**

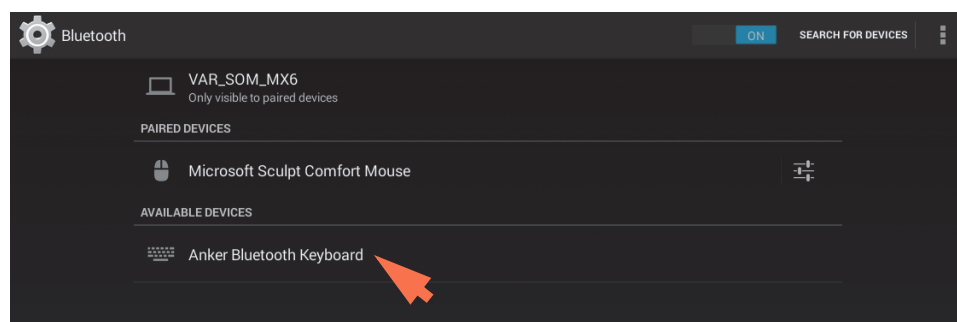
- from instrument Home screen, tap 
- tap **System** tab
- tap **Bluetooth**
- to disconnect paired Bluetooth device, tap its Profiles button 



- tap **Unpair**



device is no longer listed under “Paired Devices” but remains in Available Devices list



- tap **Back** to return to System settings
- tap **Done** to close Settings

## Set up Ethernet Connection

The instrument Ethernet port can be used to set up a wired connection between the instrument and a personal computer (or PC). The connected computer can then be used to store or view data acquired with the NanoDrop One instrument. ([NanoDrop One Viewer software](#) must be installed on the computer.)

Tools needed:

- Standard (straight through) Ethernet cable (CAT5e or newer is recommended)

**Note** If the computer is an older model, you may need a crossover Ethernet cable instead. Most newer model computers are designed to automatically detect and work with both cable types. However, a straight through cable will provide best performance.

### Set up Ethernet connection


- connect Ethernet cable between Ethernet port on instrument back panel (see image above) and Ethernet port on computer

## Set up Wireless Connections

Use Wi-Fi™ to connect the instrument to a remote computer through a wireless local area network (WLAN). The remote computer can then be used to store or view data acquired with a NanoDrop One instrument.

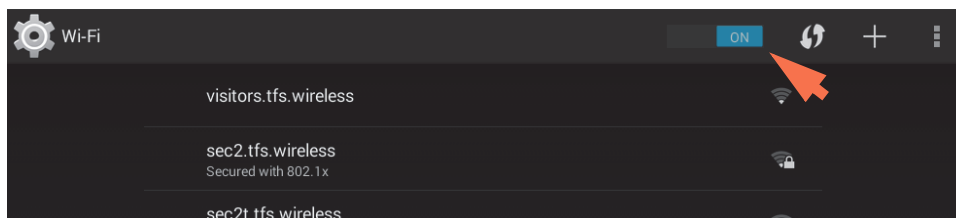
**Note** To store or view collected data on a connected computer using Wi-Fi, NanoDrop One Viewer software must be installed on the remote computer and the computer must be configured for Wi-Fi data storage. The instrument must also be connected to the remote computer's network host and have Wi-Fi enabled.

### Select Wi-Fi network on the instrument

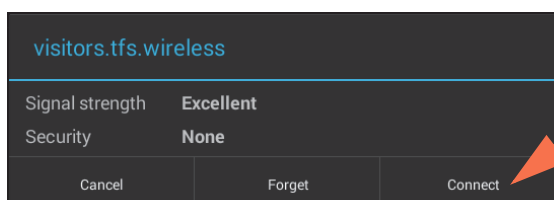
- from instrument Home screen, tap  (Settings)
- tap **System** tab
- tap **Wi-Fi** (if Wi-Fi is disabled, button in upper right is set to “OFF” and no wireless networks are listed)



- tap button to enable Wi-Fi and display available Wi-Fi networks



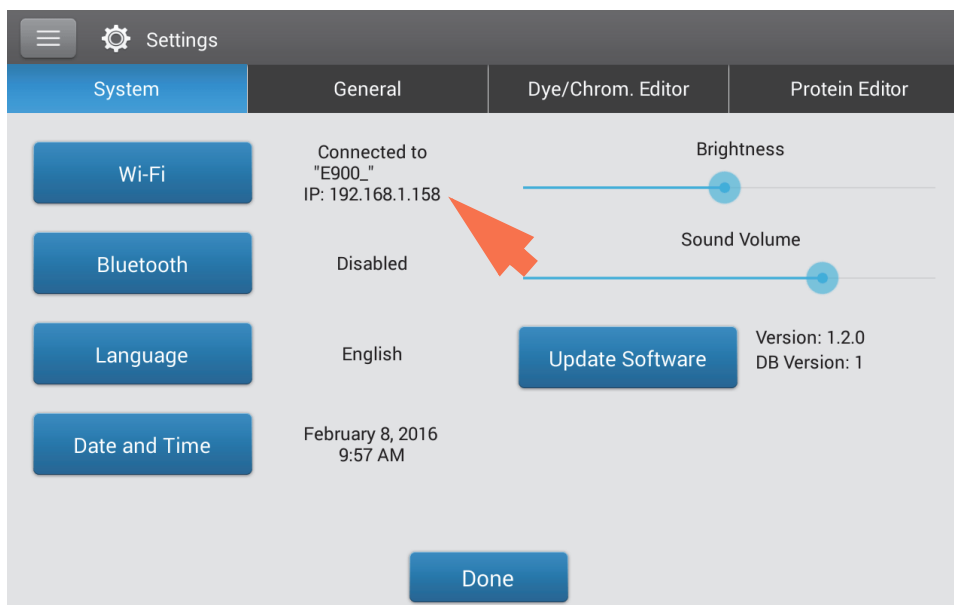
- select remote computer's Wi-Fi network host and tap **Connect** (here is an example)





- tap **Back** to exit Wi-Fi setup (if the connection is successful, the instrument is assigned an IP (Internet Protocol) address, which appears at the right of the Wi-Fi button as in the example below)

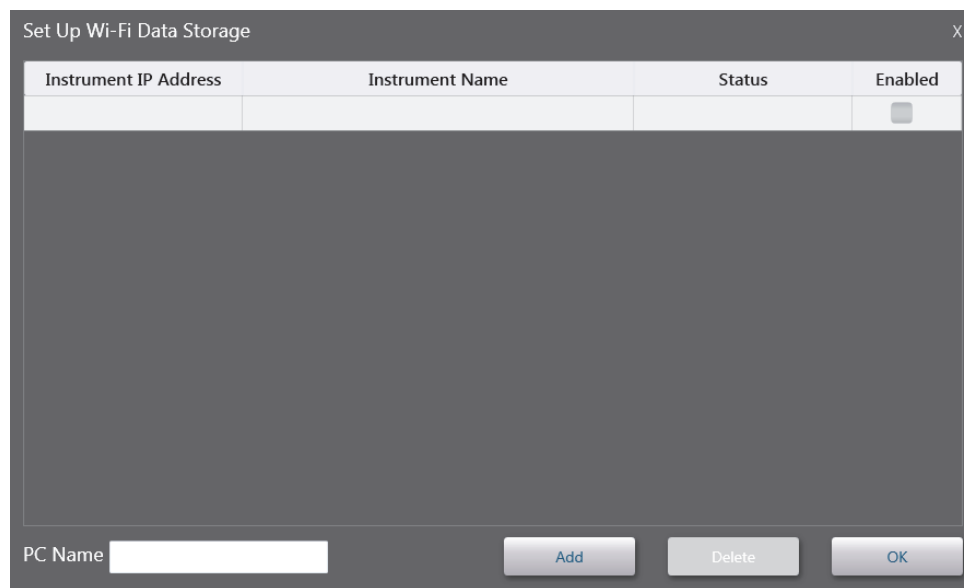
**Note** Some Wi-Fi networks may require an identity, password or other information before you can connect to them, or they may be anonymous (that is, you may have to search for them by name). For more information, see the system administrator at your work site.



- record IP address (you will need to enter it on the remote computer in the next section)
- tap **Done** to exit Settings

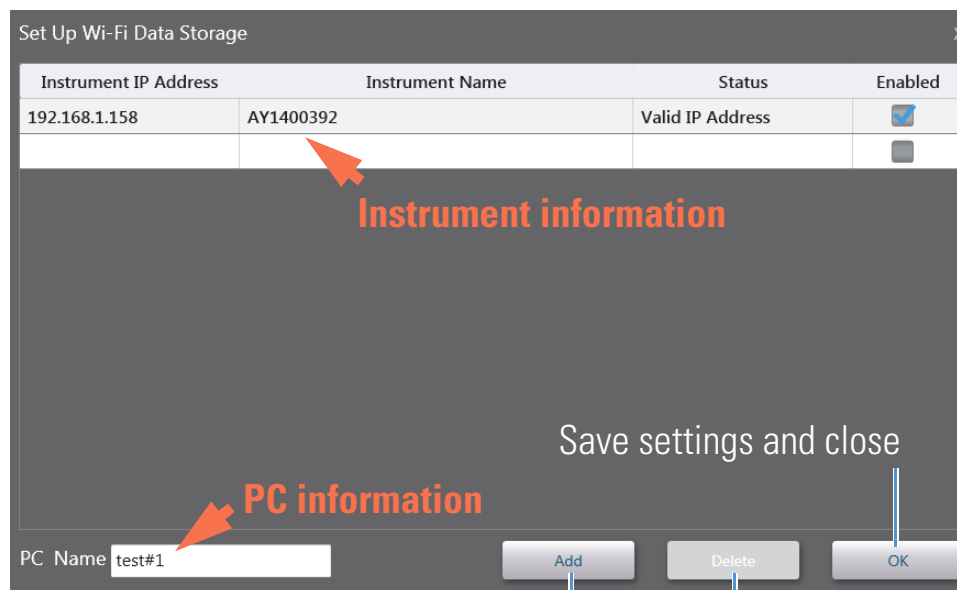
### Configure Wi-Fi data storage on the remote computer

- from remote computer, open **NanoDrop One Viewer** software
- choose **File** (menu) > **Set Up Wi-Fi Data Storage** (the following screen is displayed)



- enter the following information:
  - **Instrument IP address** (displayed on instrument in **Settings > System**, see previous section; if IP address is valid, **Status** column shows “Valid IP Address”)
  - unique **Instrument Name** (in case there are multiple instruments in the same lab on the same network)
  - **PC Name**, such as the computer’s assigned name or an invented name (the name you enter will appear in the “select a data storage location” list box on the instrument (see the next section)

- make sure the instrument's **Enabled** button is selected (see example below)



**Add** Wi-Fi connection  
(with a new instrument)


**Delete** selected  
Wi-Fi connection

- to set up another instrument, tap **Add** and then repeat steps above

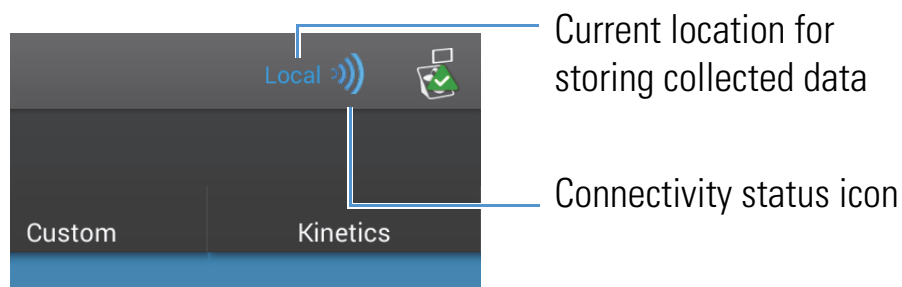
**NOTICE** You can add multiple Wi-Fi addresses to this list to make it easy to switch computers. However, only one Wi-Fi connection should be enabled during data collection to ensure the data integrity.

- to remove an item from the list, tap to select the row and then tap **Delete**
- when finished, choose **OK** to close Wi-Fi Data Storage setup

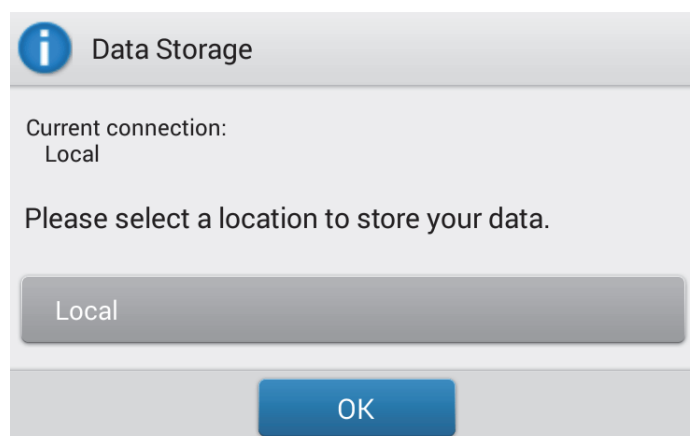
## Select location for saving collected data

- from instrument Home screen, tap **Connectivity Status** icon 

**Note** The Connectivity Status icon is active, i.e., blue, only when the instrument is connected to a personal computer (PC) with an [Ethernet cable](#) or through a properly configured wireless network, as in the example below.



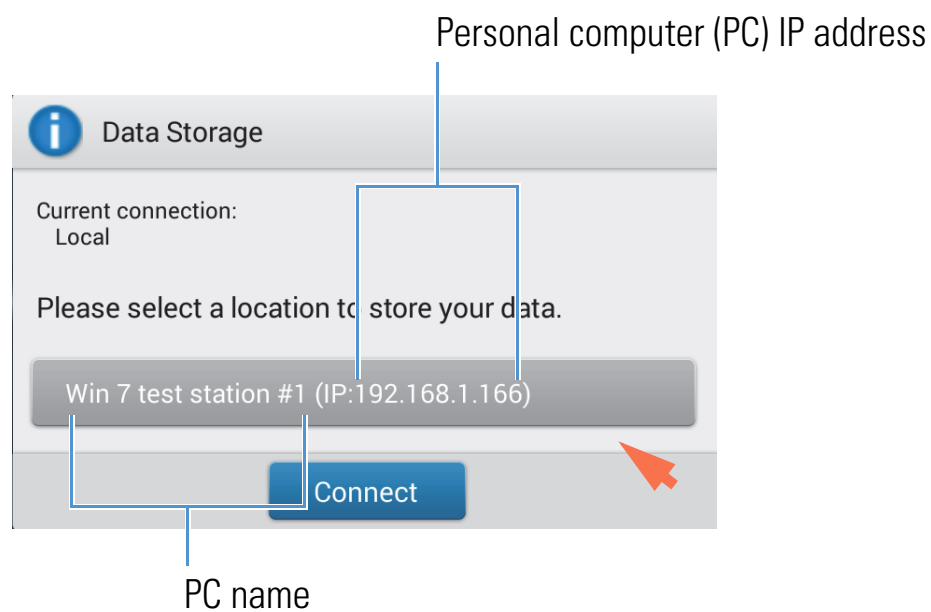
the Data Storage message box is displayed as in the example below



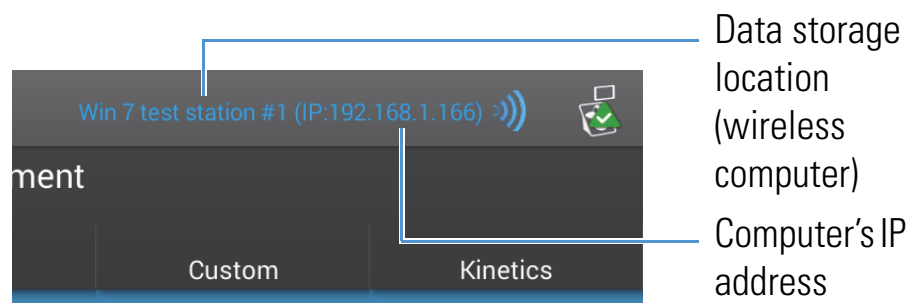
- select an available option below:
  - to store all subsequently acquired measurement results only in the NanoDrop One database on the instrument, set Data Storage to **Local** (see example above).
  - to store all subsequently acquired measurement results in the NanoDrop One Viewer database on a computer connected to the instrument with an Ethernet cable, set Data Storage to **Direct-Connect PC\*** (see [Set Up Ethernet Connection](#) for details).
  - to store all subsequently acquired measurement results in the NanoDrop One Viewer database on a computer connected to the instrument through a wireless network, set Data Storage to the **computer's assigned name\*** (see [Set Up Wi-Fi Connections](#) for details).

\* The Ethernet and wireless options listed above will also store data on the instrument as a backup.

Here is an example of a wireless configured destination computer selected for data storage



- tap **Connect** (or **OK** if connection had already been established) to close message box (new data storage location appears adjacent to Connectivity Status icon)



all subsequently acquired measurement results are saved in the NanoDrop Viewer database on the selected computer, and in the NanoDrop One database on the local instrument.

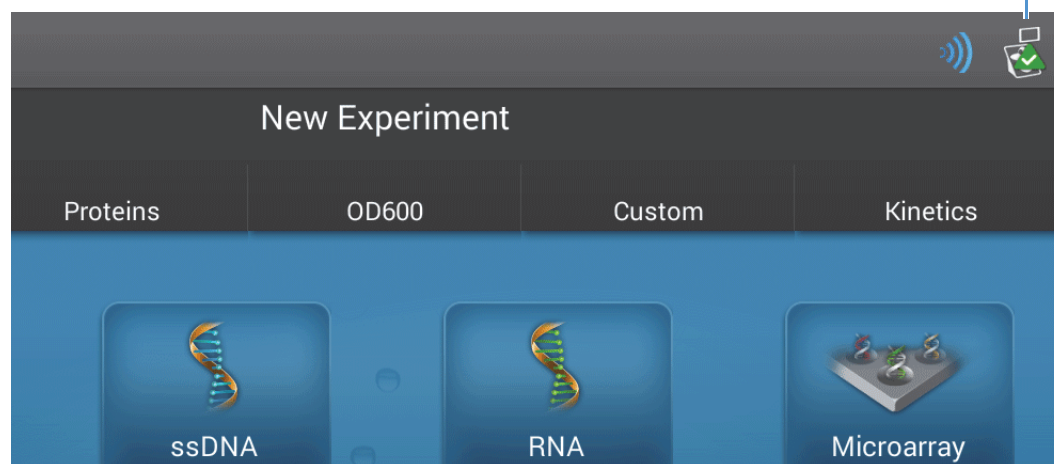
**Note**

- The NanoDrop One Viewer software does not need to be running for data from the instrument to be saved there.
- If the wireless or Ethernet connection is interrupted during a measurement, data storage switches back to the local instrument with no loss of data.
- [Custom methods](#) and [Kinetics methods](#) must reside on the connected computer when the data are configured for remote storage.
- When the instrument is connected to a computer with an Ethernet cable or through a wireless network, the Data Viewer icon on the instrument Home screen is unavailable. (You cannot use the instrument to view the NanoDrop One database on a connected computer.)


## Assess Instrument Connectivity

Use the System Status icon at the top right of the instrument Home screen to quickly assess the instrument's connectivity status including Bluetooth, Ethernet and Wi-Fi:

Tap to show connectivity status



### Show connectivity status

- tap  on instrument Home screen to open System Status box

Location of database where instrument is currently storing data (Local (instrument) or Connected PC)

System Status	
Instrument type	NanoDrop One C
Serial number	AZY1400392
Instrument status	Instrument initialization complete
Data storage location	Local
Wi-Fi status	Connected to "E900_" IP: 192.168.1.158
Bluetooth status	Enabled No paired devices
Software product version	1.2.0.358 Build 01/28/16 09:53 AM
Platform release	1.2.0.194 Build 01/28/16 09:26 AM
Firmware version	145
Android release	3.6

Wi-Fi status  
Bluetooth status

- tap **OK** to exit System Status

## Operating Specifications

The instrument operates reliably when the room environment meets these specifications:

- operating temperatures: 5 °C - 35 °C (41 °F - 95 °F)
- relative humidity (non-condensing): 20-80%

Locate the instrument away from air vents and exhaust fans to minimize evaporation.

**Note** If operating the instrument at the low end of the recommended humidity range, use adequate sample volume to avoid evaporation.

After the instrument is installed, you can leave it turned on.

### Related Topics

- [Safety and Operating Precautions](#)
- [Instrument Models and Features](#)

### 3 Learning Center

Set Up the Instrument

- [Optional Accessories](#)
  - [Instrument Settings](#)
-

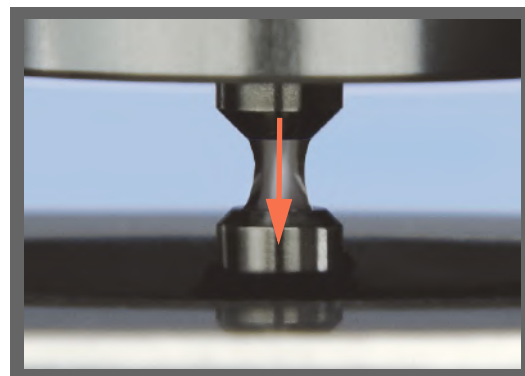


## Measure a Micro-Volume Sample

The NanoDrop One spectrophotometer uses surface tension to hold a small volume of sample between two pedestals. The patented sample retention system enables the measurement of highly concentrated samples without the need for dilutions. [Tap here](#) for details.

### Supplies needed

- NanoDrop One or NanoDrop One<sup>C</sup> spectrophotometer
- lint-free laboratory wipes
- calibrated precision pipettor (0–2  $\mu\text{L}$ )
- sample material resuspended in appropriate buffer solution (see [Preparing Samples](#))
- pure buffer solution for blanking instrument (see [Choosing and Measuring a Blank](#) or watch multimedia training [What is a blank?](#))



## Best practices for micro-volume measurements

### Cleaning pedestals for daily operation

- Before first measurement, clean both pedestals with a new laboratory wipe.
- [Run a blanking cycle](#) to verify pedestals are clean.
- After each measurement, clean both pedestals with new wipe to prevent carryover.
- After each set of measurements, clean pedestals with DI H<sub>2</sub>O (see [Clean pedestals between users](#))
- [Recondition pedestals](#) periodically to maintain their hydrophobic property.



### Pipetting Samples

- Use [recommended sample volumes](#) to ensure proper liquid column formation.
- Use calibrated precision pipettor (0–2  $\mu\text{L}$  volume range) with well-fitting, low-retention precision tips to apply sample material to instrument for measurement.

If using low accuracy (0-10  $\mu\text{L}$ ) pipettor, use 2  $\mu\text{L}$  sample volumes.

- Use new tip for each blank and sample aliquot.
- Use new aliquot of sample for each measurement.
- If solvents are used, make sure they are compatible with the pedestals. (see “Compatible Solvents” in [Hazardous Materials](#)).



### Recommended sample volumes

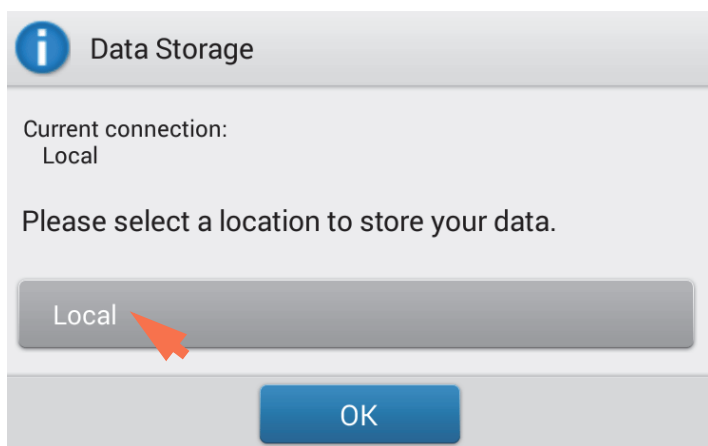
Application	Sample Volume
Nucleic acid (aqueous solution)	1 $\mu\text{L}$ <sup>a</sup>
Purified protein	2 $\mu\text{L}$
Other protein applications such as Bradford or BCA	2 $\mu\text{L}$
Microbial cell suspensions	2 $\mu\text{L}$

<sup>a</sup> Use 2  $\mu\text{L}$  for samples that contain materials that may reduce surface tension such as a surfactant.

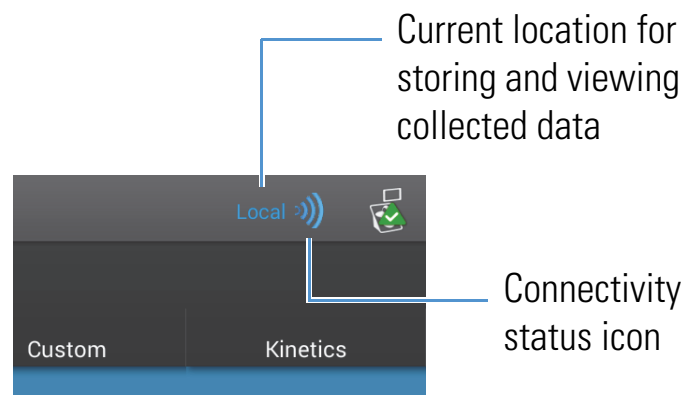
## To measure a micro-volume sample

### NOTICE

- Do not use a squirt or spray bottle on or near the instrument as liquids will flow into the instrument and may cause permanent damage.
- Do not use hydrofluoric acid (HF) on the pedestals. Fluoride ions will permanently damage the quartz fiber optic cables.

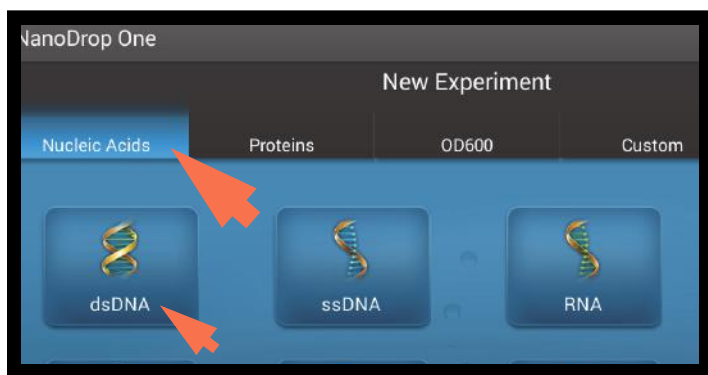


1. If the instrument has a working **Ethernet** or **wireless** connection to a personal computer (PC), the Connectivity Status icon is blue and shows the **currently selected location for storing and viewing data collected with the instrument.**



If the Connectivity Status icon is blue, **tap the icon** and set **Data Storage** to Local as shown at the left.

2. From the instrument Home screen, select an application tab such as Nucleic Acids and tap an application name such as dsDNA or RNA.





3. Lift the instrument arm and clean the upper and lower pedestals with new laboratory wipe.



4. Measure a blank:
  - Pipette 1–2  $\mu\text{L}$  blanking solution onto the lower pedestal and quickly lower the arm.
  - Tap **Blank** and wait for the measurement to complete.

**Tip:** If **Auto-Blank** is On, blank measurement starts automatically after you lower the arm.

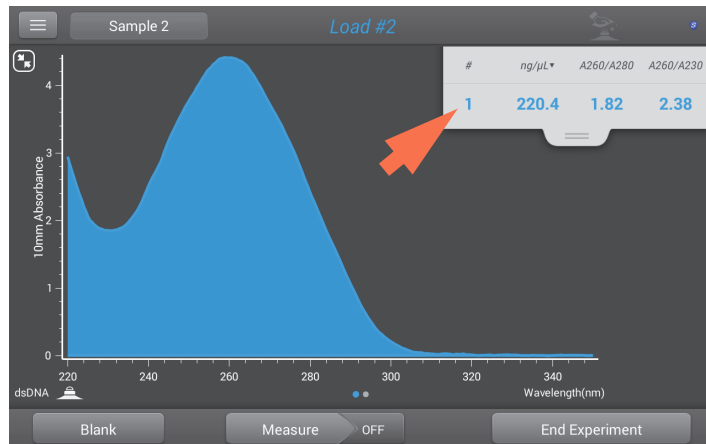
  - Lift the arm and clean both pedestals with a new laboratory wipe.



5. Measure the first sample:
  - Pipette 1-2  $\mu\text{L}$  sample solution onto the pedestal and quickly lower the arm (see [Recommended Sample Volumes](#) for more information).
  - Start the sample measurement:
    - if **Auto-Measure** is On, lower arm
    - if Auto-Measure is off, lower arm and tap **Measure**
  - When the sample measurement is completed, the spectra and reported values are displayed.

### 3 Learning Center

#### Measure a Micro-Volume Sample



If one of these symbols appears next to a sample ID, tap the symbol for any alerts or additional information about the measurement:



contaminant information available



on-demand technical support available



invalid result

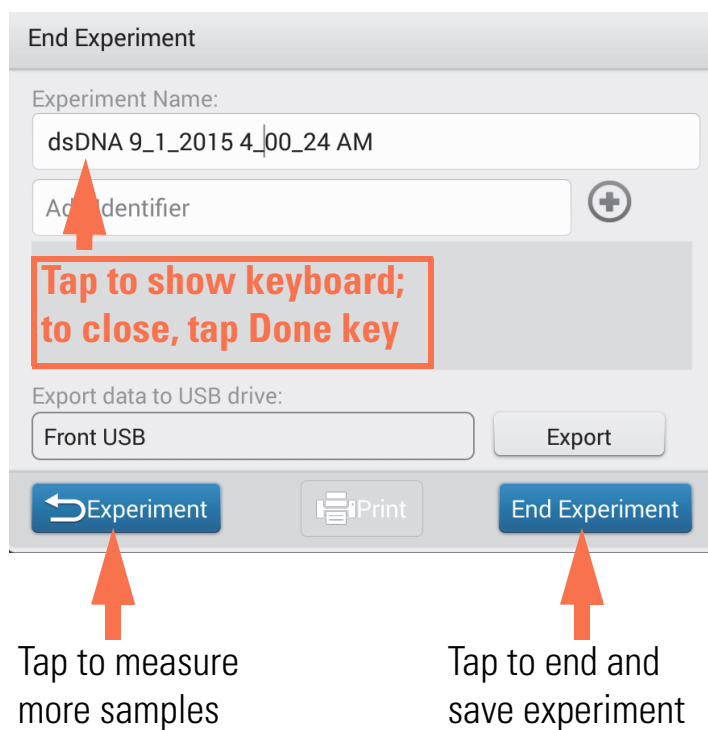


Tap to end experiment

6. To measure another sample:

- Lift the arm.
- Clean both pedestals with new wipe.
- Load the next sample and quickly lower the arm.
- Start the sample measurement.
- Wait for the measurement to complete.

The new spectrum replaces the previous one on the spectral display and the new reported values appear under the previous ones in the table. (Drag tab down to show both sets of data.)



7. When you are finished measuring samples:

- Tap **End Experiment**.
- Enter an experiment name (tap **Experiment Name** box, use displayed keyboard to type name, tap **Done** key), or leave the default experiment name
- Tap **End Experiment**
- Lift the arm and clean both pedestals with a new wipe.

If finished with the instrument for the day, clean the pedestals with DI H<sub>2</sub>O (see [Clean pedestals between users](#)).

Acquired data are automatically saved in an experiment with the entered name. In the default configuration, experiments are stored in a database on the local instrument according to acquisition date, experiment name, [application used](#) and any assigned labels (see [Manage identifiers on the instrument](#)).

### Related Topics

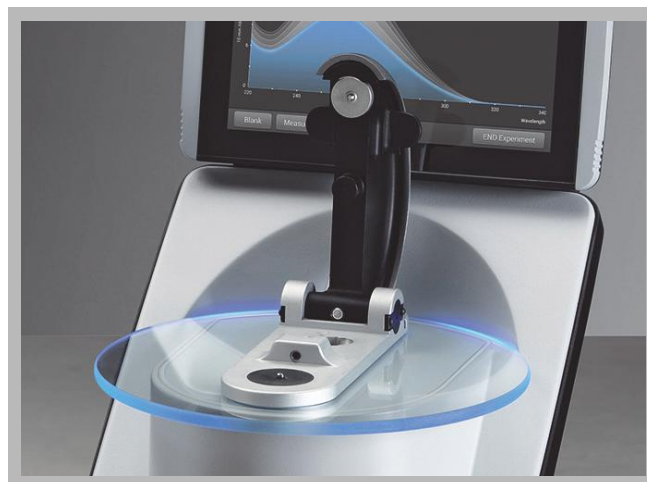
- [Micro-Volume Sampling—How it Works](#)
- [Absorbance Detection Limits](#)
- [Prepare Samples and Blanks](#)
- [Auto-Measure and Auto-Blank](#)
- [Acclaro Sample Intelligence](#)
- [Cleaning the Pedestals](#)
- [Search Experiment Database](#)
- [Export Data](#)
- [Measure a Sample Using a Cuvette](#)

### 3 Learning Center

Measure a Sample Using a Cuvette

## Measure a Sample Using a Cuvette

The NanoDrop One<sup>C</sup> spectrophotometer includes a cuvette holder for measuring dilute samples, colorimetric assays, cell cultures and kinetic studies. The cuvette system offers an extended lower [detection limit](#) and an optional 37 °C heater and micro-stirrer.



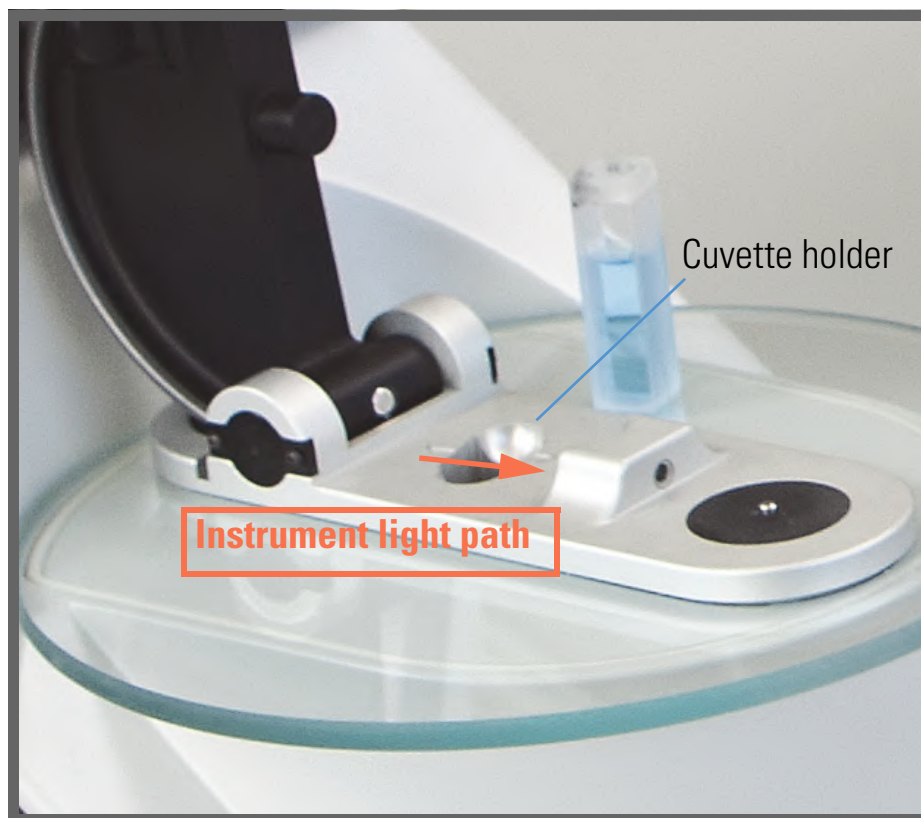
### Supplies needed

- NanoDrop One<sup>C</sup> spectrophotometer
- lint-free laboratory wipes
- two [compatible cuvettes](#)
- sample material resuspended in appropriate buffer solution (see [Preparing Samples](#))
- pure buffer solution for blanking instrument (see [Choosing and Measuring a Blank](#) or watch multimedia training [What is a blank?](#))



## Best practices for cuvette measurements

- The instrument arm can be up or down for cuvette measurements.
- Use 10 mm, 5 mm, 2 mm or 1 mm cuvettes up to 48 mm tall.
- Clean and dry cuvette after each measurement.
- Use cuvettes that are free of scratches and avoid fingerprints which may affect results.
- Use quartz cuvettes or UV-grade plastic cuvettes to measure samples with analysis wavelengths in the UV range (<340 nm).
- Micro, semi-micro, and ultra-micro cuvettes should be masked.
- Fill cuvettes with enough blanking or sample solution to cover instrument optical path (2 mm sample beam is 8.5 mm above cuvette bottom).
- Lift instrument arm and make sure cuvette holder is free of debris.
- When inserting quartz or masked plastic cuvettes, align cuvette light path with instrument light path.



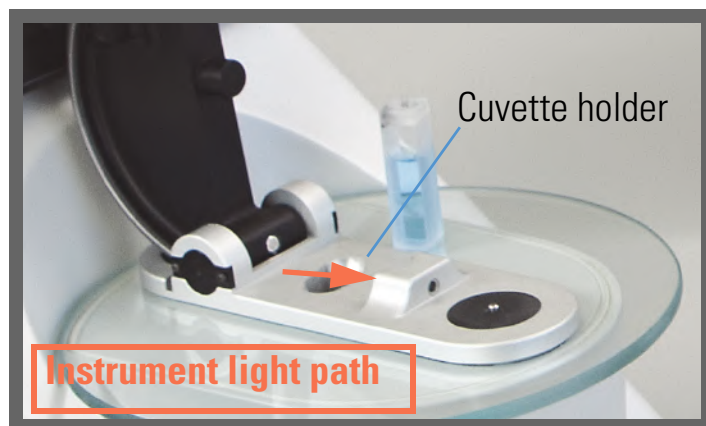
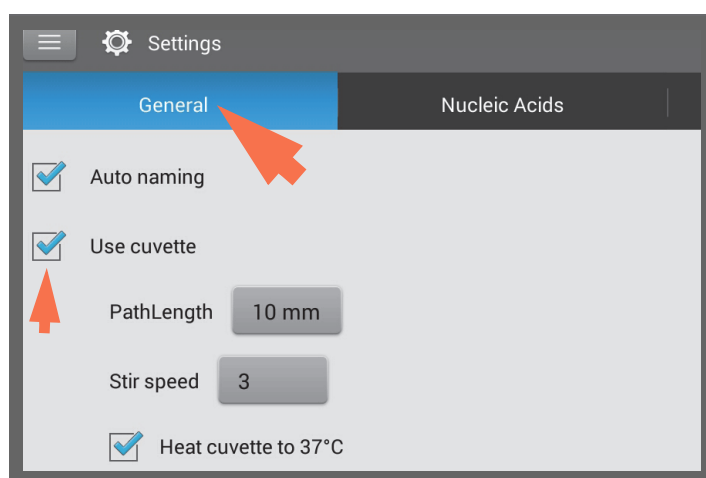
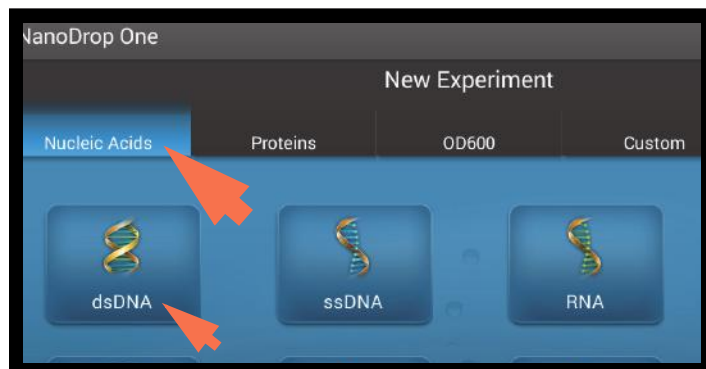
## To measure a sample using a cuvette

### NOTICE

- To prevent damage from spills, keep containers of liquids away from the instrument.
- Do not use a squirt or spray bottle on or near the instrument as liquids will flow into the instrument and may cause permanent damage.


### 3 Learning Center

#### Measure a Sample Using a Cuvette



1. From the Home screen, select an application tab such as Nucleic Acids and tap an application name such as dsDNA or RNA.

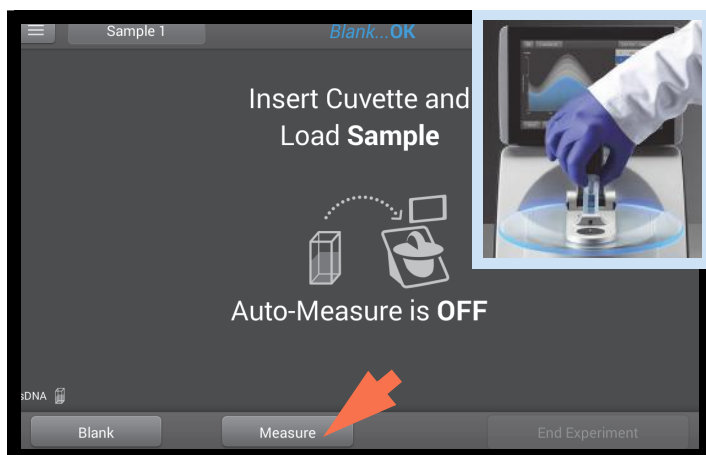
2. Specify the cuvette options:

- From Home screen, tap  (Settings).
- tap **General**.
- select **Use Cuvette**.
- set **Pathlength** to pathlength (width) of cuvette (see cuvette manufacturer for specifications).
- set stirrer and heater if desired.
- tap **Done**.

See [General settings](#) for details.

3. Measure a blank:

- Fill clean, dry cuvette with enough blanking solution to cover [instrument optical path](#).
- Lift instrument arm and insert blanking cuvette into cuvette holder, making sure to align light path of cuvette with light path of instrument.
- Tap **Blank** and wait for the measurement to complete.



4. Measure a sample:

- Fill clean cuvette to same height with sample solution.
- Replace blanking cuvette with sample cuvette, making sure to align light paths.
- Tap **Measure**.
- Wait for measurement to complete.
- Remove cuvette.
- Clean cuvette according to manufacturer specifications.

**Related Topics**

- [Instrument Models and Features](#)
- [Absorbance Detection Limits](#)
- [Prepare Samples and Blanks](#)
- [Acclaro Sample Intelligence](#)
- [Instrument Settings](#)
- [Search Experiment Database](#)
- [Export Data](#)
- [Measure a Micro-Volume Sample](#)

## Prepare Samples and Blanks

### Preparing Samples

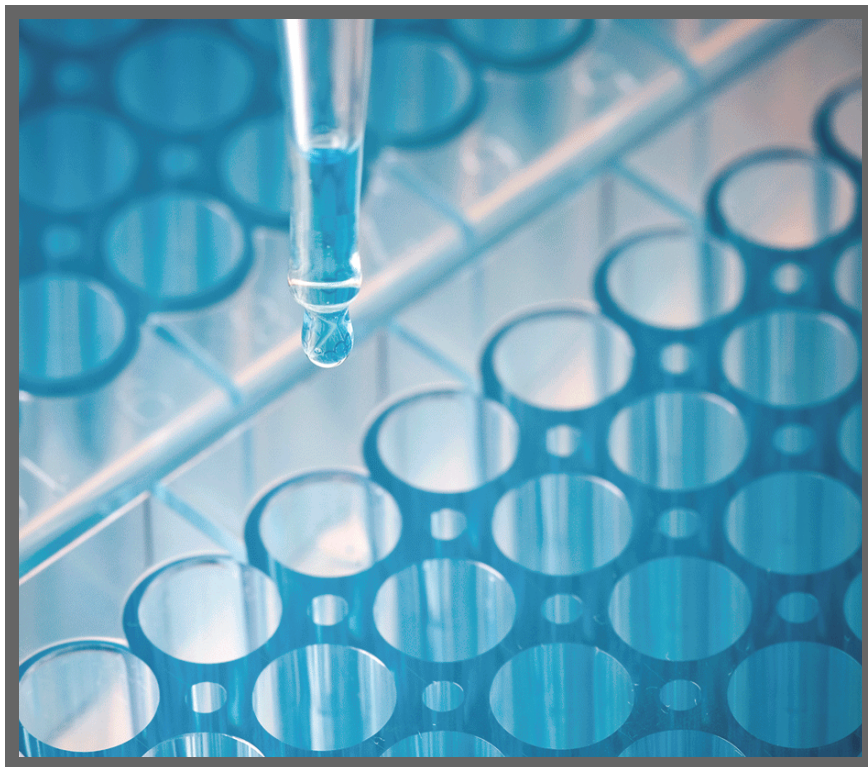
- Isolate and purify samples before measuring them with the instrument. Commercial sample isolation kits are available for these purposes, or use an in-house protocol. After purification, analyte of interest is typically dissolved in aqueous buffer solution before it is measured.

**Tip:** Any molecule that absorbs light at analysis wavelength will contribute to total absorbance value used to calculate sample concentration.

- Ensure final analyte concentration is within instrument's [absorbance detection limits](#).
- For micro-volume measurements, gently (but thoroughly) vortex each sample before taking a measurement.

**Tip:** Heat highly concentrated or large molecule nucleic acid samples, such as genomic or lambda DNA, to 63 °C (145 °F) before vortexing them.

- Avoid introducing bubbles when mixing and pipetting. For more information, watch multimedia training [Effects of Bubbles in Samples](#).



**Note** Samples dissolved in extremely volatile solvent such as hexane may work best with [cuvette sampling option](#) (NanoDrop One<sup>C</sup> instruments only).

### Choosing and Measuring a Blank

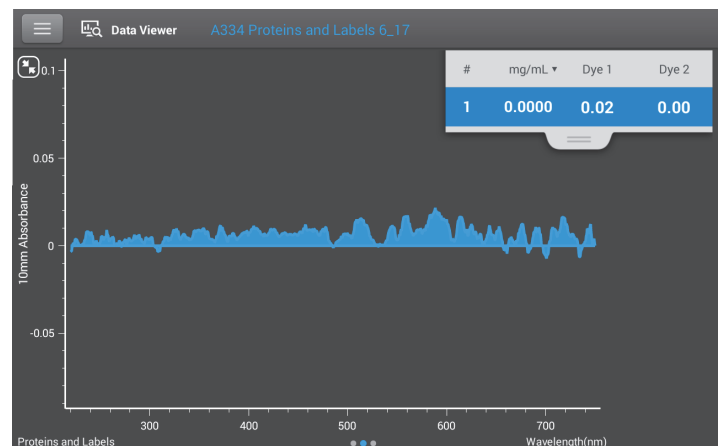
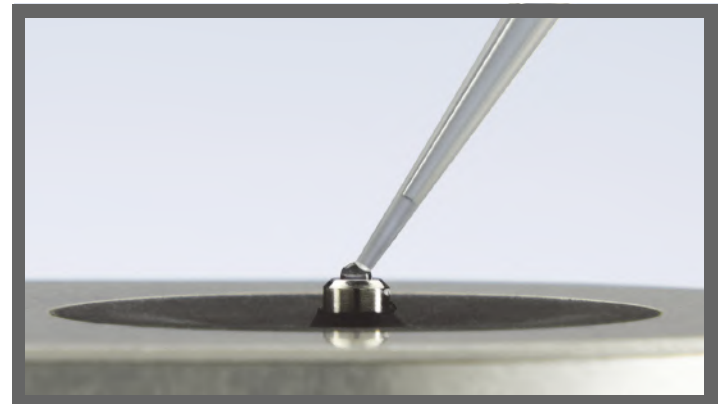
The buffer used to resuspend a sample analyte can contribute absorbance. Blanking minimizes any absorbance contribution due to the buffer components from the sample measurement. The resulting sample spectrum represents the absorbance of only the analyte of interest. For more information, watch the multimedia training [What is a blank?](#)

**For best results:**

- For most applications, blank with the same buffer solution used to resuspend the analyte of interest. The blanking solution should be a similar pH and ionic strength as the analyte solution. For details, see “To measure samples” in the application used.
- Measure new blank before each set of samples. It is not necessary to blank the instrument before each sample measurement unless the samples are dissolved in different buffer solutions.
- Measure a new blank every 30 minutes.
- Run a **blanking cycle** to assess the suitability of your blanking solution before using it to perform sample measurements. For a quick demonstration, watch the multimedia training [Evaluating a Blanking Solution for Suitability](#).

The resulting spectrum should vary no more than 0.04 A (10 mm equivalent) across the spectrum, especially at the analysis wavelength as in the example at the right.

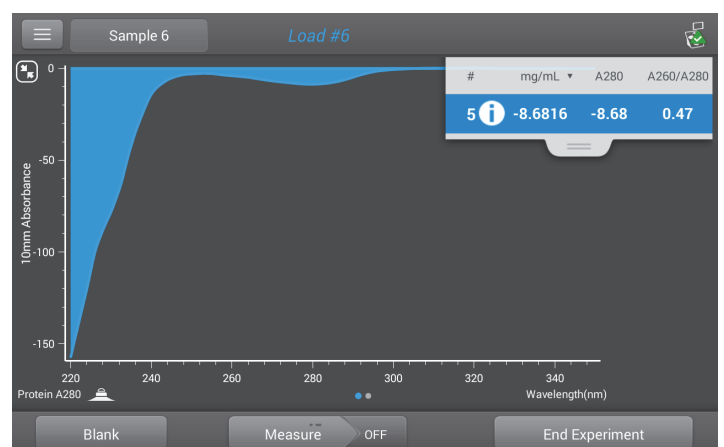
If the resulting spectrum is greater than 0.04 A around the analysis wavelength, that buffer solution may interfere with the sample analyses, especially for low concentration samples. See below for details.



**Good blanking buffer (measured abs < 0.04)**

**Problems associated with blanking**

- Residual sample was left on pedestal or in cuvette before blank measurement was performed. (Resulting sample spectra may exhibit negative absorbance values, indicating blank had more absorbance than sample in that region of spectrum.)
- Blank measurement exhibits higher absorbance than unknown sample at analysis wavelength. (If buffer used as blank differs in composition from that used to resuspend sample, measurement results will be incorrect.)
- Sample was inadvertently used to blank instrument. (Resulting sample spectra may exhibit negative absorbance values or, in some cases, resemble a mirror image of a typical pure nucleic acid or protein spectrum as in example at right.)



**Protein sample solution used to blank instrument results in “mirror image” spectrum**

### Solutions for blanking problems

- Thoroughly [clean](#) and/or [recondition both pedestals](#) and then:
  - rerun blanking cycle, or
  - measure new blank using new aliquot of appropriate buffer solution, then measure new aliquot of unknown sample
- For most applications, blank with the same buffer solution used to resuspend the analyte of interest. The blanking solution should be a similar pH and ionic strength as the analyte solution. For details, see “To measure samples” in the application used.
- If blanking problems persists, use an application that may be more suitable such as a fluorescence assay using the NanoDrop 3300 or a colorimetric assay if measuring proteins.

## Run a Blanking Cycle

Run a blanking cycle to verify the following:

- instrument is operating normally (with flat baseline)
- pedestals are clean (i.e., no dried-down sample material on pedestals)
- absorbance contribution of buffer solution you plan to use for sample analyses

### Supplies needed

- lint-free laboratory wipes
- calibrated precision pipettor (0–2  $\mu$ L)
- buffer solution for evaluation

### ❖ To run a blanking cycle

For quick demonstration, watch multimedia training [Evaluating a Blanking Solution for Suitability](#).

**NOTICE**

- Do not use a squirt or spray bottle on or near the instrument as liquids will flow into the instrument and may cause permanent damage.
- Do not use hydrofluoric acid (HF) on the pedestals. Fluoride ions will permanently damage the quartz fiber optic cables.

### 3 Learning Center

#### Prepare Samples and Blanks

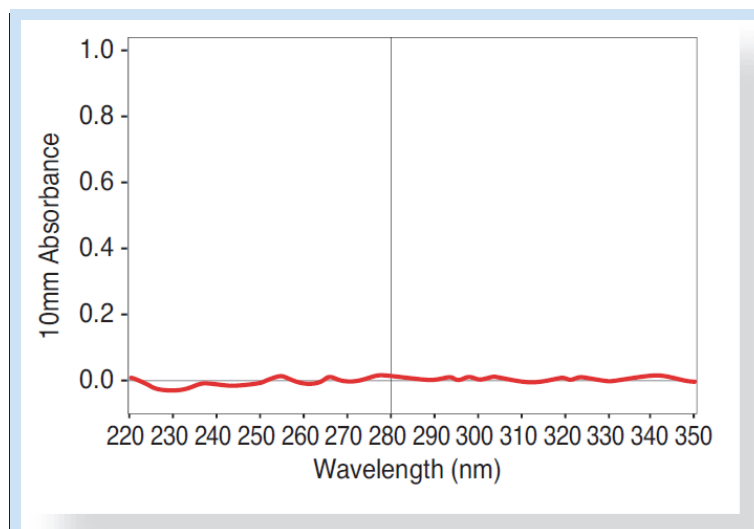
1. From the Home screen, select an application tab such as Nucleic Acids and tap an application name such as dsDNA or RNA.
2. Lift the instrument arm and clean the upper and lower pedestals with new laboratory wipe.
3. Measure a water blank:
  - Pipette exactly 1  $\mu\text{L}$  deionized water ( $\text{DI H}_2\text{O}$ ) onto the lower pedestal and lower the arm.
  - Tap **Blank** and wait for the measurement to complete.
  - Lift the arm and clean both pedestals with new laboratory wipe.
4. Measure the buffer solution:
  - Pipette 1-2  $\mu\text{L}$  buffer solution onto the pedestal and lower the arm.
  - Start the sample measurement:
    - if **Auto-Measure** is On, lower arm
    - if Auto-Measure is off, lower arm and tap **Measure**
  - Wait for measurement to complete.

The resulting spectrum should vary no more than 0.04 A from the baseline at the analysis wavelength (260 nm for nucleic acids; 280 nm for proteins).

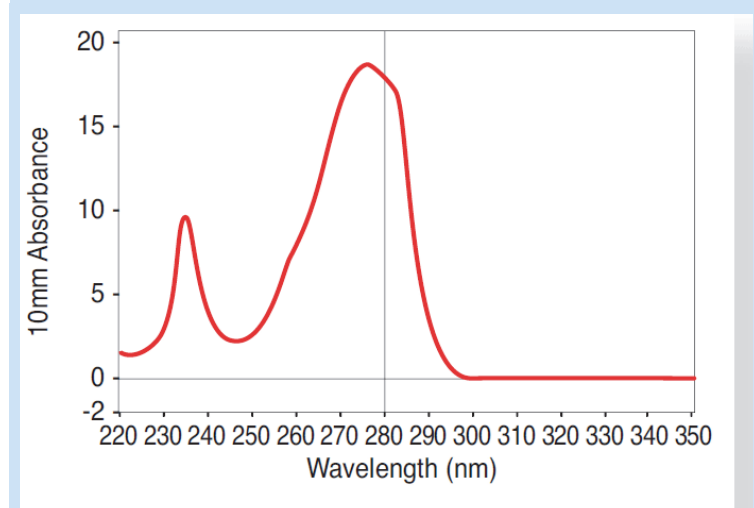
If your spectrum does not meet these criteria, repeat steps 2–4.

If spectrum is still outside specifications, see [Solutions for Blanking Problems](#).

5. When you are finished with the blanking cycle, tap **End Experiment**.
6. Lift the arm and clean both pedestals with a new wipe.



**Example spectrum of buffer suitable for Protein A280 protein quantification**



**Example spectrum of buffer unsuitable for Protein A280 protein quantification**

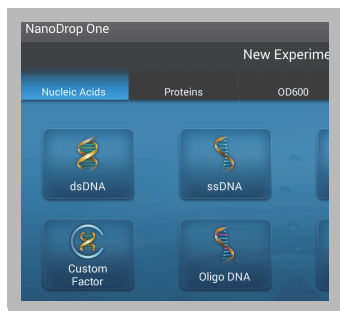
#### Related Topics

- [Absorbance Detection Limits](#)

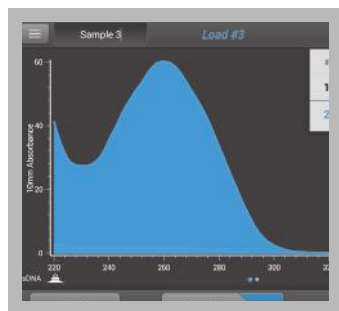


- Effects of Bubbles in Samples
  - What is a Blank?
  - Evaluating a Blanking Solution for Suitability
  - Maintaining the Pedestals
  - Measure a Micro-Volume Sample
  - Measure a Sample Using a Cuvette
-

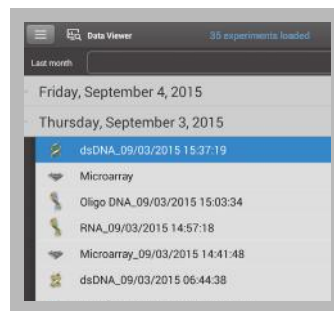
## Basic Instrument Operations



Home Screen



Measurement screens



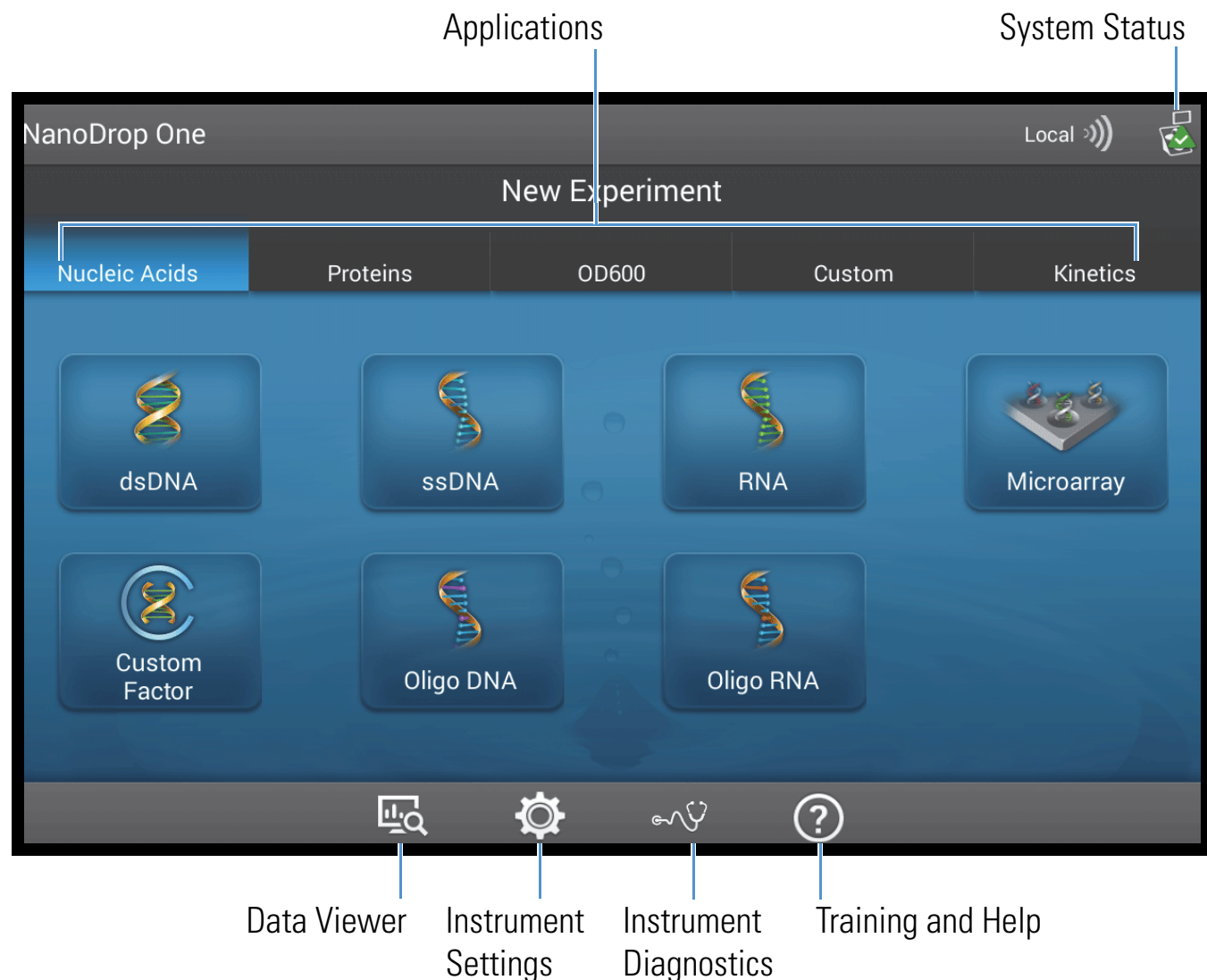
Data Viewer



General Operations

## NanoDrop One Home Screen

These operations are available from the NanoDrop One Home screen.




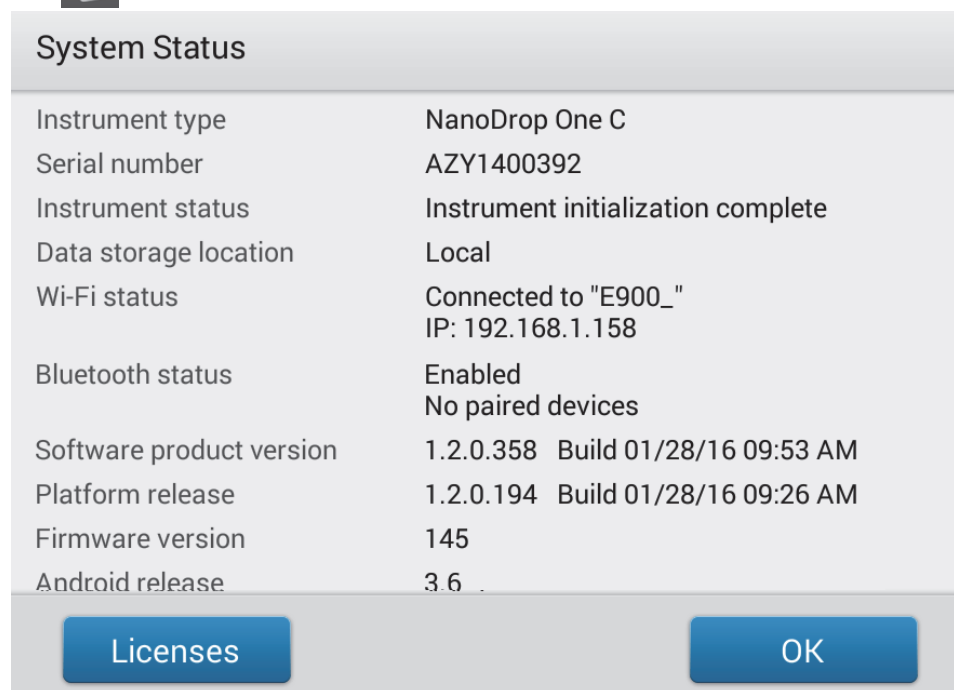
## Applications

The NanoDrop One offers a broad range of applications for measuring samples with the instrument. To select an application, tap an **Application tab** such as Nucleic Acids and then tap an **application name** such as dsDNA.

[Tap here](#) for detailed information about each available application.

## System Status

Tap  on the instrument Home screen to open the system status box. Here is an example:




The available information is described below.

Instrument type	Instrument model (NanoDrop One or NanoDrop One <sup>C</sup> )
Serial number	Instrument serial number
Instrument status	Current status of the instrument
Data storage location	Indicates location of database where instrument is currently storing data. These options are available: <ul style="list-style-type: none"> <li>Local (instrument)</li> <li>Connected PC* (personal computer connected through Ethernet cable or wireless network)</li> </ul> <p>* the Ethernet and wireless options listed above also store data on the instrument as a backup.</p>
Wi-Fi status	Status of <a href="#">WiFi connections</a> for the instrument (“Connected to...”, “Enabled and not connected” or “Disabled”)
Bluetooth status	Status of <a href="#">Bluetooth connections</a> for the instrument (“Connected to...”, “Enabled-[list of any paired devices]” or “Disabled”)
Software product version	Version of NanoDrop One software installed
Platform release	Platform release to support NanoDrop One instruments


Firmware version	Version of instrument firmware installed
Android release	Custom version of Android release
Android version	Version of Android operating system software installed

## Data Viewer


Tap  on the Home screen to view any data acquired earlier today, last week, last month, last six months, last year or in a specific date range. [Tap here](#) for more information about the Data Viewer on the instrument.

**Note** The instrument will only allow you to view data in its local NanoDrop One database. When the instrument is connected to a computer with an Ethernet cable or through a wireless network, the Data Viewer icon on the instrument Home screen is unavailable.


## Instrument Settings

Tap  on the Home screen to access general instrument settings such as WiFi and using cuvettes. [Tap here](#) for detailed information about all available instrument settings.

## Instrument Diagnostics

Tap  on the Home screen to verify instrument operation. Instrument diagnostics should be run periodically according to the recommended [maintenance schedule](#). [Tap here](#) for information about how to run the available instrument diagnostics.

## Training and Help

Tap  on the Home screen to access this Help system. The NanoDrop One software comes with comprehensive embedded training and support. [Tap here](#) for information on how to navigate the available information.

### Related Topics

- [Applications](#)
- [Set Up the Instrument](#)
- [NanoDrop One Data Viewer](#)
- [Instrument Settings](#)
- [Instrument Diagnostics](#)
- [About this Help System](#)
- [Measure a Micro-Volume Sample](#)
- [Measure a Sample Using a Cuvette](#)

## NanoDrop One Measurement Screens

These operations are available from any measurement screen within an [Application](#).

Menu of options; **tap** to open

Sample name; **tap** to edit

Measurement results; see [Applications](#) for details

Measurement alert; **tap** to learn more

**Tap row** to select sample and update spectrum; **tap more rows** to overlay up to five spectra. **Press and hold** sample row to view sample details.

**Drag tab down/up** to see more/less sample data

Sample pathlength

UV absorbance spectrum for selected sample

10mm Absorbance

Wavelength (nm)

dsDNA

Blank

Measure

Auto-Measure

End Experiment

**Tap** to measure blank solution

**Tap** to measure sample solution

Auto-Measure

**Tap** to end experiment and export data

Selected application

**Pinch and zoom** to adjust axes

Page control; **swipe screen left** to view table with more measurement results

#	ng/ul	A260/A280	A260/A230
1	96.2	1.97	1.04
2	3005.4	1.80	2.20

## Menu

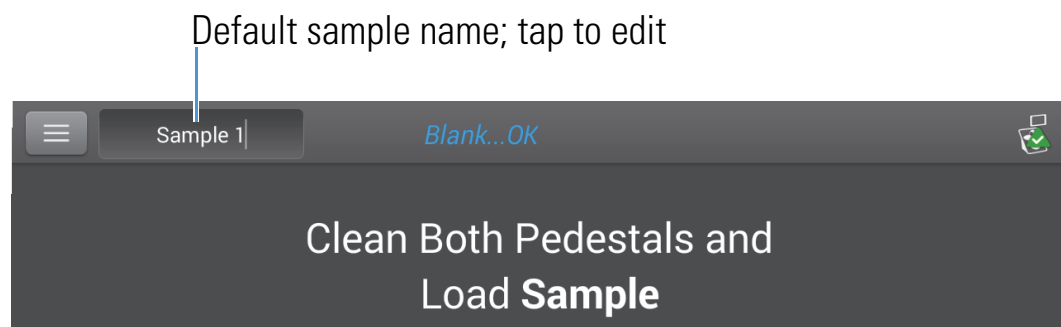
Tap in any measurement screen to see the available menu options.

Home	Return to NanoDrop One Home screen
[application] Setup	View or change settings for selected application
Settings	View or change <a href="#">instrument settings</a>
Print	<a href="#">Print</a> selected measurement results

## Sample Name

Tap the Sample Name field in any measurement screen to edit the sample name.

When Auto-Naming is On (see [General Settings](#)), each sample is automatically assigned a sample name using the default base name followed by a unique number starting with “1.” The first time this appears is after the first blank measurement and before the first sample measurement in each experiment as shown below.



In this example, the first sample would be named “Sample 1” followed by “Sample 2,” etc. You can edit the default base name and overwrite any sample name.


**Note** If you edit the sample base name during an experiment when Auto-Naming is selected, the assigned sample ID numbers restart.

### Edit default sample base name

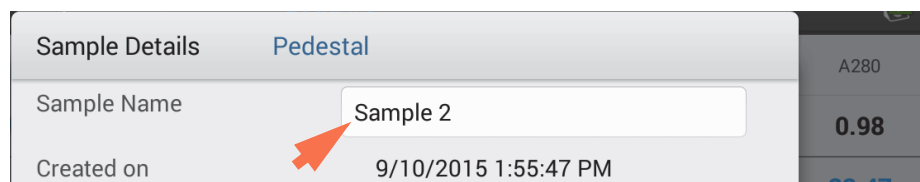
After you measure a blank and before the first sample is measured:

- tap **Sample Name** field to display keyboard
- enter new base name
- tap **Done** key

### Edit sample name

- from Home screen, tap  to open Data Viewer
- select experiment
- **swipe left** to show data table
- press and hold **sample name** to show Sample Details box
- tap **Sample Name** field to display keyboard





- enter new sample name
- tap **Done** key

## Measurement Results

The types of results that appear in the measurement screens depend on the selected application. For details, see:

Applications > [application group] > Measure [application name] > Reported Results

Here is an example for [dsDNA](#).

## Absorbance Spectrum

For each measured sample, each application shows the UV or UV-visible absorbance spectrum and a summary of the results. The vertical axis shows absorbance in absorbance units (A). The horizontal axis shows wavelength in nm.

## Sample Pathlength

All applications display the sample pathlength along the spectrum's vertical axis. Micro-volume absorbance measurements and measurements taken with nonstandard cuvettes are normalized to a 10.0 mm pathlength equivalent.

## Measurement Alerts

The [Acclaro Sample Intelligence technology](#) built into the NanoDrop One instruments provides important features to help you assess sample integrity. Tap a Sample Intelligence icon in the software to view its associated information. For more information, tap a link below.



[contaminant analysis](#) is available to help qualify a sample before use in downstream applications



[on-demand technical support](#) is available for measurements that are atypical or very low concentrations



[invalid-results alert](#)

## Blank

Tap **Blank** to measure a blank for the selected experiment.

A blank must be measured before each group of similar samples. The blank solution is typically the pure buffer that was used to resuspend the sample. For more information, see [Choosing and Measuring a Blank](#).

## Measure

Tap **Measure** to measure a sample for the selected experiment.

Samples must be properly isolated and prepared before they can be measured with the instrument and the concentration must be within the instrument's absorbance detection limits. For more information, see [Preparing Samples](#), and [Measure a Micro-Volume Sample](#) or [Measure a Cuvette Sample](#) and [Absorbance Detection Limits](#).

**Note** The **Measure** button is enabled after a valid blank measurement is completed.

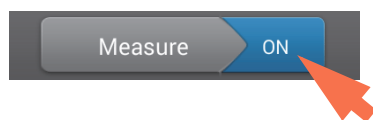
## Auto-Measure and Auto-Blank

Speed up sample analysis with the NanoDrop One Auto-Measure and Auto-Blank features, which cause the instrument to start the measurement immediately after you lower the instrument arm. These options eliminate the need for repetitive Measure or Blank operations for large batches of samples.

**Note** Auto-Measure and Auto-Blank are available for micro-volume measurements only.

### Auto-Measure

To select or deselect Auto-Measure, from any sample measurement screen, tap the **On** or **Off** button at the right of the Measure button.



### Auto-Blank

To select or deselect Auto-Blank, from any blank measurement screen, tap the **On** or **Off** button at the right of the Blank button.



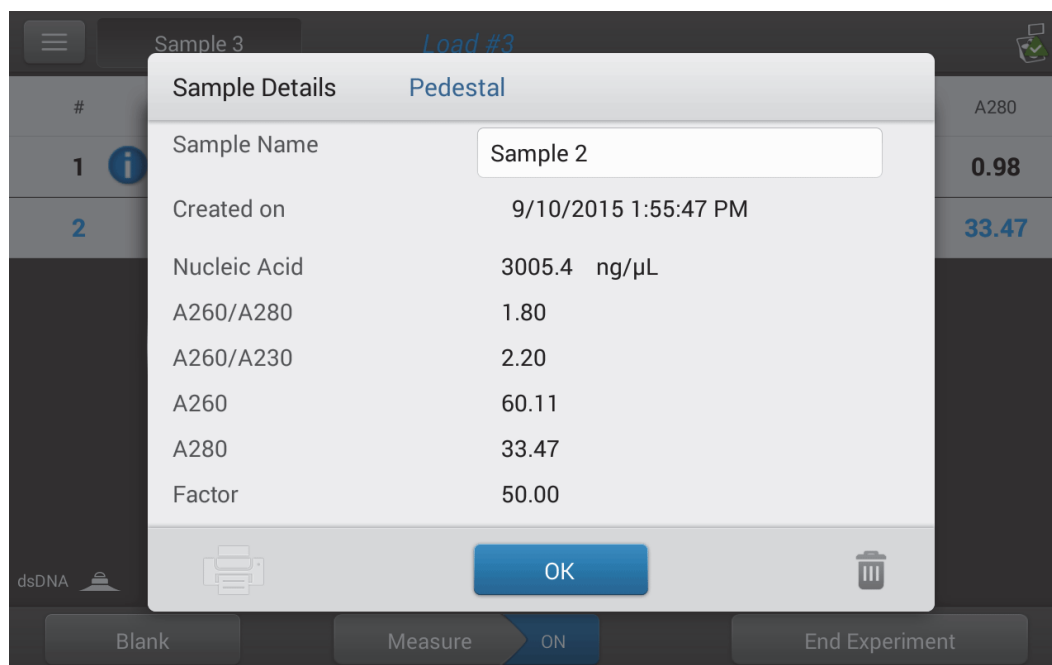
## End Experiment

Tap **End Experiment** when you are ready to name and save your experiment, add a label to help you locate the experiment later (see [Manage identifiers on the instrument](#)), or [export the data](#).

**Note** The **End Experiment** button is enabled after the first sample measurement is completed.

## Sample Details

Press and hold a **sample row** in any measurement screen or [data table](#) to show the sample details, which include all available measurement results and associated details for the selected sample. Here is an example:



**Note** You can also [edit the sample name](#) from the Sample Details box.

## Data Table

Swipe left in any measurement screen to see the data table for the current experiment. The data table contains the measurement results for all samples in the experiment. The image below highlights the available features.

The screenshot shows the data table interface with the following callouts:

- Menu of options; tap to open**: Points to the hamburger menu icon in the top left.
- Sample name; tap to edit**: Points to the 'Sample 3' header.
- Measurement results; see Applications for details**: Points to the 'Load #3' header.
- Measurement alert; tap to learn more**: Points to the information icon in the first row.
- Tap row to select sample; Press and hold row for sample details**: Points to the first row of the table.
- Application used**: Points to the 'dsDNA' label and the 'Blank' button in the bottom bar.
- Page control; swipe screen right to return to measurement screen**: Points to the 'ON' button in the bottom bar.

#	Sample Name ▾	ng/μL ▾	A260/A280	A260/A230	A260	A280
1	<b>i</b> Sample 1	96.2	1.97	1.04	1.92	0.98
2	Sample 2	3005.4	1.80	2.20	60.11	33.47

### Related Topics

- [Measure Nucleic Acids](#)
- [Measure Proteins](#)
- [Instrument Settings](#)
- [Print Data](#)
- [Acclaro Sample Intelligence](#)

- [Prepare Samples and Blanks](#)
- [Search Experiment Database](#)
- [Export Data](#)
- [Measure a Micro-Volume Sample](#)
- [Measure a Sample Using a Cuvette](#)

## NanoDrop One Data Viewer

The Data Viewer opens the database that stores sample data measured with the instrument. The data are saved according to acquisition date, experiment name, [application used](#) and any assigned labels (see [Manage Identifiers](#)).

From the Data Viewer, you can locate and select any experiment to see the measurement data it contains, or [export](#) selected experiments to a variety of locations and formats.

These operations are available from the Data Viewer.

Menu of options; **tap** to open

Current time range filter

Search for an experiment or change time range filter

Select experiments to export or delete

Date	Experiments Found
Tuesday, September 8, 2015	4 experiments found
Monday, September 7, 2015	1 experiment found
Sunday, September 6, 2015	1 experiment found
Saturday, September 5, 2015	3 experiments found
Friday, September 4, 2015	1 experiment found
Thursday, September 3, 2015	2 experiments found
Wednesday, September 2, 2015	6 experiments found


**Tap row** to view experiments acquired on this date; **tap an experiment** to open it

## Open Data Viewer

Whether you collect one sample or many in a row, after you choose End Experiment, the acquired data are automatically saved in an experiment with an experiment name. In the default configuration, experiments are stored in the NanoDrop One database on the local instrument according to acquisition date, experiment name, [application used](#) and any assigned labels.


Use the Data Viewer to open the database on the local instrument in order to view acquired spectra and associated data from any experiment at any time.

### Open instrument database of measurement results

- to open NanoDrop One database on instrument, tap  (Data Viewer) on instrument Home screen

**Note** The Data Viewer icon is not available on the instrument Home screen when the instrument is connected to a computer with an Ethernet cable or through a wireless network (see [Setting Up the Instrument](#) for details).

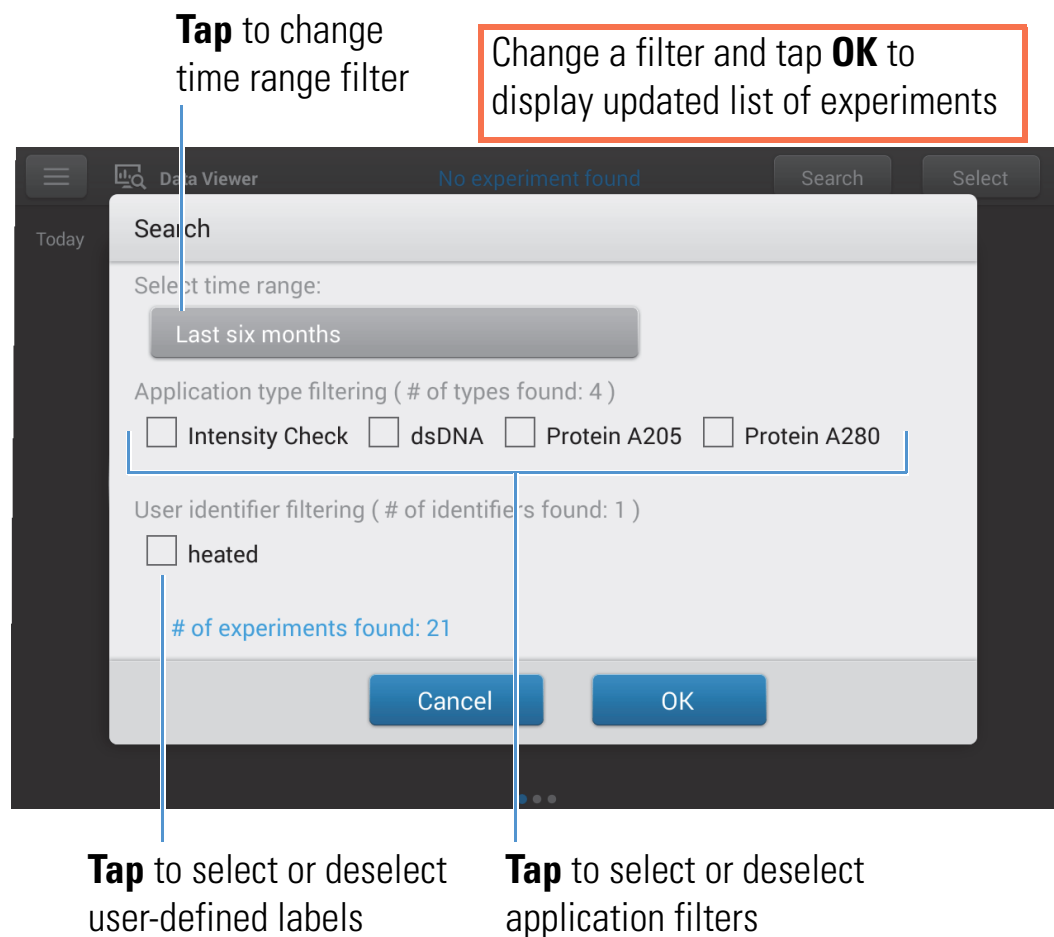
## Menu

Tap  in the Data Viewer to see the available menu options.

Home	Return to NanoDrop One Home screen
Settings	View or change <a href="#">instrument settings</a>
Import	Import data from a USB flash drive
Disk Status	View remaining space available for storing measurement data on the instrument

## Search Experiment Database

Tap **Search** in the Data Viewer to search the [selected database](#) for an experiment or to change the time range or other search filters. The database is filtered using the current settings in the Search box. Filters include time range, application type and any user-defined labels (see [Manage Identifiers](#) for information about adding and deleting labels). Here is an example:



## Export Selected Experiments

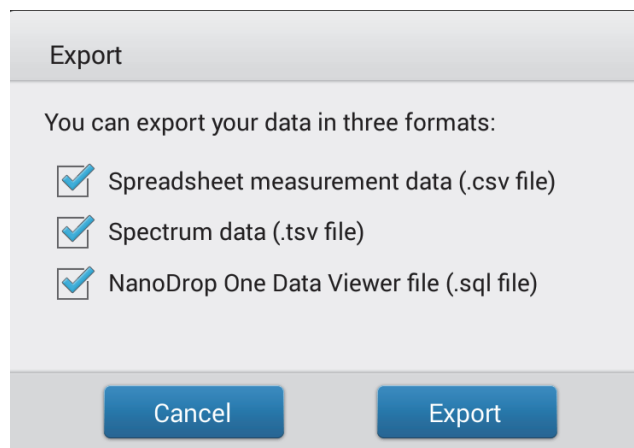
Use **Select** in the Data Viewer to select experiments to be exported.

### Export selected experiments

- tap **row** in Data Viewer to list experiments acquired on that date, or use [Search](#) feature to find experiment
- insert USB memory device into available USB port on instrument (front, back-left or back-right)
- tap **Select**



- tap to select one or more experiments to export (tap again to deselect an experiment)
- tap **Export**
- select one or more formats to export to (see “Export Data” in [General Operations](#) for details)



- tap **Export**
- after “Export Success” message, tap **OK**

## Delete Selected Experiments

Use **Select** in the Data Viewer to select experiments to be deleted.

### Delete selected experiments

- tap **row** in Data Viewer to list experiments acquired on that date, or use [Search](#) feature to find desired experiment
- tap **Select**
- tap to select one or more experiments to delete (tap again to deselect an experiment)
- tap **Delete** and **OK**

**NOTICE** Deleted data cannot be recovered.

## Open Experiment and View Associated Data

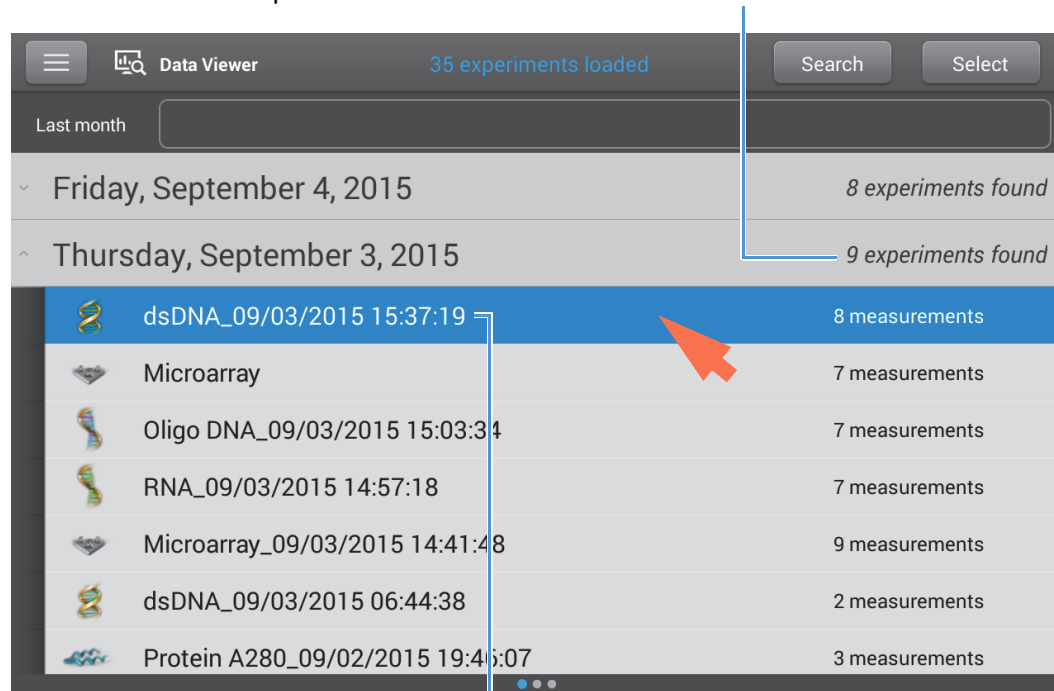
Use the Data Viewer to locate and open any experiment to see the measurement data it contains.

### Open an experiment

- tap **row** in Data Viewer to list experiments acquired on that date, or use [Search](#) feature to find desired experiment
- tap **experiment name** to open the experiment

Here is an example:

Nine experiments measured on this date



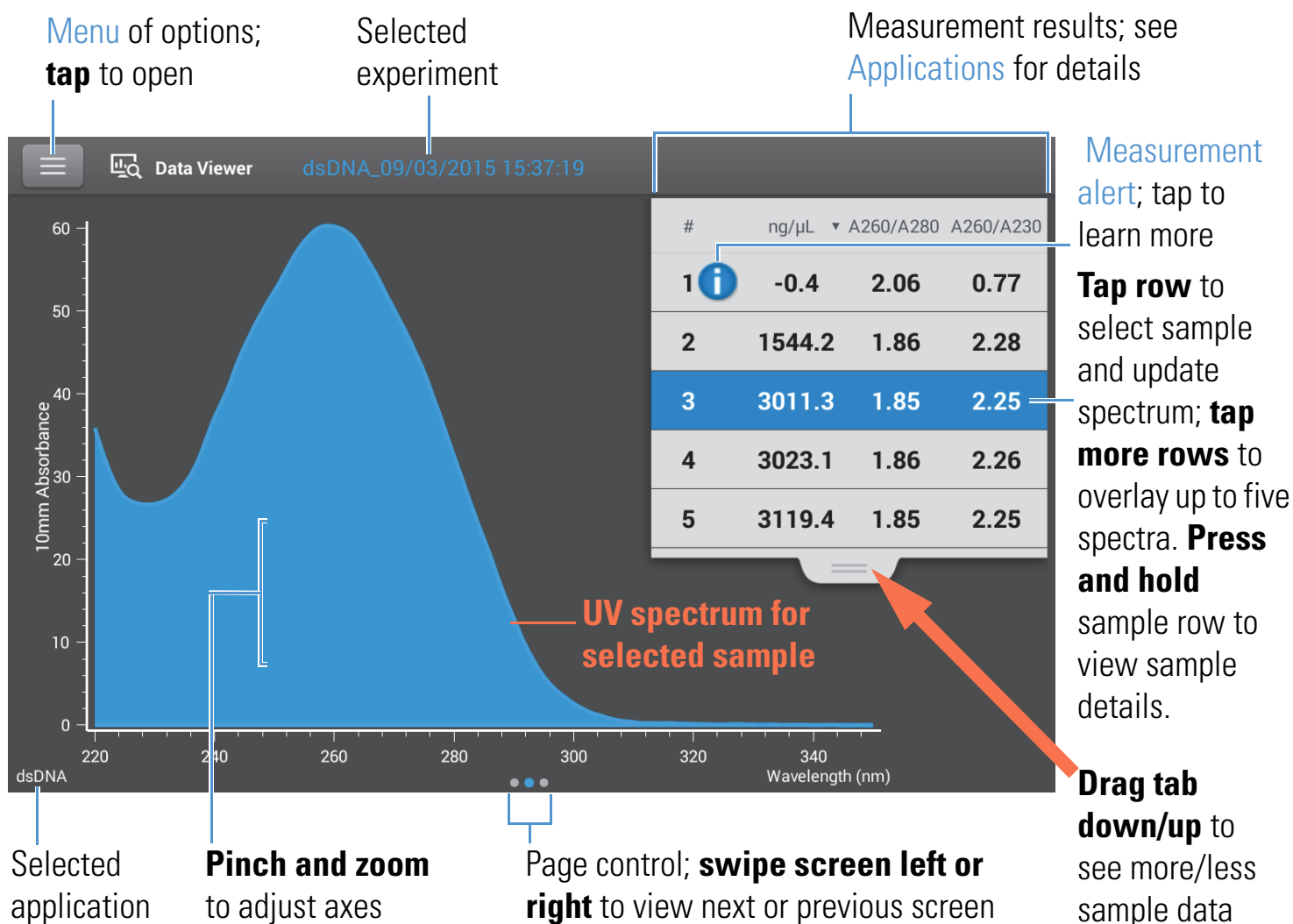
**Tap** to open this experiment; **press and hold** to view experiment details including any assigned labels

The Data Viewer provides measurement data as [spectral data](#) and [data tables](#), similar to what you see after you complete a measurement.

**Note** The data shown are dependent upon the application used to measure the samples (nucleic acids in these examples). For more information, see the [application](#) details.

**Spectral data—**

After you open an experiment, the software shows the UV or UV-visible absorbance spectrum and a summary of the associated data for the first sample measurement, much like it appears during a measurement. The image below describes the available features.



**Data Table—**

Swipe left in any Spectral Data screen to see the data table for the current experiment. The data table contains the measurement results for all samples in the experiment. The image below describes the available features.

Menu of options; tap to open

Selected experiment

Tap to select unit

Measurement results; see Applications for details

Measurement alert; tap to learn more

Tap row to select sample; Press and hold row for sample details.

Application used

Page control; swipe screen right to view previous screens (2)

#	Sample Name	ng/μL	A260/A280	A260/A230	A260	A280
1	Sample 1	-0.4	2.06	0.77	-0.01	0.00
2	Sample 2	1544.2	1.86	2.28	30.88	16.60
3	Sample 3	3011.3	1.85	2.25	60.23	32.51
4	Sample 4	3023.1	1.86	2.26	60.46	32.46
5	Sample 5	3119.4	1.85	2.25	62.39	33.64
6	Sample 6	3030.9	1.86	2.26	60.62	32.61
7	Sample 7	0.2	0.38	1.73	0.00	0.01
8	Sample 8	-0.2	0.43	-5.09	0.00	-0.01

**Menu**

Tap from any Spectral Data or Data Table screen to see the available menu options.

Home	Return to NanoDrop One Home screen
Manage Identifiers	Add or delete labels for selected experiment to make it easier to find (see <a href="#">Manage identifiers on the instrument</a> )
Export	<a href="#">Export selected experiment</a> to USB device
Print	<a href="#">Print</a> selected measurement results (Print option appears only when one or more measurements results are selected in Data Table)

Settings	View or change <a href="#">instrument settings</a>
Disk Status	View remaining space available for storing measurement data on the instrument

### Related Topics

- [Instrument Settings](#)
- [Search Experiment Database](#)
- [Export Data](#)
- [Print Data](#)

## NanoDrop One General Operations



These operations are available from any measurement screen or from the [Data Viewer](#).

### Manage Identifiers (on the instrument)




You can add one or more “identifiers” (i.e., labels or metadata tags) to an experiment to make the experiment easier to find. Labels can be added from the NanoDrop One software running on the instrument, or from the NanoDrop One Viewer software installed on a personal computer (see [Manage Identifiers on a PC](#)).

Use the Data Viewer to add labels to experiments, assign existing labels, view assigned labels and remove or delete labels on the instrument. You can filter the list of experiments in the Data Viewer based on one or more user-defined labels.

#### Label new experiment when you save it

- after the last sample has been measured, tap 
- in End Experiment box, tap **Add Identifier** field
- use displayed keyboard to enter label and tap 
- tap **Done** key
- tap **End Experiment**


### Label experiment in Data Viewer

- from Home screen, tap  to open Data Viewer
- tap to open an experiment
- tap  and choose **Manage Identifiers**
- in Manage Identifiers box, tap **Add Identifier** field
- use displayed keyboard to enter label and tap 
- tap **Done** key
- tap **OK**




### View assigned labels for an experiment

- from Home screen, tap  to open Data Viewer
- press and hold selected experiment to see Experiment Details

### Find labeled experiments

- from Home screen, tap  to open Data Viewer
- tap **Search**
- in Search box, select date range, select application (only applications that have associated data are shown), select one or more identifiers from scrollable list and tap **OK**

### Remove a label

- from Home screen, tap  to open Data Viewer
- tap to open an experiment
- tap  and choose **Manage Identifiers**
- in Manage Identifiers box, select label and tap .
- tap **OK**

## Export Selected Measurements

You can export measurement data from one or more experiments when you save the experiment, or afterwards from the [Data Viewer](#).

**Note** Data exported during a save are still saved to a database (local or remote, depending on the Data Storage setting; see [Select location for saving or viewing collected data](#) for more information).

Measurement data can be exported in three formats:

- as a comma-separated values (.csv) file, containing the measurement results and details
- as a tab-separated values (.tsv) file, containing x,y coordinates for every spectral data point
- as a NanoDrop One Viewer (.sql) file, containing spectra and measurement results that can be imported to the [NanoDrop One Viewer software](#) running on a personal computer

The filenames are the same as the [experiment names](#). The files are stored in a folder named “NanodropOne” followed by the instrument serial number. (Use [System Status](#) to view instrument serial number.)

If you select multiple experiments for export in the CSV and TSV formats, each exported experiment has a corresponding CSV and TSV file. If the SQL option is also selected, the exported SQL file contains all the selected experiments.

Use any spreadsheet or word processing application to open a CSV or TSV file. Here is an example of several sample measurement results in CSV format:

	A	B	C	D	E	F	G	H	I	J
1	Date	Sample Name	Nucleic Acid	A260/A280	A260/A230	A260	A280	Nucleic Acid Factor	Baseline (nm)	
2	4/21/2015 15:37	Sample 1	0.3	0.7	0.56	0.01	0.01	33	340	
3	4/21/2015 15:42	Sample 2	0.37	0.94	0.86	0.01	0.01	33	340	
4	4/21/2015 15:44	Sample 3	0.43	0.98	0.74	0.01	0.01	33	340	
5	4/21/2015 15:44	Sample 4	0.18	2.1	0.83	0.01	0	33	340	
6	4/21/2015 15:45	Sample 5	0	0.07	0.02	0	0	33	340	
7	4/22/2015 8:57	Sample 6	-0.52	2.11	0.66	-0.02	-0	33	340	
8										


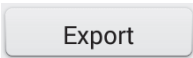
**Note** The types of data exported are dependent upon the application used to measure the samples (nucleic acids in this example). For more information, see the [application](#) details.

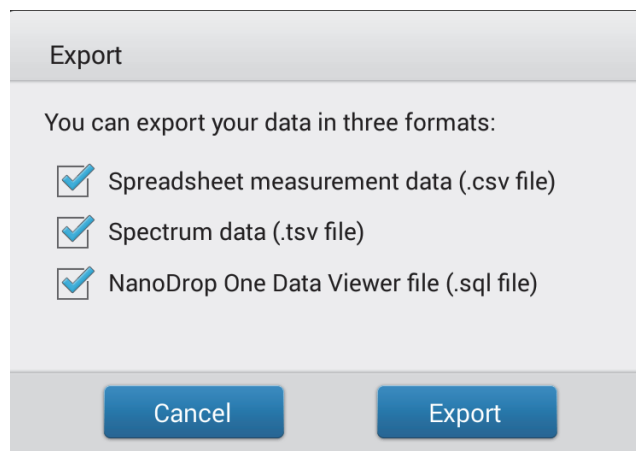
The SQL file can be opened only using our NanoDrop One Viewer software, and only after the file has been imported.

Data can be exported to a USB device connected to any USB port on the local instrument (front, back-left or back-right), and then transferred to any computer that has an installed spreadsheet or word processing application (for CSV and TSV files) or the NanoDrop One Viewer application (for SQL files).

### Export data at end of experiment


- insert USB memory device into available USB port on instrument (front, back-left or back-right)

- when finished measuring samples, tap 
- from End Experiment box, tap 
- select one or more formats to export to (see above for details)



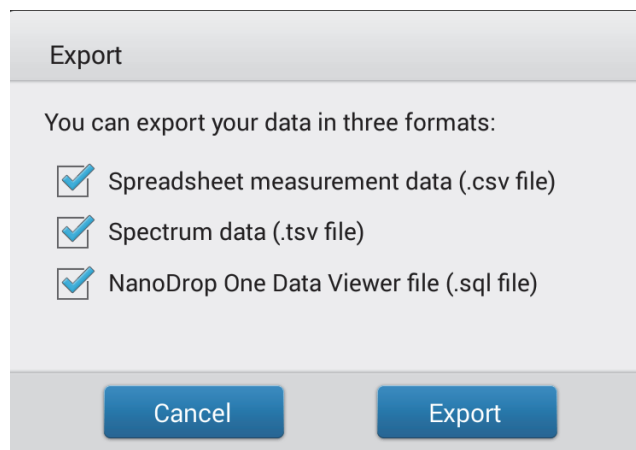
- tap **Export**
- after “Export Success” message, tap **OK**
- remove USB device
- tap **End Experiment**

#### Export data from Data Viewer

- from Home screen, tap  to open Data Viewer
- tap **row** in Data Viewer to list experiments acquired on that date, or use [Search](#) feature to find experiment
- insert USB memory device into available USB port on instrument (front, back-left or back-right)
- tap **Select**
- tap to select one or more experiments to export (tap again to deselect an experiment)
- tap **Export**



- select one or more formats to export to (see above for details)




- tap **Export**
- after “Export Success” message, tap **OK**

## Delete Selected Measurements



You can delete a sample measurement from any experiment.

**NOTICE** Deleted data cannot be recovered.

### Delete data from any measurement screen

- press and hold sample row to open Sample Details box
- tap 



### Delete data from Data Viewer

- from Home screen, tap  to open Data Viewer
- tap **row** in Data Viewer to list experiments acquired on that date, or use [Search](#) feature to find desired experiment
- press and hold sample row to open Sample Details box
- tap 

## Print Selected Measurements




Connect a [compatible printer](#) to the instrument to quickly print measurement results, including spectral data and sample details, to include in a laboratory notebook or post on a bulletin board.

### Print data from any measurement screen

- after you have measured a sample, display the measurement results to be printed such as the spectral data or data table (see [NanoDrop One Measurement Screens](#))
- tap to select one or more sample rows to print (tap again to deselect a sample row)
- tap  and choose  **Print**
- in the Print Information box, choose **OK**

One label is printed for each selected measurement.

### Print data from Data Viewer




- from Home screen, tap  to open Data Viewer
- tap **row** in Data Viewer to list experiments acquired on that date, or use [Search](#) feature to find desired experiment
- tap **experiment name** to open the experiment
- from the [spectral data](#) or [data table](#) in any measurement screen or from the [Data Viewer](#), tap to select one or more sample rows to print (tap again to deselect a sample row)
- tap  and choose  **Print**
- in the Print Information box, choose **OK**

One label is printed for each selected measurement.

### Print sample details

- from the [spectral data](#) or [data table](#) in any measurement screen or from the [Data Viewer](#), press and hold sample row to open Sample Details box

Sample Details	Pedestal
Sample Name	<input type="text" value="Sample 3"/>
Created on	9/3/2015 3:34:32 PM
Nucleic Acid	3011.3 ng/μL
A260/A280	1.85
A260/A230	2.25
A260	60.23
A280	32.51
Factor	50.00

- tap 
- in the Print Information box, choose **OK**




One label is printed for this measurement.

### Related Topics

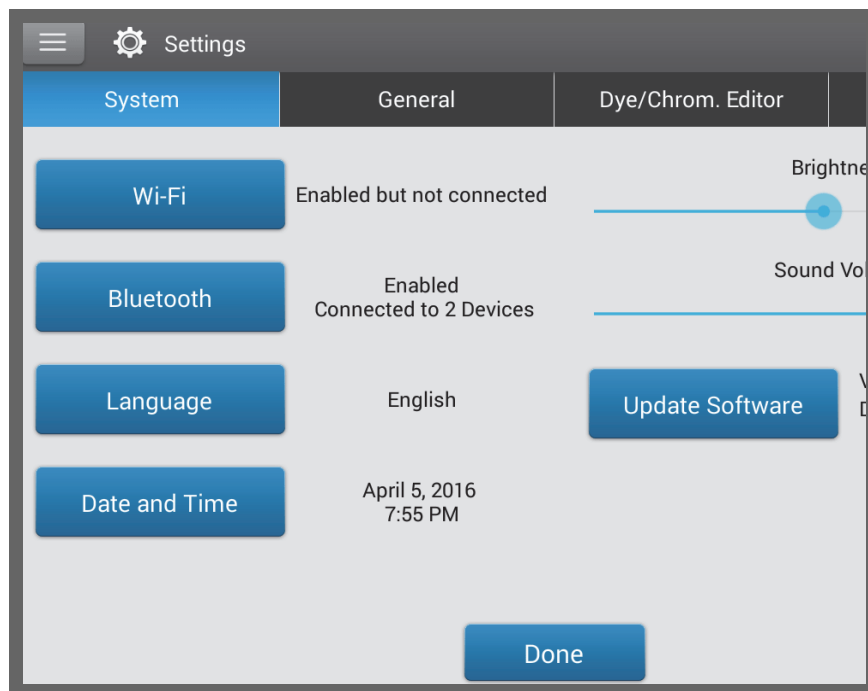
- [Instrument Settings](#)
- [NanoDrop One Data Viewer](#)
- [Search Experiment Database](#)
- [Select Experiments to Export or Delete](#)
- [Open Experiment](#)

## Instrument Settings

### View or change instrument settings

- from Home screen, tap 
- -or-
- from any measurement screen or the Data Viewer, tap  and choose  **Settings**

These instrument settings are available:



## System Settings

These options are available:

### Wi-Fi

Set up wireless local area network (WLAN) connection on the instrument

### Bluetooth

Set up Bluetooth connections to wireless input devices for the instrument such as a wireless keyboard, mouse or barcode scanner

### Language

Select language for displaying NanoDrop One software and for any connected input device such as a keyboard, mouse or barcode scanner

**Notice:** Changing the language requires a software restart.

<b>Date and Time</b>	<p><b>Automatic date &amp; time:</b> synchronize instrument date and time with available network</p> <p><b>Automatic time zone:</b> synchronize instrument time zone with available network</p> <p><b>Set date:</b> manually set instrument date (this option is disabled when Automatic Date &amp; Time is selected)</p> <p><b>Set time:</b> manually set instrument time (this option is disabled when Automatic Date &amp; Time is selected)</p> <p><b>Select time zone:</b> manually select instrument time zone (this option is disabled when Automatic Time Zone is selected)</p> <p><b>Use 24-hour format:</b> use 24-hour time format</p> <p><b>Choose date format:</b> choose an available date format</p>
<b>Brightness</b>	Adjust brightness of instrument touchscreen
<b>Sound Volume</b>	Adjust volume of instrument touchscreen
<b>Update Software</b>	<p>Update NanoDrop One software via USB device connected to instrument; if connected USB device contains multiple eligible update files, you can choose which files to update (see <a href="#">Update Software</a> for details)</p> <p><b>Version:</b> version of NanoDrop One instrument operating software currently installed on this instrument</p> <p><b>Database version:</b> version of NanoDrop One database on this instrument</p>

## General Settings

These options are available:

<b>Auto-naming</b>	Assign sample names automatically using base name followed by unique number starting with “1.” Uses default (“Sample”) or user-specified base name. For details, see <a href="#">Sample Name</a> .
--------------------	--

### Use cuvette

Select cuvette sampling mode (available for NanoDrop One<sup>C</sup> instrument model only). When selected, these additional options are available:

**Pathlength:** Enter cuvette [pathlength](#) (width) before taking blank or sample measurements with cuvettes (see cuvette manufacturer for cuvette specifications)

**Stir Speed:** If using automatic stirring, drop micro-stir bead into sample cuvette and set Stir Speed (levels 1 through 9 correspond with range from 10 RPM to 850 RPM with controlled ramping from zero)

**Heat cuvette to 37 °C:** Select this option if sample cuvettes require heating. Cuvette heater increases from room temperature to 37 °C at rate of 5 °C/minute.

## Dye/Chrom. Editor

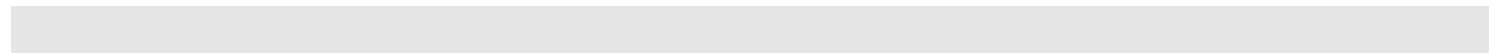
Use the [Dye/Chromophore Editor](#) to add a custom dye to the list of available dyes in [Microarray Setup](#) or [Proteins & Labels Setup](#). You can also specify which dyes are available in that list.

## Protein Editor

Use the [Protein Editor](#) to add a custom protein to the list of available proteins in the [Protein A280](#) application.

### Related Topics

- [Set Up the Instrument](#)
- [Update Software](#)
- [Measure a Sample Using a Cuvette](#)
- [Set Up Ethernet Connection](#)
- [Dye/Chromophore Editor](#)
- [Protein Editor](#)



## Acclaro Sample Intelligence

The Thermo Scientific™ Acclaro™ Sample Intelligence technology built into the NanoDrop One instruments provides these exclusive features to help you assess sample integrity:



**contaminant analysis** to help qualify a sample before use in downstream applications



**on-demand technical support** for measurements that are atypical or very low concentration



**invalid-result alerts** (a column sensor monitors for the presence of bubbles or reflective particles that can compromise measurement results)



Use these embedded resources to quickly troubleshoot possible problem measurements and make informed decisions on whether to use, re-purify or take other actions with an atypical sample result. The Sample Intelligence feature also serves as a resource for further study and a learning tool for new or novice users.

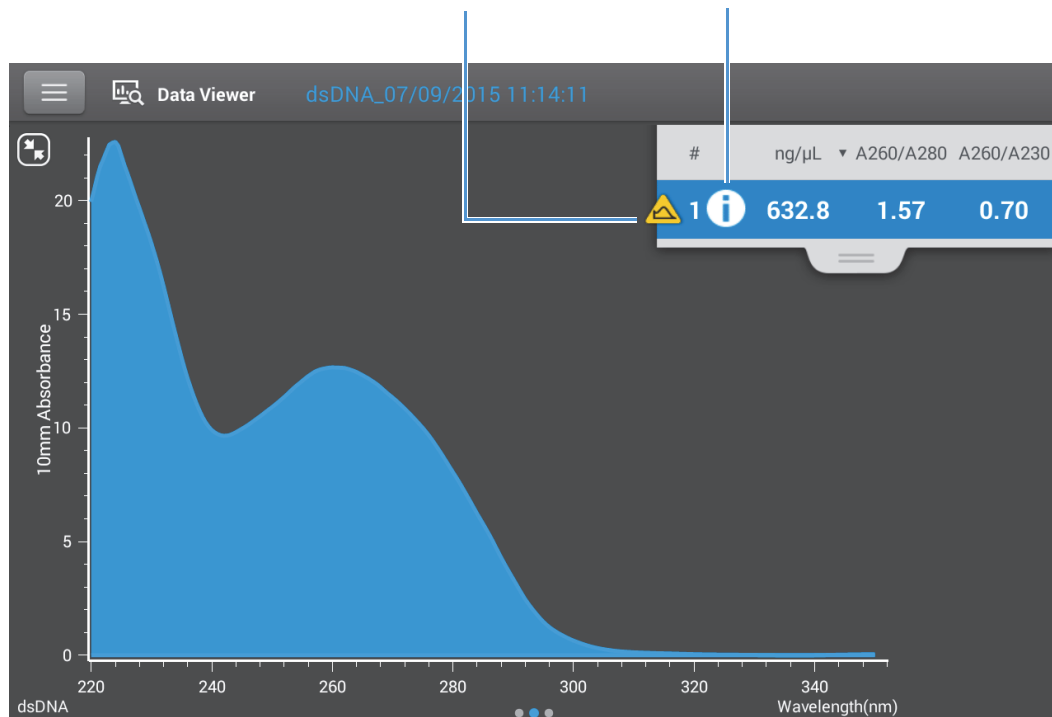


## View Acclaro Sample Intelligence Information

Measurements that include a contaminant analysis or technical information are flagged automatically (see examples below). Tap the icon to review the associated data or information.

Contaminant analysis is available for this measurement

Technical information is available for this measurement



The icons appear next to the [measurement results](#) (see above), and in the [data table](#), as well as the [Data Viewer](#) (see below).


#	Sample Name	ng/μL	A260/A280	A260/A230	A260	A280
1	Sample 1	632.8	1.57	0.70	12.66	8.05
2	Sample 2	633.7	1.57	0.70	12.67	8.06
3	Sample 3	518.2	1.56	0.69	10.36	6.63
4	Sample 4	519.3	1.56	0.70	10.39	6.64
5	Sample 5	516.4	1.56	0.69	10.33	6.63
6	Sample 6	876.3	1.80	2.24	17.53	9.71

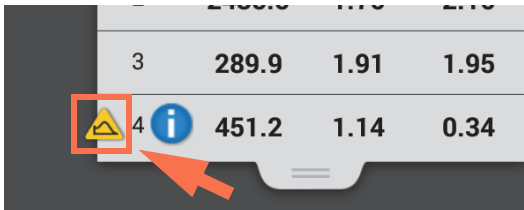
The icons are active in all three places; the information remains with the data indefinitely, even after it has been exported.

## Contaminant Analysis

For the dsDNA, RNA and Protein A280 applications, the NanoDrop One software automatically initiates a spectral analysis for several known contaminants during the measurement. Examples of known contaminants include:

- for dsDNA and RNA measurements:
  - in the analysis region: protein and phenol
  - also detects presence of guanidine HCl and guanidinium isothiocyanate
- for protein measurements:
  - in the analysis region: nucleic acids and phenol

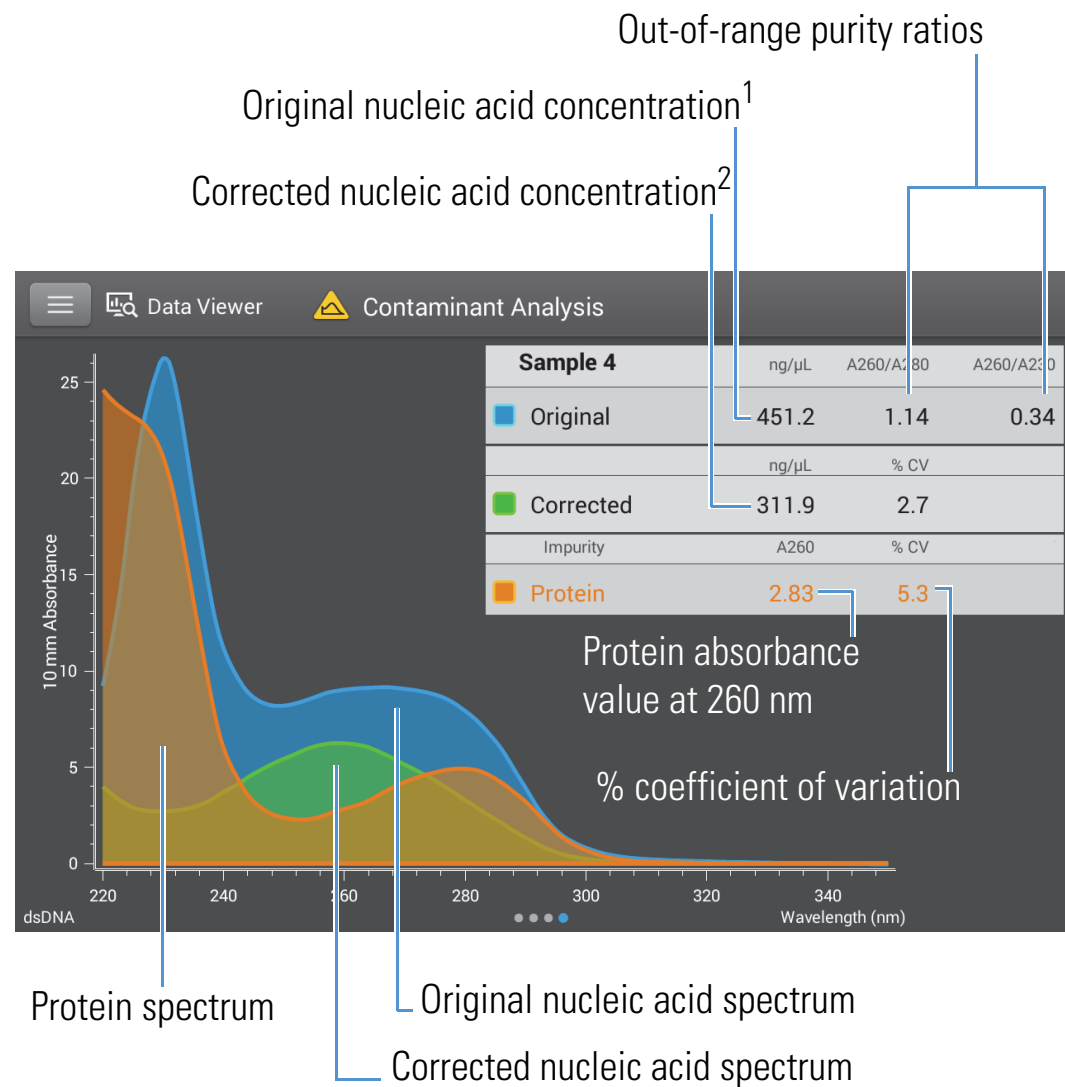
If contaminants are identified in a sample, the “Contaminant Analysis” icon  appears to the left of the measurement results.



3	289.9	1.91	1.95
 4 	451.2	1.14	0.34

Tap the icon to view the contaminant analysis and associated information.

Here is an example of results from a nucleic acid contaminant analysis that contains enough protein contaminant to affect the measurement results.



<sup>1</sup>Based on total sample absorbance (sample plus contaminant)

<sup>2</sup>Based on corrected sample absorbance (sample minus contaminant)

Since proteins absorb light near the analysis wavelengths for nucleic acid (230 nm, 260 nm, and 280 nm), the presence of protein in the nucleic acid sample shown above has pushed the A260/A280 and A260/A230 ratios out of range and caused the reported nucleic acid concentration to be higher than the real value. The software identifies the impurity (protein), and reports the following:

- baseline-corrected absorbance due to protein (2.83) at the analysis wavelength (260 nm)
- % coefficient of variation for the measurement result (uncertainty x 100/measurement result = 5.3%; a high %CV indicates the measurement result is close to the instrument detection limit or there is an interfering component)

- original nucleic acid concentration (451.2 ng/μL), which is based on the total baseline-corrected absorbance (sample plus contaminant) at the analysis wavelength
- corrected nucleic acid concentration (311.9 ng/μL), which is based on the corrected absorbance (sample minus contaminant) at the analysis wavelength

### Theory behind contaminant analysis

UV and UV-visible absorbance measurements are used to quantify nucleic acid and protein samples at 260 nm and 280 nm, respectively. The analysis is based on the fact that the total absorbance of a mixture solution at a given wavelength is the sum of the absorbance values of each component in the mixture.

An ongoing challenge of this method is that a number of materials used in the extraction process can absorb in various regions across the spectrum. When these contaminants are present in a sample, they can interfere with the analysis by artificially inflating the absorbance at the wavelength of interest, which causes the analyte concentration to be overestimated.

Traditionally, purity ratios are used to detect the presence of contaminants that could affect downstream applications. However, purity ratios do not always provide a complete picture of possible contamination. When a purity ratio falls outside the expected range, the spectral profile is often examined qualitatively.

Our Acclaro technology applies a quantitative approach to contaminant analysis. Through sophisticated mathematical algorithms, Acclaro analyzes the spectral data to identify probable contaminants in a sample and removes any contribution due to the contaminant from the sample result. This results in a more accurate concentration value of the analyte of interest and a more qualitative analysis of the level of contamination.


Since the spectrum of a pure compound is unique to that compound, a mixture spectrum of mostly known materials that have few interactions can be mathematically broken down into its component spectra and the components identified. The contaminant analysis algorithm uses a narrow spectral region (220-285 nm) around the analysis wavelength (260 nm for nucleic acids, 280 nm for proteins) to determine any absorbance contribution from possible known contaminants (protein or nucleic acid, and phenol) that absorb in that region. The entire spectrum is analyzed to determine the presence of other possible contaminants such as guanidine HCl and/or guanidinium isothiocyanate, which are common reagents used for nucleic acid purification.

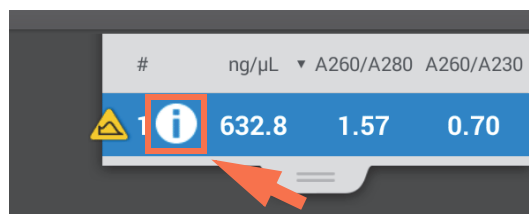
**Note** Achieving consistent, high quality contaminant analysis results is dependent on the quality of the measured sample spectra, which is dependent on the maintenance status of the instrument. For more information, see [Maintenance Schedule](#).

## On-Demand Technical Support

For the dsDNA and Protein A280 applications, the NanoDrop One software monitors all sample measurements for the presence of contaminants or other anomalies that may affect the measurement. Examples of monitored characteristics include:

- absorbance ratios, which indicate the presence of compounds that may interfere with sample measurements (also referred to as “purity ratios”). For more information, watch the multimedia training [What is a Purity Ratio?](#).
- bubble check, which looks for bubbles or other reflective materials in a sample or blank. For more information, watch the multimedia training [Effects of Bubbles in Samples](#).

If technical information is available, the “information” icon  appears to the left of the measurement results.

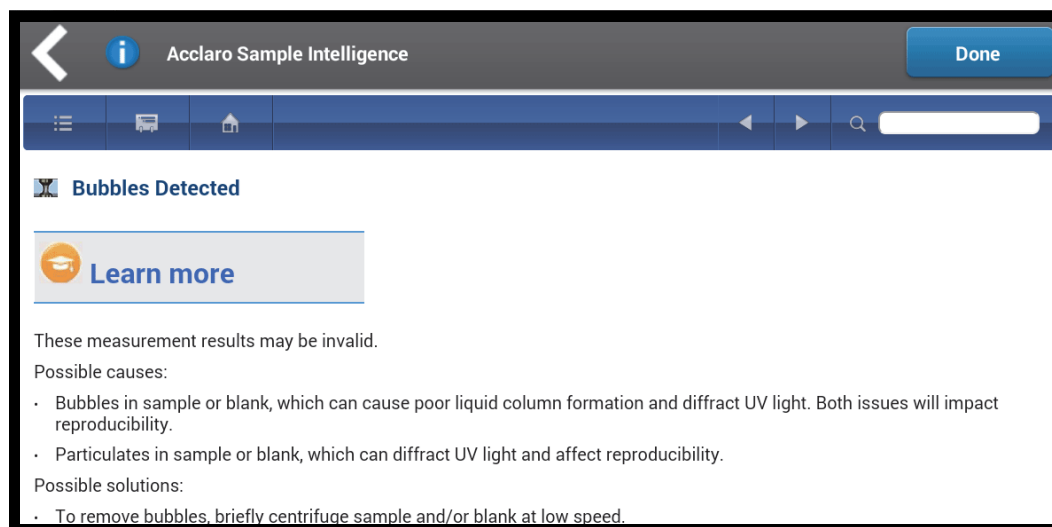


Tap the icon to view the information.

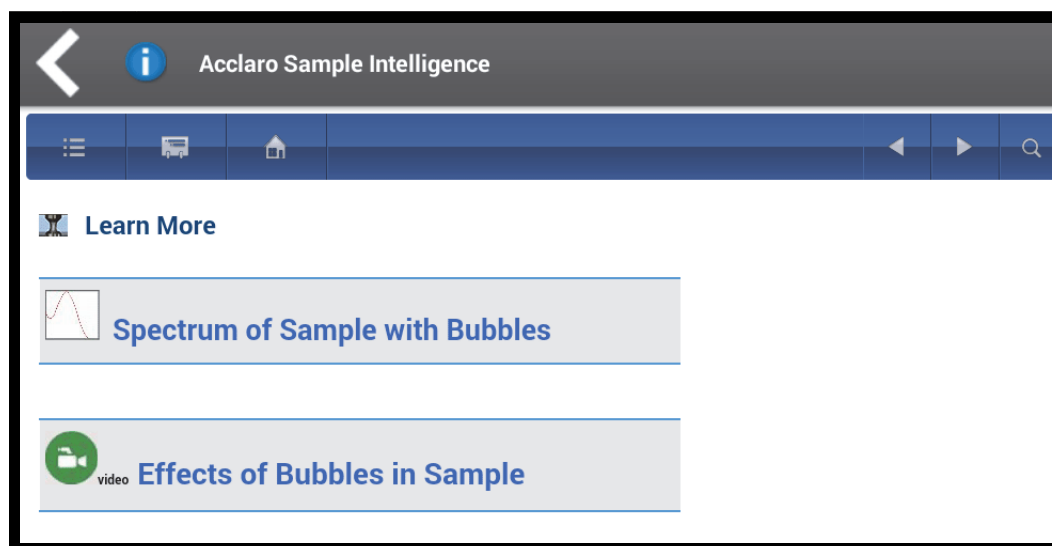
Here are results from a nucleic acid analysis for which two measured purity ratios are below the expected value and the sample contained enough bubbles to possibly affect the measurement results.



Tap an information button for more information. Here is the information provided for the bubble error:




Tap **Learn More** for the next level of information which, for this example, includes a link to a multimedia training video.



## Invalid-Results Alerts

The NanoDrop One software uses an embedded image sensor to monitor all measurements for conditions (such as a broken liquid column) that are likely to invalidate the measurement results.

After an invalid-results alert, the Invalid Results icon  is displayed and the measurement is stopped. See [Troubleshooting](#) for more information.

### **Related Topics**

- [NanoDrop One Measurement Screens](#)
  - [NanoDrop One Data Viewer](#)
  - [Maintenance Schedule](#)
  - [Maintaining the Pedestals](#)
  - [Troubleshooting](#)
-

## NanoDrop One Viewer Software

The NanoDrop One Viewer software gives you the flexibility to work with data acquired with the NanoDrop One instrument at your location and convenience. Use the Viewer software to:

- view or print data acquired using the NanoDrop One instrument on any personal computer
- create, edit, import, and delete custom measurement methods
- easily search the NanoDrop One Help system for information

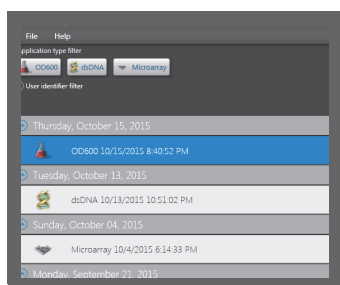
Data can be imported from the instrument at any time (see [Import Data from the Instrument](#) below), or saved directly on a connected computer after each measurement is completed (see “Set Up Ethernet Connections” or “Set Up Wi-Fi Connections” in [Set Up the Instrument](#) for details).

### Install the Viewer software

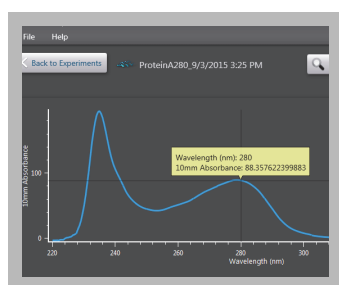
The Viewer software can be installed on any computer running the Windows™ operating system software. [See our website](#) for compatible versions of Windows software.

#### ❖ To download and install the Viewer software

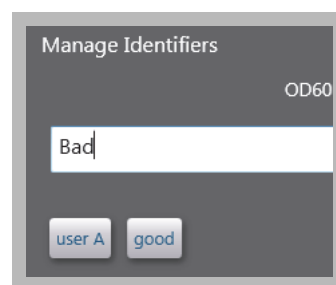
1. From a compatible PC that is connected to the Internet, use any web browser to navigate to our website.
2. On our website, locate NanoDrop One software downloads, select to download NanoDrop One Viewer software and follow the instructions to download and run the installer.



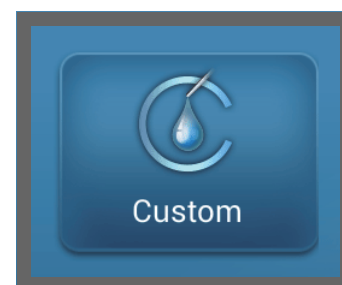
Home Screen



Manage Data



Manage Identifiers

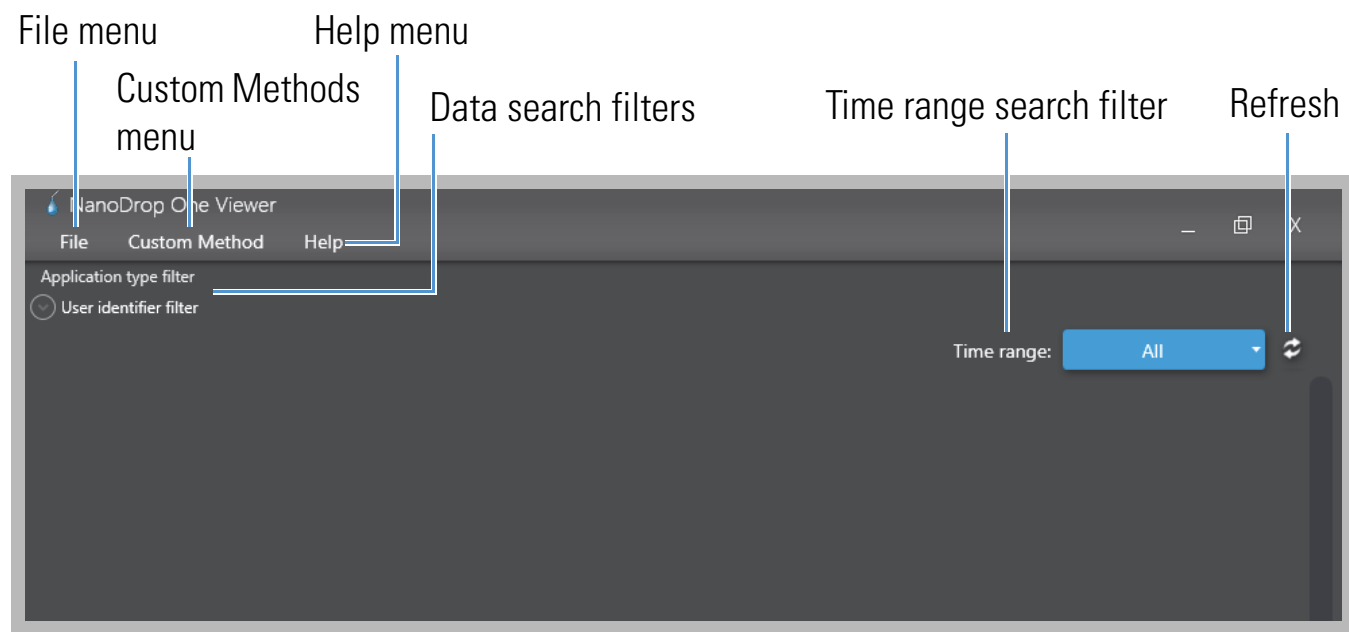


Manage Custom Methods



## Viewer Home Screen

After you install the Viewer software, it opens with a blank screen if there are no custom methods or saved or imported data in its database. These operations are available from the Viewer Home screen.



## File Menu

File menu options:

Import Data	For <a href="#">importing experiments</a> from the instrument
Set Up Wi-Fi Data Storage	Set up this computer as a potential data storage location for samples measured with the instrument (see “Set Up Wi-Fi Connections” in <a href="#">Set Up the Instrument</a> for more information)
Exit	Closes the Viewer software

## Custom Methods Menu

Custom Methods menu option:

<a href="#">Manage Custom Methods</a>	For creating, importing, editing and deleting custom methods, which can be used to acquire data with the instrument using the available custom settings
---------------------------------------	---

## Help Menu

Help menu options:

NanoDrop One Website	Opens a local web browser, if available, and navigates to the NanoDrop One website
Help	Displays the full NanoDrop One Help system including detailed information about the instrument, the NanoDrop One software, and the Viewer software
About	Displays version numbers for the NanoDrop One Viewer software

## Data Search Filters

Filters for searching the Viewer database on this computer based on the application used or any user-assigned identifiers. To turn off the data search filters, make sure none of the buttons are selected. For more information, see [Search Viewer Database](#).

## Time Range Search Filter

Filter for searching the Viewer database by experiment acquisition date (for example, last six months or in a specific date range). To turn off the time range filter, set it to **All**. For more information, see [Search Viewer Database](#).

## Refresh

Updates the list of experiments and measurement results in the Viewer software after new data have been [imported](#).

## Right-Click Menu

Right-click an experiment for these additional menu options:

Export Experiment	Export spectra and results for selected measurements in several formats
Manage Identifiers	Add user-defined labels to experiments, view assigned labels and remove or delete labels
Experiment Details	Display information about the open experiment including application type, date and time measured, number of measurements, instrument serial number, software and firmware version numbers, and any assigned labels
Delete Experiment	Delete selected experiment

**Notice:** Deleted data cannot be recovered.

## Manage Experiments and Associated Data

Use the Viewer software to open and view stored spectra and associated data from any experiment that was either exported from the instrument and then imported to the PC, or saved directly on the PC immediately after the measurement. Experiments are stored in a database on the computer according to acquisition date, experiment name, [application used](#) and any [assigned labels](#).

## Import Experiments

You can import data acquired with the NanoDrop One instrument to the NanoDrop One Viewer software installed on a personal computer, in order to view or print the data at your location and convenience.

### Note

- The data must first be exported from the instrument in the database (SQL) format to a portable USB memory device (see “Export Data” in [General Operations](#) for details).
- To learn how to save data directly on a personal computer after each measurement is completed, see “Set Up Ethernet Connections” or “Set Up Wi-Fi Connections” in [Set Up the Instrument](#).

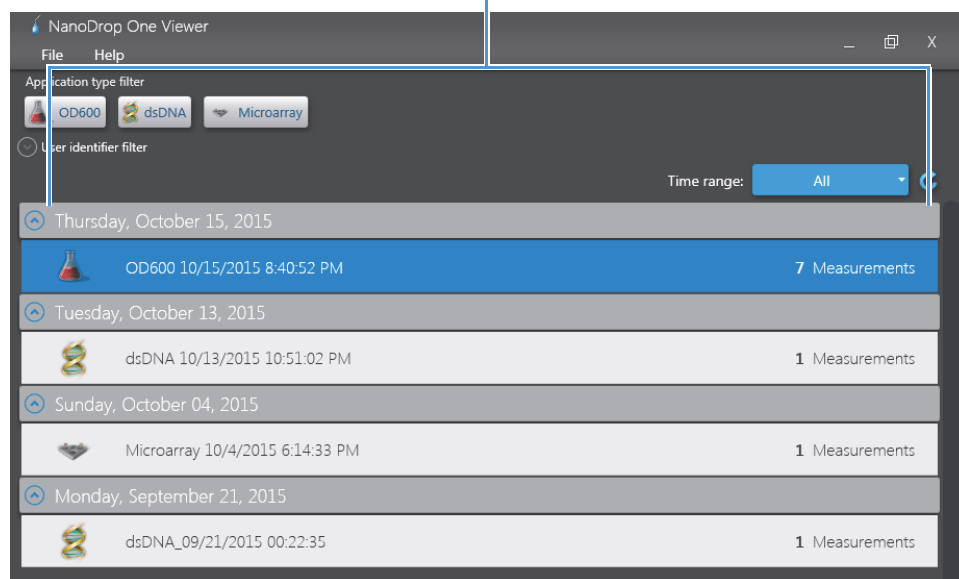
### Import experiments to Viewer software

- connect portable USB memory device with exported SQL file to personal computer that has NanoDrop One Viewer software installed
- from Viewer software, choose **File > Import Data**
- navigate to portable USB device, select exported SQL file and choose **Open**

**Note** By default, exported SQL files are stored on the USB memory device in a folder named “NanodropOne” followed by the instrument serial number.

- the NanoDrop One experiments stored in the SQL file are added to the Viewer Home screen. Here is an example:

### Imported experiments



## Search Viewer Database

A list of experiments that match the current filter settings appears on the Viewer Home screen. Filters include time range, application type and any user-defined labels (see [Manage Identifiers on a PC](#) for information about adding and deleting labels).

### Search experiment list

To search the experiment list, change a filter setting on the Viewer Home screen. The list is updated automatically. These filters are available:

- **Application type.** Only applications that have associated experiments in the Viewer database are available. To list only the experiments acquired using the OD600 application, for example, select **OD600** under the Application Type filter (selected filter buttons are blue). To turn off the Application Type filter, make sure none of the buttons are selected.

- **User identifier.** Only labels assigned to experiments in the Viewer database are available. To list only the experiments that contain the “Good” label, for example, select **Good** under the User Identifier filter (selected filter buttons are blue). To turn off the User Identifier filter, make sure none of the buttons are selected.
- **Time range.** To list only the experiments acquired during a particular date range (during the last six months, for example), select the date range from the drop down list. To turn off the time range filter, set it to **All**.

Here is an example of database filtering:

**Click** to select or deselect application filters

Change a filter to display updated list of experiments

**Click** to open and select time range filter

The screenshot shows the NanoDrop One Viewer interface. At the top, there is a menu bar with 'File' and 'Help'. Below the menu bar, there are three filter buttons: 'OD600', 'dsDNA', and 'Microarray'. The 'dsDNA' button is highlighted in blue and has an orange arrow pointing to it with the text 'Selected filter'. Below these are two more filter buttons: 'user A' and 'good'. To the right of these filters is a 'Time range' dropdown menu set to 'Last six months'. Below the filters is a list of experiments. The first experiment is 'dsDNA 10/13/2015 10:51:02 PM' with '1 Measurements'. The second experiment is 'dsDNA\_09/21/2015 00:22:35' with '1 Measurements'. The interface is annotated with several callouts: 'Click to select or deselect application filters' points to the filter buttons; 'Change a filter to display updated list of experiments' is a red-bordered box around the 'dsDNA' button; 'Click to open and select time range filter' points to the 'Time range' dropdown; 'Click to select or deselect user-defined label filters' points to the 'user A' and 'good' buttons; and 'Filtered list of experiments' points to the list of experiments.

**Click** to select or deselect user-defined label filters

Filtered list of experiments

## Open Experiment and View Associated Data

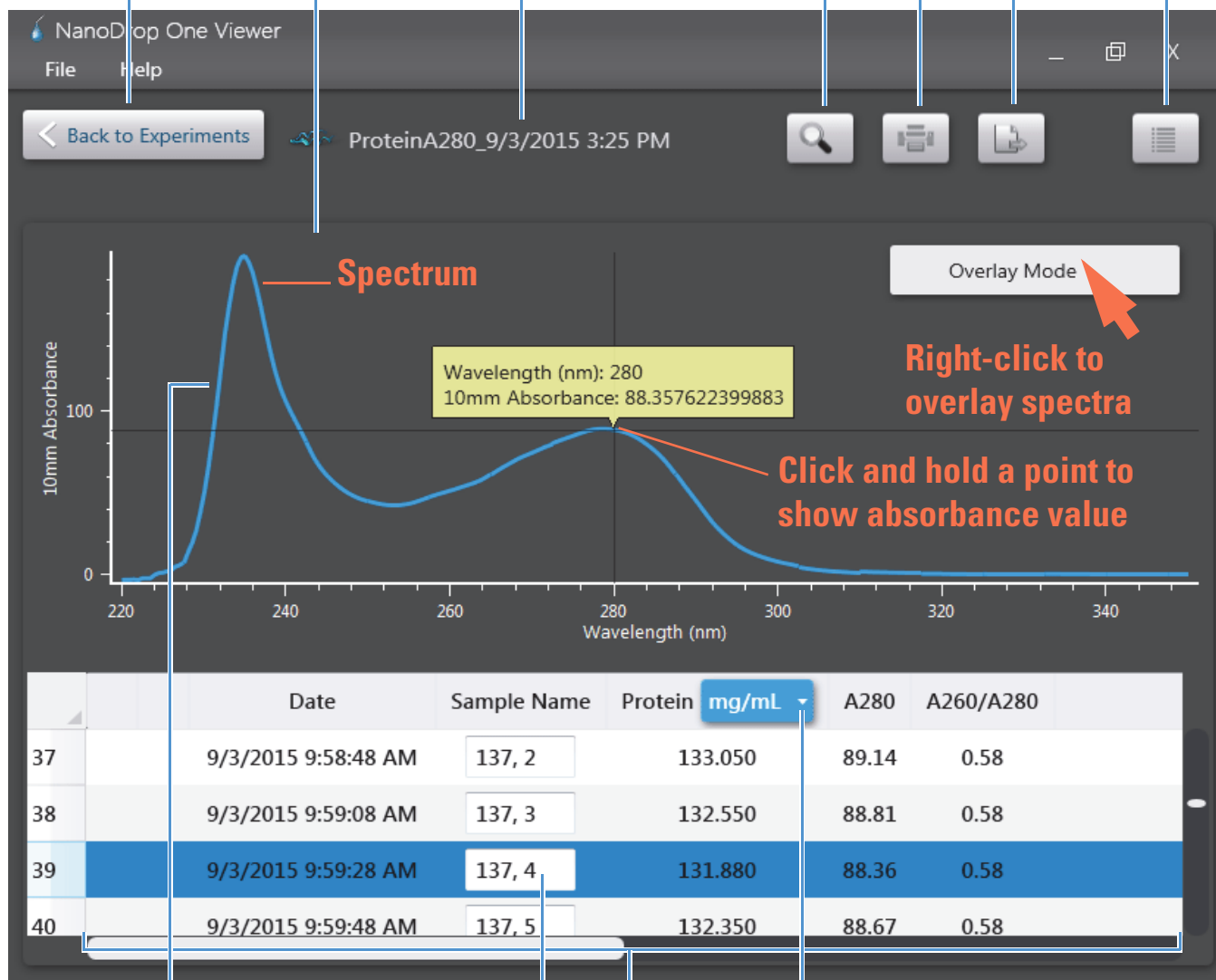
Use the Viewer software to open experiments stored in the Viewer database in order to view, print or export the spectra and associated data. The Viewer Home screen shows a list of experiments that match the current filter settings.

### Open experiment

- use available filters to locate the experiment (see [Search Viewer Database](#) for details)
- double-click the experiment name in the filtered experiment list (the experiment opens and the software displays the measurement screen)

These options are available from the Viewer measurement screen.

Return to Viewer Home screen    Spectral pane    Experiment name    Manage Identifiers    Print    Experiment details    Export



Click to edit sample name

Click to change displayed unit

Use mouse scroll wheel to expand or contract spectrum; double-click to reset

Measurement details (see individual Applications for more information)

Right-click to overlay spectra

Click and hold a point to show absorbance value

## Print Data

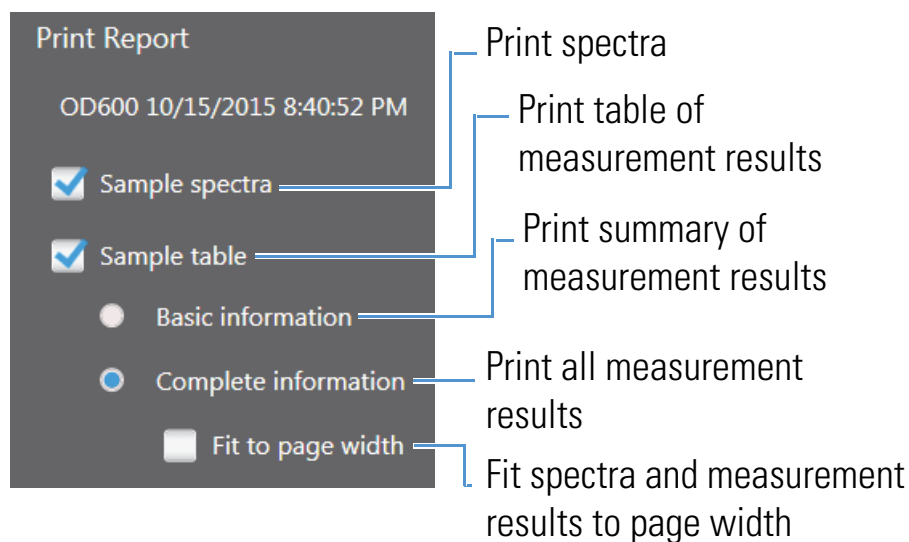
You can print selected measurements in an open experiment using standard Windows print tools.

### Print selected measurements

- open the experiment
- click to select a measurements to print (use Shift+click, or click and drag, to select sequential measurements; use Ctrl+click to select nonsequential measurements)

- click 

The Print Report window is displayed with a preview of the first page, along with these options:



These standard Windows Print options are also available:

- Page Setup (to select paper size and adjust margins and page orientation)
- Print Preview (allows all pages to be previewed)
- click **Print**
- select a printer
- click **Print**




## Export Data

You can export spectra and results for selected measurements to these formats:

- measurement results only to comma-separated values spreadsheet (.csv) file
- spectral data only (absorbance value at each wavelength) to tab-separated values spreadsheet (.tsv) file
- spectral data to tsv file and measurement results to csv file
- NanoDrop One database (.sql) file containing spectra and measurement results that can be opened from the instrument or from the NanoDrop One Viewer software
- spectral data to xml spreadsheet (.xml) file

The filenames are the same as the [experiment names](#). Use any spreadsheet or word processing application to open a CSV, TSV or XML file. The SQL file can be opened only using our NanoDrop One Viewer software, and only after the file has been imported. The XML file can also be opened with an XML reader application.

### Export selected measurements

- open the experiment
- click to select a measurement to export (use Shift+click to select sequential measurements; use Ctrl+click to select nonsequential measurements)
- click 
- in Export Experiments box:
  - navigate to a location for saving the exported data
  - set **Save As Type** to the desired format (see above for descriptions of available options)
- choose **Save**

**Note** The Export Data feature is unavailable in the NanoDrop One Viewer software when the computer is connected to the instrument with an Ethernet cable.

## Delete Data

You can delete an experiment from the Viewer database.

### Delete selected experiment

- use available filters to locate the experiment (see [Search Viewer Database](#) for details)
- right-click the experiment name in the filtered experiment list
- choose **Delete Experiment**

**NOTICE** Deleted data cannot be recovered.

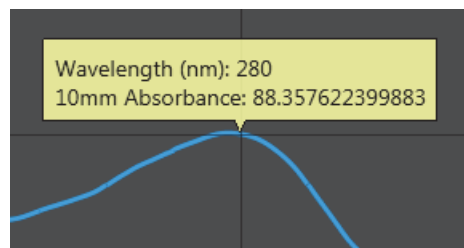
## Find Absorbance Values on a Spectrum

You can easily view the absorbance value that corresponds with any wavelength in a displayed spectrum.

### Find absorbance values on a spectrum

- open the experiment
- select the measurement
- click and hold the point on the displayed spectrum

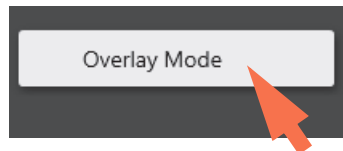
The wavelength and corresponding absorbance value are displayed in a popup box:



**Note** You can also drag the mouse along the spectrum's X-axis to display absorbance values sequentially.

## Overlay Spectra

If you want to display the spectra for all measurements in the experiment layered on top of each other in the spectral pane, open the experiment, right-click the spectral pane and select **Overlay Mode**. The spectra are displayed in a variety of colors.



**Note** To display multiple selected spectra layered on top of each other without using Overlay Mode, simply select the measurements in the open experiment.

## Expand or Contract Displayed Spectra

After you open an experiment, you can use the **scroll wheel on your mouse** to expand or contract a displayed spectrum or spectra along the X- and Y-axis.

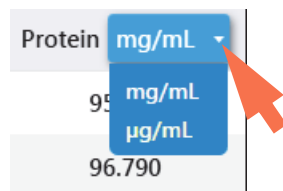
To reset both axes, double-click the spectral pane.

## Change Concentration Unit

Many applications offer a choice of concentration units.

### Change concentration unit for selected experiment

- open the experiment
- use the drop down menu, if available, in the measurement table to change the displayed unit



After the unit is changed, all reported concentration results are recalculated to comply with the new unit.

## View Experiment Details

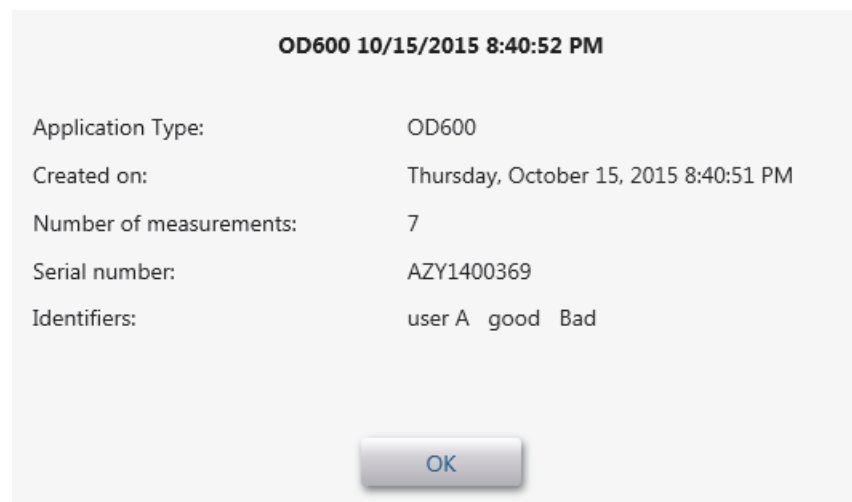
You can display information about the open experiment including application type, date and time measured, number of measurements, instrument serial number and any assigned labels.

### View experiment details

- open the experiment

- click 

Here is an example:



## Manage Identifiers on a PC

You can add one or more “identifiers” (i.e., labels or metadata tags) to an experiment to make the experiment easier to find. Labels can be added from the NanoDrop One software running on the instrument (see [Manage identifiers on the instrument](#)), or from the NanoDrop One Viewer software installed on a personal computer.

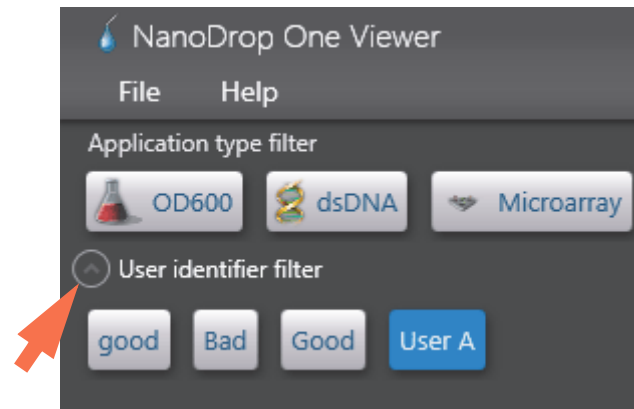
Use the Viewer software to add labels to experiments, assign existing labels, view assigned labels and remove or delete labels on a personal computer. You can filter the list of experiments based on one or more user-defined labels.

## Show or Hide User Identifier Filter Buttons

The user identifier filters can be shown or (if you have a lot of them) hidden to allow more space for the experiment list.

### Show User Identifier filter buttons

- click the adjacent arrow so the arrow points up




### Hide User Identifier Filter buttons

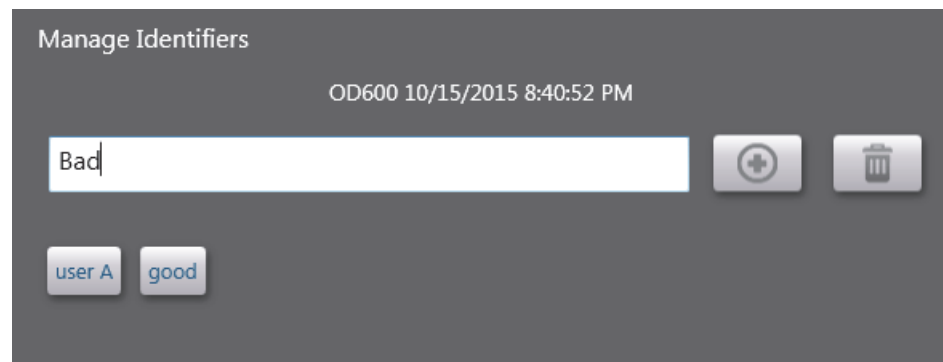
- click the adjacent arrow so the arrow points down

## Label Experiment in Viewer

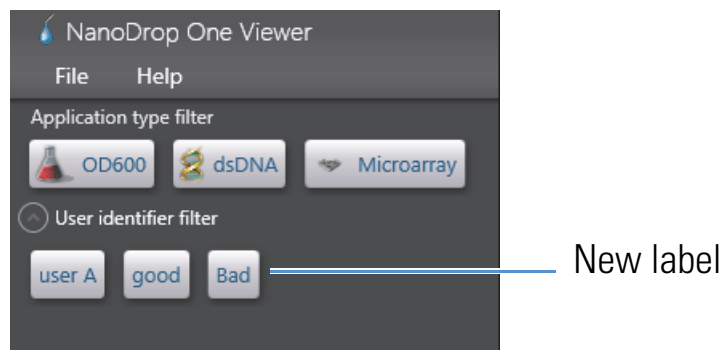
You can use the Viewer software to add user-defined labels to experiments. The list of experiments can then be filtered based on those labels (see [Find labeled experiment](#) for details).

### Add new label to experiment

- from Viewer Home screen, right-click experiment in experiment list and choose **Manage Identifiers**
- in Manage Identifiers box, enter label and tap  or press Enter key (new label appears below entry box)

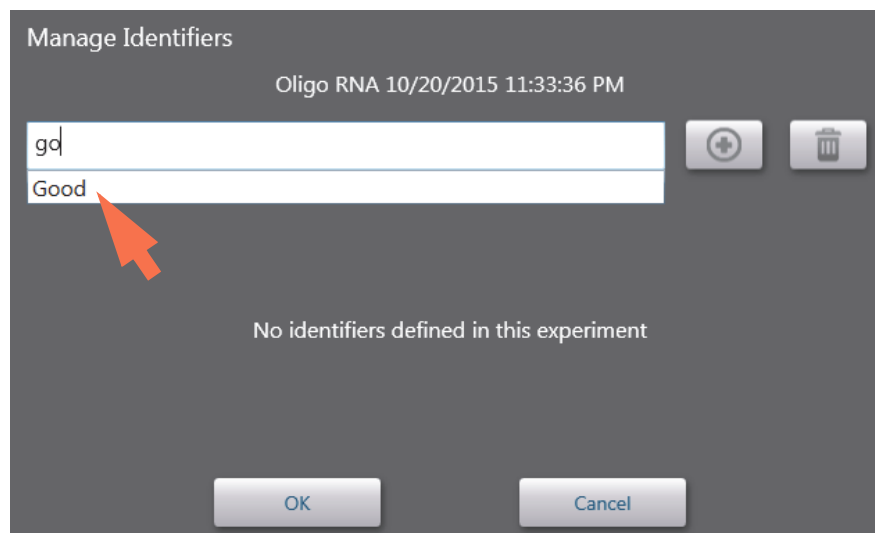


- choose **OK** (new label appears in User Identifier Filter group on Viewer Home screen)



### Assign existing label to experiment

- from Viewer Home screen, right-click experiment in experiment list and choose **Manage Identifiers**
- in Manage Identifiers box, start typing existing label name (actual name of existing label appears below entry box)



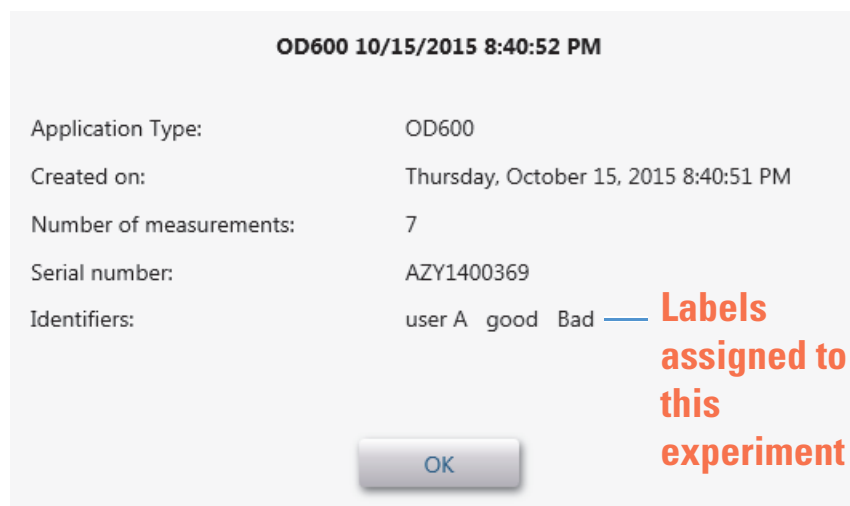
- select auto-filled existing label and choose **OK** (existing label is added to selected experiment)

## View Labels Assigned to an Experiment

You can use the Viewer software to see all the user-defined labels assigned to an experiment.

### View assigned labels

- from Viewer Home screen, right-click experiment in experiment list and choose **Experiment Details**



- choose **OK**

## Find Labeled Experiments

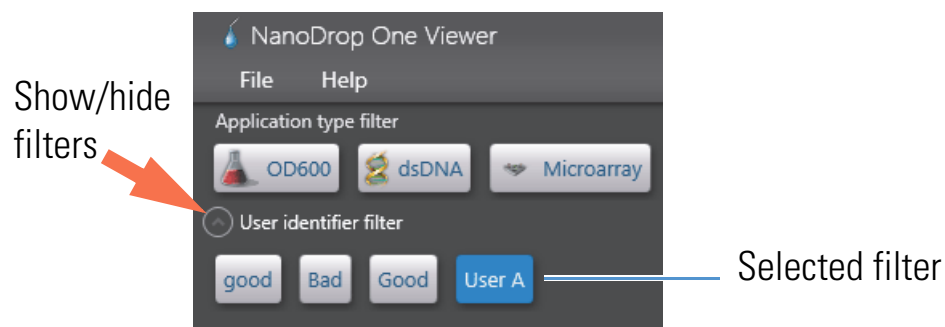
You can use the Viewer software to find experiments with assigned user-defined labels. The database is automatically filtered using the current filter settings.

### Find experiments that have a particular user-defined label

from Viewer Home screen, set search filters:

- deselect any **Application Type filters**, if desired, so the experiments acquired with all applications are listed
- set Time Range filter, if desired (only experiments acquired in selected range are listed)

- click each **User Identifier filter** button to select it (selected filter buttons are blue)  
(if the buttons are hidden, click the adjacent arrow to show them)




The list of experiments is filtered and updated automatically so only experiments that match the selected filters are listed.

## Remove a Label

You can use the Viewer software to easily remove a user-defined label from an experiment. A removed label remains in the User Identifier Filter list if it is still assigned to other experiments.

### Remove a label

- from Viewer Home screen, right-click experiment in experiment list and choose **Manage Identifiers**
- in Manage Identifiers box, select one or more label buttons (selected label buttons are blue)
- tap  (selected label(s) no longer appear below entry box)
- choose **OK**

**Note** To delete a user-defined label from the software, you must remove it from all the experiments it is assigned to.



## Manage Custom Methods

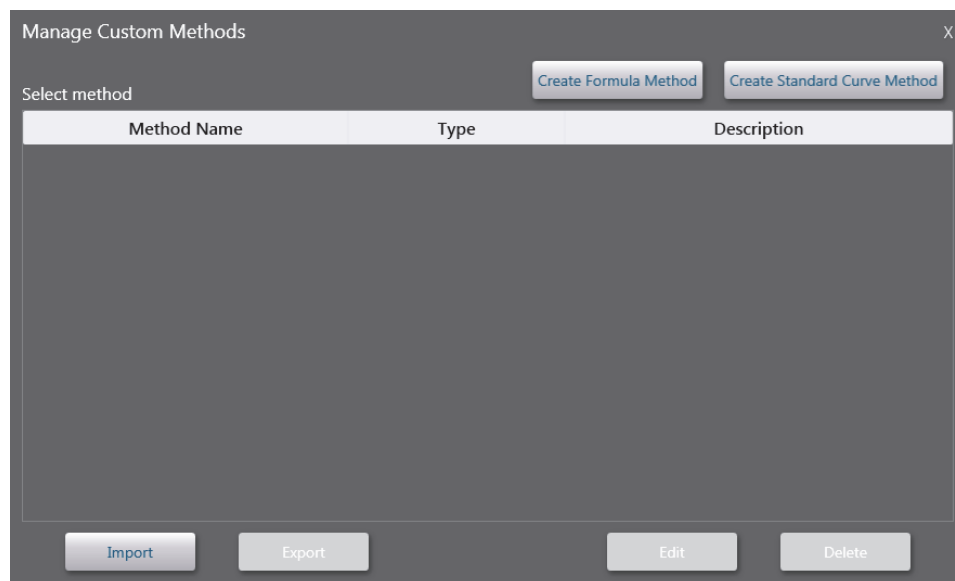
The Viewer software is your tool for creating and managing custom methods, which contain user-defined settings that can be used to acquire data with the instrument. Custom methods can be made with or without standards.

### Create Custom Method

Create method to be used for sample measurements with user-defined settings.

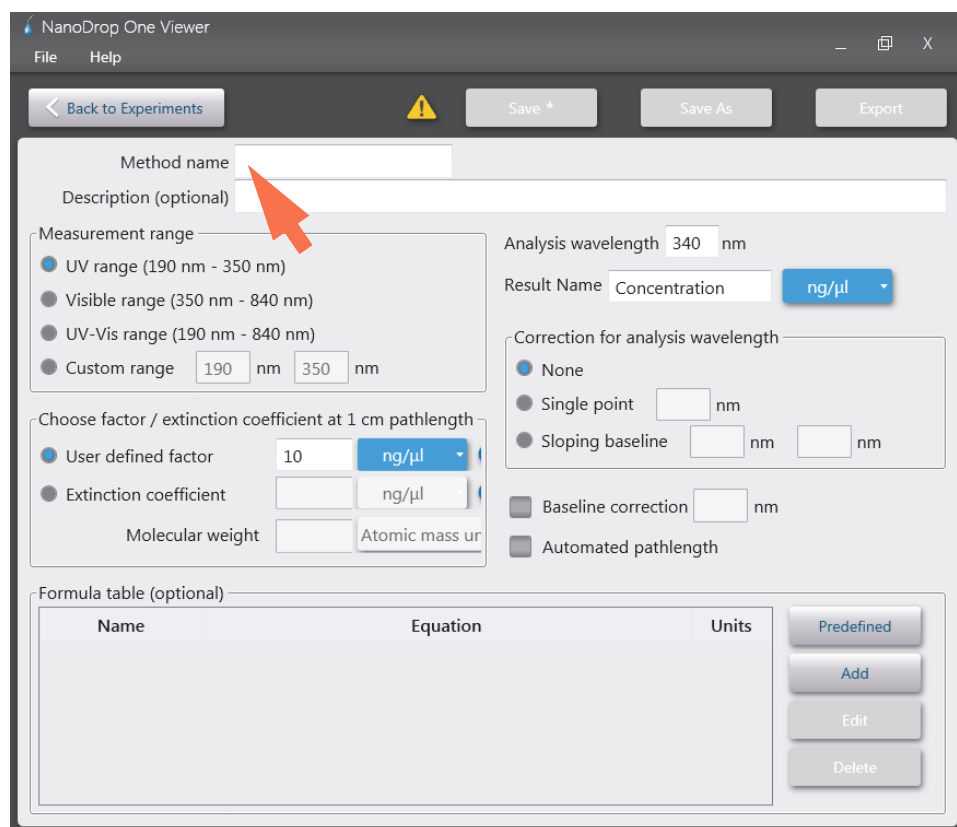
#### Create new custom method

- from Viewer Home screen, choose **Custom Methods** (menu) > **Manage Custom Methods**



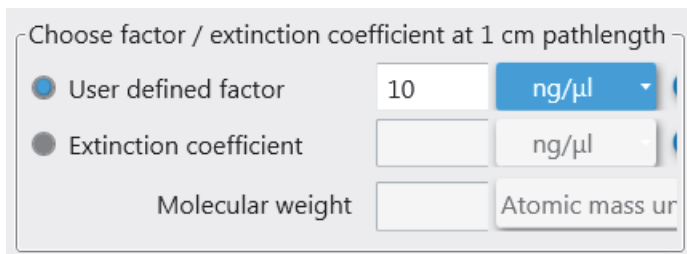
- in Manage Custom Methods box, choose one of the following:
  - **Create Formula Method** (if your method will not have standards)
  - **Create Standard Curve Method** (if your method will have standards)

- in the setup window, enter **Method Name** (this name appears in the [Custom Setup](#) box on the instrument after the method has been transferred there)



### Custom Method Setup for Create Formula Method selection


- enter detailed **Description** of method, if desired
- specify how to calculate and report the method results:
  - if method does not have standards, specify [factor or extinction coefficient of analyte](#) (enter “1” to report absorbance measurements only)



- if method has standards, enter name and concentration of each standard and select the curve fit type

Standard ID	Concentration (ng/μl)
Reference	0.00
Standard 1	
Standard 2	
Standard 3	
Standard 4	
Standard 5	

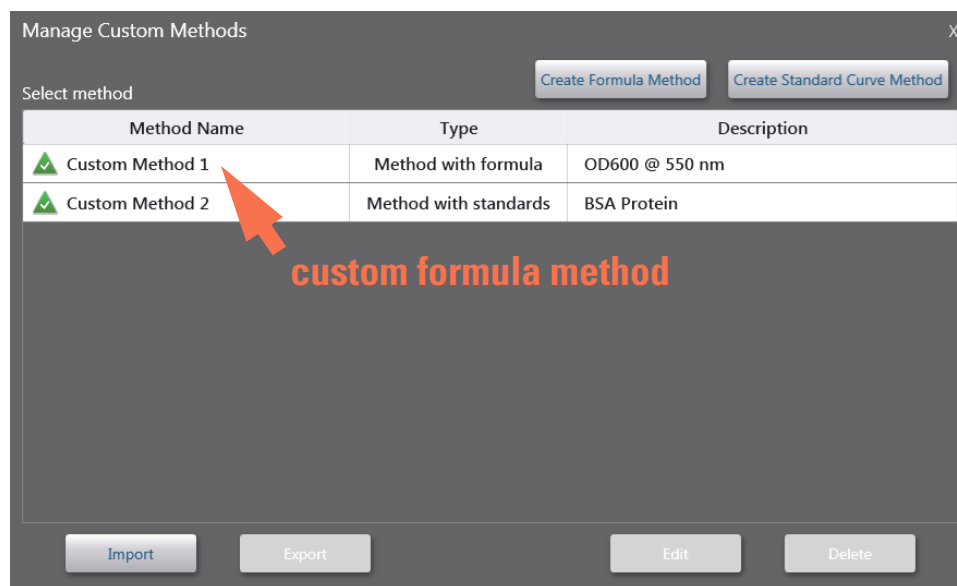
- enter or choose remaining custom settings as needed (see below)
- choose **Save**

**Note** If this icon  appears next to the Save button instead of a green check mark icon, the method is invalid because it contains an error. Hover your mouse over the icon for suggested solutions.

if the method has a green check mark icon at the top, tap **Close** to exit method setup

### View or edit custom method

- choose **Custom Methods** (menu) > **Manage Custom Methods** (existing methods are listed in Select Method box along with their type (formula or standards) and Description)



### Custom method settings

These settings are available for creating custom methods.

Setting	Available Options
Measurement range	<p>Select spectral range in which method will acquire data.</p> <p>Available options:</p> <ul style="list-style-type: none"> <li>• Ultra-violet only (190 nm - 350 nm)</li> <li>• Visible only (350 nm - 850 nm)</li> <li>• Ultra-violet and visible (190 nm - 850 nm)</li> <li>• Custom (specify starting and ending point in nanometers)</li> </ul> <p><b>Notes:</b></p> <ul style="list-style-type: none"> <li>• If a <a href="#">Baseline correction</a> and/or <a href="#">Analysis wavelength correction</a> are used, make sure your selected spectral range includes your specified baseline correction and/or analysis correction wavelength.</li> <li>• For micro-volume absorbance measurements and measurements taken with nonstandard (other than 10 mm) cuvettes, the spectra are normalized to a 10 mm pathlength equivalent.</li> </ul>
Analysis wavelength	<p>Monitor absorbance at specified wavelength (enter the wavelength in nanometers).</p> <p><b>Note:</b> The specified wavelength must fall within the selected <a href="#">measurement range</a>.</p> <p>The measurement results or the concentration will be calculated automatically using the absorbance value at the specified wavelength and applying the selected method type (factor or standard curve).</p>
Result name	<p>Enter descriptive name for calculated concentration result (for example, “Nucleic Acid”) and use adjacent drop down list to select appropriate unit. Result name appears as column heading for reported concentration value.</p>

**Setting** Available Options

Factor or Extinction coefficient at 1 cm pathlength (Formula methods only)

Specify whether to use factor or extinction coefficient to calculate concentration result:

Choose factor / extinction coefficient at 1 cm pathlength

User defined factor    10    ng/µl

Extinction coefficient       ng/µl

Molecular weight    Atomic mass ur

- **User-defined factor.** Enter **factor** for 1 cm pathlength and use adjacent drop down list to select appropriate **unit**. Equation below shows how factor is used to calculate sample concentration:

$$c = (A * f) / b$$

where:

c = analyte concentration

A = absorbance in absorbance units (A)

f = factor (typically 1/ε, where ε = wavelength-dependent molar absorptivity coefficient, or extinction coefficient)

b = pathlength in cm (determined at measurement time, then normalized to 10 mm (1 cm) pathlength equivalent)

- **Extinction coefficient and molecular weight.** Enter **extinction coefficient** for 1 cm pathlength and use adjacent drop down list to select appropriate **unit**. Equation below shows how extinction coefficient is used to calculate sample concentration:

$$c = A / (\epsilon * b)$$

where:

c = analyte concentration

A = absorbance in absorbance units (A)

ε = wavelength-dependent molar absorptivity coefficient (or extinction coefficient)

b = pathlength in cm (determined at measurement time, then normalized to 10 mm (1 cm) pathlength equivalent)

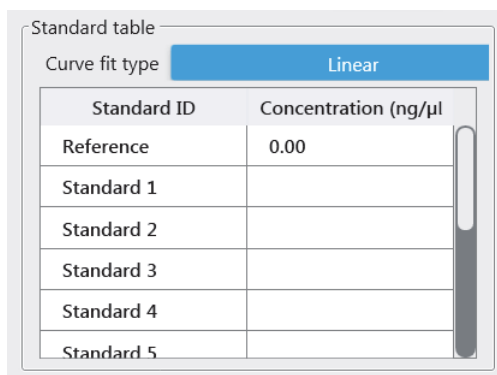
**Setting Available Options**

**Notes:**

- Refer to product literature for information about factors and extinction coefficients for specific materials.
- To set up a method that reports absorbance measurements only, select Factor or Extinction Coefficient with the factor or extinction coefficient set to “1”.
- If specified unit for factor or extinction coefficient is based on mass (such as mg/mL) and specified unit for calculated result is based on molarity (such as pmol/μL) or vice versa, enter **molecular weight** and use adjacent drop down list to select appropriate **unit**.

Standards (Standard curve methods only)

Define the standards:



- Enter name and analyte concentration of each standard and a reference, if desired:
  - Depending on the Curve Type setting, a standard curve can be generated using two or more standards. (The software **allows a reference and up to 7 standards**.)
  - **All reference and standards solutions** should be in the same buffer used to resuspend the samples plus the same volume of reagent added to the samples.
  - **First standard** can be a reference measurement. The reference solution should contain none of the analyte of interest. (The reference measurement is not the same as a blank measurement.)
  - **Concentration values for standards** can be entered in any order but the standards must be measured in the order in which they were entered; however, best practice dictates that standards be measured from the lowest concentration of the standard analyte stock to the highest.
  - **Concentration range of the standards** must cover the dynamic range of the assay and the expected range of the unknown samples. Sample analyte concentrations are not extrapolated beyond the concentration of the highest standard.

For more information, see [Working with Standard Curves](#).

Setting	Available Options
	<ul style="list-style-type: none"><li>• Select curve fit type.</li></ul> <p>Specify type of equation used to create standard curve from standard concentration values. Available options:</p> <ul style="list-style-type: none"><li>– <b>Linear:</b> Draws the linear least squares line through all measured standards (requires reference measurement and at least one standard)</li><li>– <b>Interpolation:</b> Draws a series of straight lines to connect all measured standards (requires reference measurement and at least one standard)</li><li>– <b>2<sup>nd</sup> order polynomial:</b> Draws the 2<sup>nd</sup> order least squares polynomial using all measured standards (requires reference measurement and at least two standards)</li><li>– <b>3<sup>rd</sup> order polynomial:</b> Draws the 3<sup>rd</sup> order least squares polynomial using all measured standards (requires reference measurement and at least three standards)</li></ul>
Baseline correction	<p>Select this option to correct offset caused by light scattering particulates by subtracting the absorbance at a specified baseline point. Then specify wavelength for baseline correction.</p> <p><b>Note:</b> Software subtracts absorbance value at specified baseline correction wavelength from absorbance values at all wavelengths in sample spectrum. As a result, absorbance of sample spectrum is zero at specified baseline correction wavelength.</p>
Analysis wavelength correction	<p>Use this option to specify absorbance correction at analysis wavelength only. Available options:</p> <ul style="list-style-type: none"><li>• <b>None.</b> No correction at analysis wavelength.</li><li>• <b>Single point.</b> Enter wavelength for analysis correction. (Absorbance value at specified analysis correction wavelength is subtracted from absorbance value at analysis wavelength. Corrected value is used to calculate sample concentration.)</li><li>• <b>Sloping baseline.</b> Enter two wavelengths that define sloping baseline for analysis correction. (Absorbance value of sloping baseline at analysis wavelength is subtracted from absorbance value at analysis wavelength. Corrected value is used to calculate sample concentration.)</li></ul>

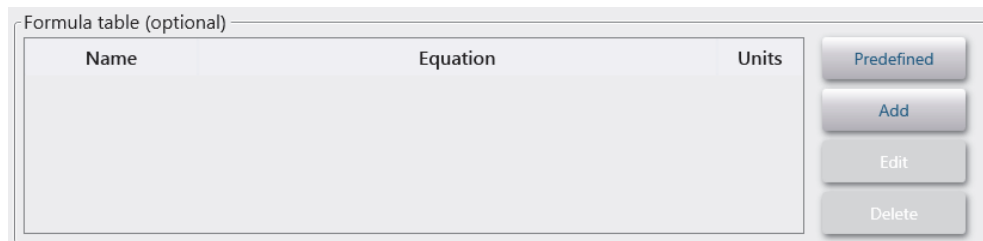


Setting	Available Options
Automated pathlength	<p>Affects micro-volume measurements only.</p> <ul style="list-style-type: none"><li>When Automated Pathlength is selected, software selects the optimal pathlength (between 1.0 mm and 0.03 mm) based on sample absorbance at the analysis wavelength. For example, when sample absorbance at the analysis wavelength is less than or equal to 12.5 (10 mm pathlength equivalent), the optimal longer pathlength is used. When sample absorbance is greater than 12.5, the optimal shorter pathlength is used. Recommended for samples that are highly absorbing at the analysis wavelength. (This option may cause reduced sensitivity when the sample spectra have a large absorbance peak that is not at the analysis wavelength.)</li></ul> <p><b>Note:</b> When the analysis wavelength is between 190 nm and 219 nm, the optimal longer pathlength is used when sample absorbance is less than or equal to 10 (10 mm pathlength equivalent), and the optimal shorter pathlength is used when sample absorbance is greater than 10.</p> <ul style="list-style-type: none"><li>When Automated Pathlength is deselected, the software uses a 1 mm pathlength regardless of the sample absorbance. This can cause detector saturation (resulting in jagged peaks) for highly absorbing samples (e.g., ~15 A at 10 mm pathlength equivalent).</li></ul>

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**Setting Available Options**

Formula table (optional) Use the Formula table to specify additional reported results, such as a purity ratio, for each sample.



Available options:

- **Predefined.** Select from a list of predefined formulas, which can be used as is or edited, and choose **Add**. The predefined formula is listed in the Formula Table.
- **Add.** Create formula for current method. Available options:
  - **Formula Name.** Enter a name for the formula. After a measurement, the name is reported in Data Table and Sample Details screens.
  - **Formula.** Enter valid formula (see below for rules and examples). After a measurement, the measured or calculated value is reported in Data Table and Sample Details screens.
  - **Unit.** Enter unit for reported result. After a measurement, the unit is reported in Data Table and Sample Details screens.
- **Edit.** Edit selected formula for current method.
- **Delete.** Delete selected formula from current method.

---

Formula rules

Custom formulas can include the following operators and functions:

- **Path()**. Returns sample pathlength in cm.
- **A(nm)**. Returns sample absorbance at specified wavelength (for example, enter A(650) to add the measured absorbance at 650 nm to your equation).
- **Operators:** + (add), - (subtract), \* (multiply), / (divide).
- **Functions:** Log(x), Pow(x,y).

**Notes:** Follow these additional rules for all languages:

- Use period “.” decimal separators for floating point and double-floating point numbers.
- Use comma “,” list separators (for example, “POW(2,8)”).
- Do not use comma “,” group separators for large numbers (for example, enter 1000 rather than 1,000).

## Copy Custom Method

To create a custom method that is similar to an existing one, save the existing method with a new name and then edit the new method.

### Copy custom method

- from Manage Custom Methods box, select custom method
- choose **Edit**
- choose **Save As**
- enter new **Method name** and **Description** (optional)

## Run Custom Method


If you want to run a custom method and store the measurement results on the instrument, the method must also reside on the instrument (see [To Load a Custom Method](#) for details). (This is the only way to run a custom method if your instrument is not connected to the computer with an Ethernet cable or through a wireless network.)

**Note** If the computer is connected to the instrument with an Ethernet cable or through a wireless network, custom methods can reside on the computer and the measurement results will be stored in the NanoDrop One Viewer database on that computer. For more information, see “Set Up Ethernet Connection” or “Set Up Wi-Fi Connections” in [Set Up the Instrument](#).

## Export Custom Method

Export a custom method in order to run it and store the measurement results on the NanoDrop One instrument.

- from Manage Custom Methods box, select custom method

**Note** If this icon  appears next to the method name in the Manage Custom Methods box, the method is invalid because it contains an error. Hover your mouse over the icon for suggested solutions.

- choose **Export** (if method is invalid, an error message is displayed; errors must be fixed before method can be exported)
- in Export Custom Method box, choose **Save** (method is exported to method file (\*.method filename extension) in proprietary format; default folder is “C:\[user name]\My Documents\Thermo\NanoDrop One”)

To transfer the method to the NanoDrop One instrument, copy the method file to a USB memory device and then load the method (see [To Load a Custom Method](#) for details)

## Import custom method

Import a custom method back to a computer running the NanoDrop One Viewer software in order to edit the method settings.

- from Manage Custom Methods box, choose **Import**
- locate and select “.method” file
- choose **Open** (imported method is added to end of Select Method list)

## Edit custom method

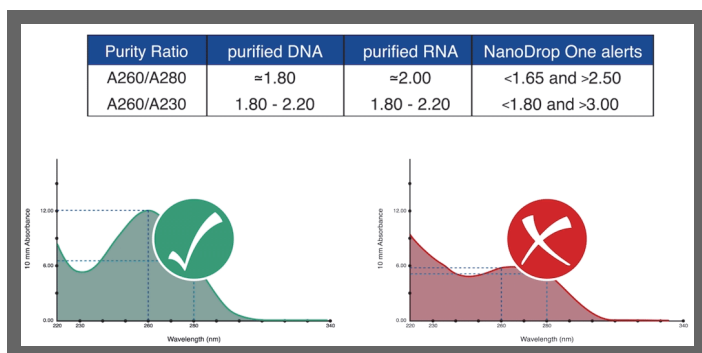
Edit a custom method in order to change the method settings.

- from Manage Custom Methods box, select custom method
- choose **Edit**
- edit method settings as desired
- choose **Save**

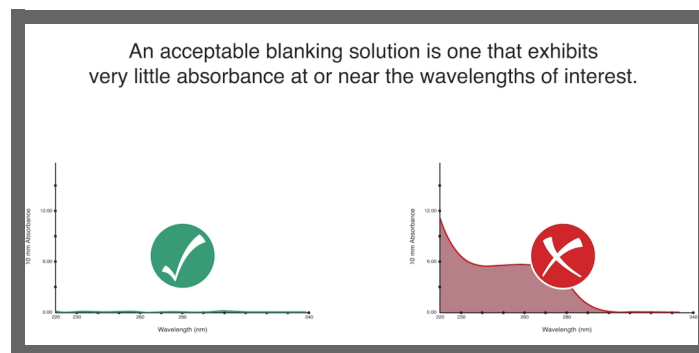
## Delete custom method

- from Manage Custom Methods box, select custom method
- choose **Delete**
- after confirmation message, choose **Yes**

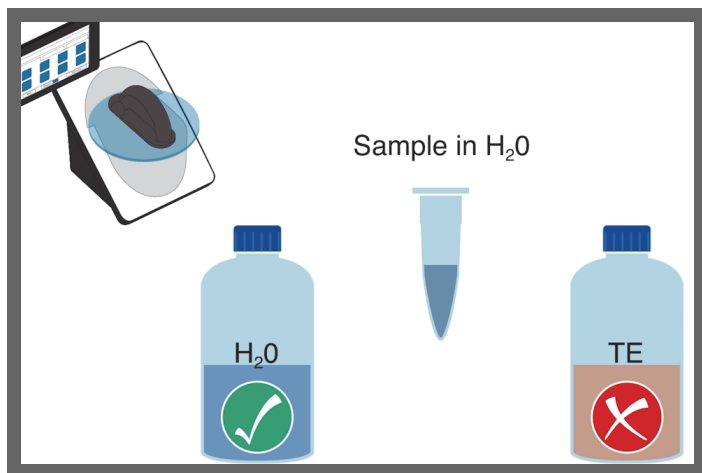
## Multimedia



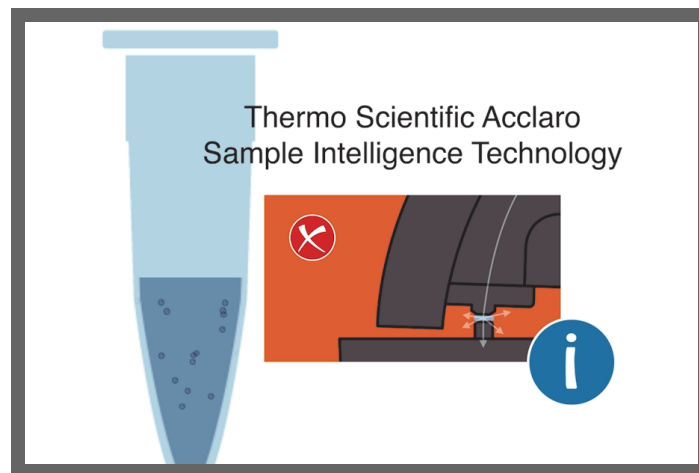
What is a Purity Ratio?



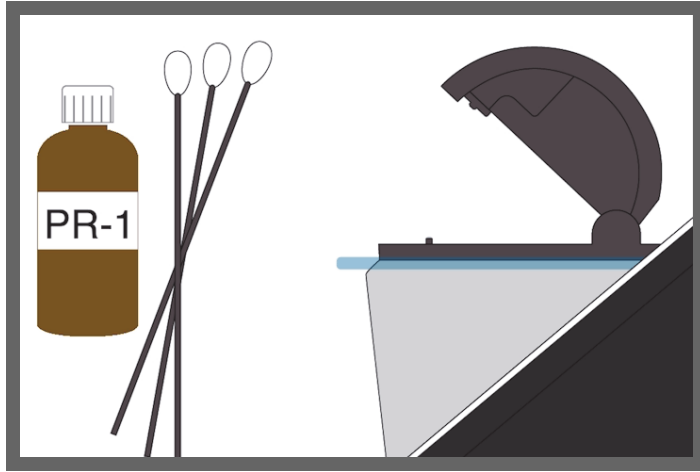
Evaluating a Blanking Solution for Suitability



What is a Blank?



Effects of Bubbles in Samples



### Pedestal Cleaning and Reconditioning

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## Maintaining Your Instrument



**Maintenance Schedule**



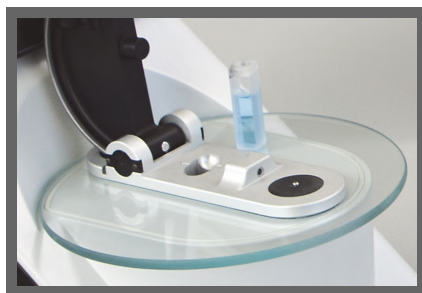
**Clean Touchscreen**



**Maintain Pedestals**



**Decontaminate**



**Cuvette System**



**Instrument Diagnostics**

## Maintenance Schedule

### Daily Maintenance

- Clean pedestals with deionized water

### Periodic Maintenance

- Clean touchscreen
- Clean pedestals with 0.5M HCl
- Recondition pedestals



### Every 6 Months

- Recondition pedestals
- Run [Intensity Check](#)
- Run [Performance Verification](#)
- Run [Pedestal Image Check](#)

If you are experiencing an issue with your system, refer to the troubleshooting information. If the issue persists, contact us. If you are outside the U.S.A. and Canada, please contact your local distributor.

If your instrument requires maintenance or repair, [contact us](#) or your local distributor.



## Cleaning the Touchscreen

**NOTICE** To avoid causing permanent damage to the touchscreen, do not:

- clean the touchscreen with abrasive material such as paper towel
- apply excessive pressure
- spray liquid directly onto the touchscreen
- apply lubricant to the touchscreen slide mechanism

### To clean the touchscreen

Gently wipe the touchscreen with a soft, lint-free cloth such as microfiber.

If necessary, use a cleaner intended for glass LCD displays and follow the manufacturer's recommendations.

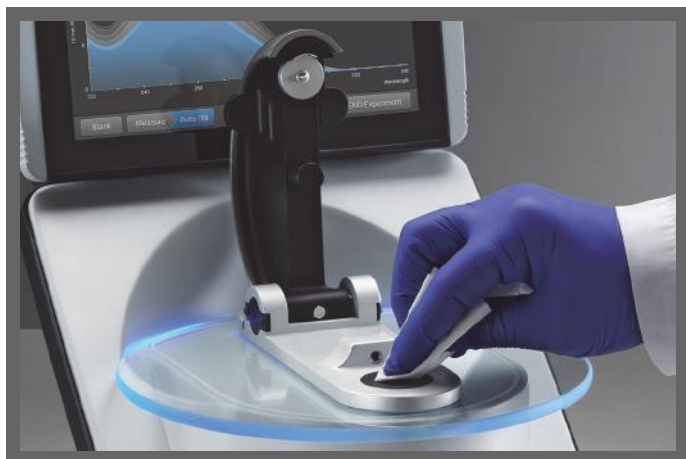
### Related Topics

- [Clean Pedestals](#)
- [Recondition Pedestals](#)
- [Decontaminate Instrument](#)



# Maintaining the Pedestals

The pedestals require periodic maintenance to maintain measurement integrity. Time lines and procedures for cleaning and reconditioning the pedestals are provided below.



Clean Pedestals



Recondition Pedestals

## Cleaning the Pedestals

To avoid carryover and cross contamination, clean the pedestals before the first blank or sample measurement and at the end of each measurement. Additional cleaning (see below) or [reconditioning](#) may be required for periodic maintenance.

### NOTICE

- Do not use hydrofluoric acid (HF) on the pedestals. Fluoride ions will permanently damage the quartz fiber optic cables.
- To prevent damage from spills, keep containers of liquids away from the instrument.
- Do not use a squirt or spray bottle on or near the instrument as liquids will flow into the instrument and may cause permanent damage.
- Do not attempt to remove the diaphragm around the lower pedestal as it is permanently affixed to the instrument.
- Do not allow HCl, alcohol, bleach, acetone or any other solvent to remain on the diaphragm for more than one minute or it may loosen the seals. If the diaphragm becomes loose, [contact us](#).

**Note** Solutions containing detergent or isopropyl alcohol may uncondition the pedestals. If these are required for sample analyses, follow immediately with 3–5  $\mu\text{L}$  DI  $\text{H}_2\text{O}$ .

## 4 Maintaining Your Instrument

### Maintaining the Pedestals

#### Supplies needed

- lint-free laboratory wipes
- deionized water (DI H<sub>2</sub>O)
- for thorough cleaning: [PR-1 kit](#) or 0.5M HCl

#### To clean the pedestals between measurements

Lift the instrument arm and clean the upper and lower pedestal with a new laboratory wipe.

#### To clean the pedestals between users

1. Lift the arm and clean both pedestals with a new laboratory wipe.
2. Pipette 3–5  $\mu\text{L}$  DI H<sub>2</sub>O onto the lower pedestal.
3. Lower the arm and wait 2–3 minutes.
4. Lift the arm and clean both pedestals with a new wipe.

**Tip:** When thorough cleaning is required (for example, to remove dried sample left on the pedestals), substitute 0.5M HCl for the DI H<sub>2</sub>O in the procedure above and follow with 3–5  $\mu\text{L}$  DI H<sub>2</sub>O. You can also [recondition the pedestals](#) using PR-1 compound.



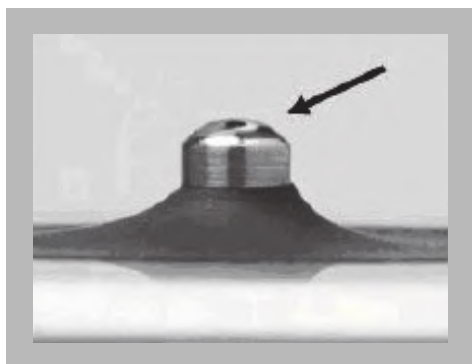
## Related Topics

- [Recondition Pedestals](#)
- [Clean Touchscreen](#)
- [Decontaminate Instrument](#)

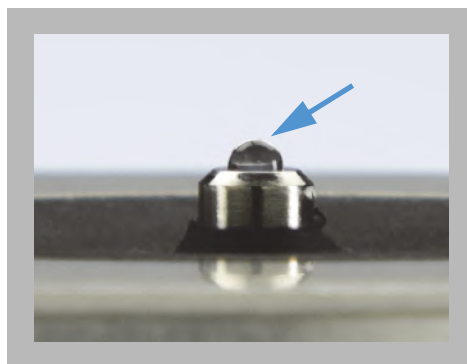
## Reconditioning the Pedestals

The pedestal surfaces may lose their “conditioned” properties over time, especially after measurements with isopropyl alcohol or solutions that contain surfactants or detergents such as the [Bradford reagent](#). An unconditioned pedestal causes droplets on the lower pedestal to “flatten out,” preventing proper formation of the liquid column when the arm is lowered. The resulting spectrum may look “rough” or “jagged.”

If samples flatten out on the pedestal (rather than “beading up” or forming a rounded droplet) or the liquid column breaks during a measurement, recondition the pedestals.



**Unconditioned pedestal**  
(droplet flattens out)



**Properly conditioned pedestal**  
(droplet beads up)

## Supplies needed

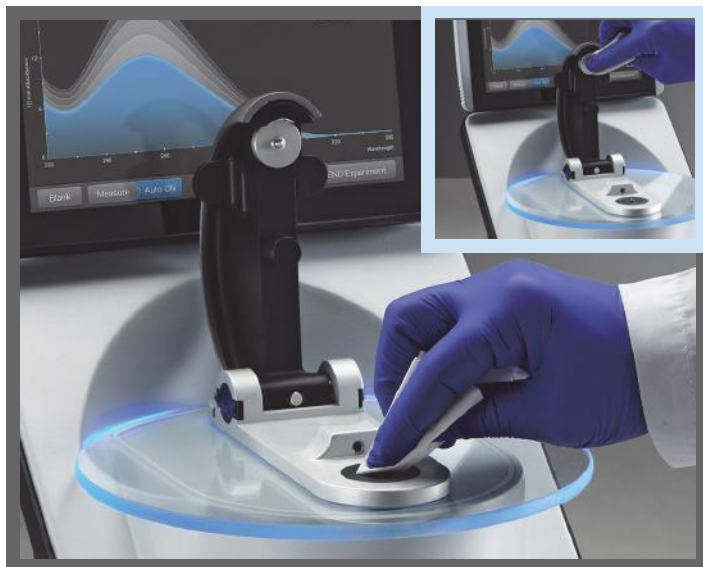
- lint-free laboratory wipes
- [PR-1 pedestal reconditioning kit](#) (available from us or a local distributor)
- calibrated precision pipettor (0-2  $\mu\text{L}$ )
- canned air

## To recondition the pedestals



1. Open the container of PR-1 compound and use the provided applicator to remove a pin-head sized amount of the compound.
2. Apply a thin, even layer of reconditioning compound to the surface of the upper and lower pedestal.

Wait 30 seconds for the PR-1 compound to dry.



3. Fold a clean laboratory wipe into quarters and use it to vigorously buff the surface of each pedestal.

**Notice:** Support the instrument arm with one hand while you buff the upper pedestal to avoid damaging the arm.

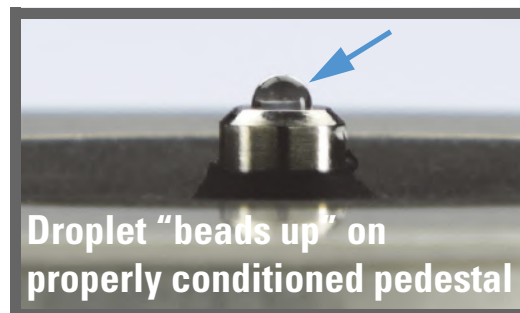
**Tip:** Black residue on the wipe is normal.

4. Repeat step 3 with a new folded wipe until all residue is removed and the pedestals buff clean.
5. Use canned air to remove any paper residue from the pedestals.



6. Pipette 1  $\mu\text{L}$  DI  $\text{H}_2\text{O}$  onto the lower pedestal.

The DI  $\text{H}_2\text{O}$  should “bead up” or form a rounded droplet.



**Tip** The PR-1 pedestal reconditioning compound is the easiest way to recondition the pedestals. If you don't have a PR-1 kit, follow these steps:

1. Lift the instrument arm and pipette 3  $\mu$ L 0.5M HCl onto the lower pedestal.
2. Lower the arm and wait 2–3 minutes.
3. Lift the arm and clean both pedestals with a new laboratory wipe.
4. Pipette 3  $\mu$ L DI H<sub>2</sub>O onto the lower pedestal.
5. Lower the arm and wait 2–3 minutes.
6. Lift the arm and clean both pedestals with a new wipe.

**NOTICE:** Support the instrument arm with one hand while you buff the upper pedestal to avoid damaging the arm.

7. Fold a clean laboratory wipe into quarters and use it to vigorously buff the surface of each pedestal at least 50 times.
8. Use canned air to remove any paper residue from the pedestals.

### Related Topics

- [PR-1 Pedestal Reconditioning Kit](#)
- [Clean Pedestals](#)
- [Clean Touchscreen](#)
- [Decontaminate Instrument](#)

## Decontaminating the Instrument

Decontaminate the instrument after measurements with samples that contain [hazardous materials](#) and before returning the instrument to us for maintenance or repair.

**Note** If your instrument requires maintenance or repair, [contact us](#) or your local distributor.

## 4 Maintaining Your Instrument

### Decontaminating the Instrument

#### NOTICE

- Do not use hydrofluoric acid (HF) on the pedestals. Fluoride ions will permanently damage the quartz fiber optic cables.
- To prevent damage from spills, keep containers of liquids away from the instrument.
- Do not use a squirt or spray bottle on or near the instrument as liquids will flow into the instrument and may cause permanent damage.
- Do not attempt to remove the diaphragm around the lower pedestal as it is permanently affixed to the instrument.
- Do not allow HCl, alcohol, bleach, acetone or any other solvent to remain on the diaphragm for more than one minute or it may loosen the seals. If the diaphragm becomes loose, [contact us](#).

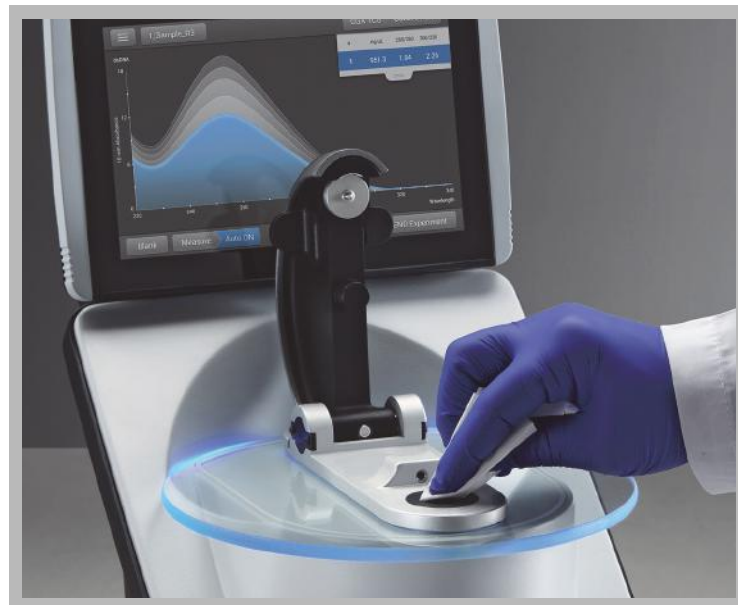
#### Supplies needed

- lint-free laboratory wipes
- deionized water (DI H<sub>2</sub>O)
- 0.5% sodium hypochlorite solution (1:10 dilution of commercial bleach, freshly prepared)
- pipettor



## To decontaminate the pedestals

1. Lift the instrument arm and clean the upper and lower pedestal with a new laboratory wipe.
2. Pipette 2–3  $\mu\text{L}$  diluted bleach solution (see [Supplies needed](#)) onto the lower pedestal.
3. Lower the arm and wait 2–3 minutes.
4. Lift the arm and clean both pedestals with a new wipe.
5. Pipette 3–5  $\mu\text{L}$  DI  $\text{H}_2\text{O}$  onto the lower pedestal.
6. Lower the arm and wait 2–3 minutes.
7. Lift the arm and clean both pedestals with a new wipe.



## To decontaminate the instrument surfaces

1. Dampen a clean, soft cloth or laboratory wipe with the diluted bleach solution (see [Supplies needed](#)) and use it to gently wipe the outside surfaces of the instrument.
2. Use a clean cloth or wipe dampened with DI  $\text{H}_2\text{O}$  to remove the bleach solution.



### Related Topics

- [Clean Pedestals](#)
- [Recondition Pedestals](#)
- [Clean Touchscreen](#)

## 4 Maintaining Your Instrument

### Maintaining the Cuvette Sampling System

## Maintaining the Cuvette Sampling System

The cuvette sampling system is included only with the NanoDrop One<sup>C</sup> model instrument. For information about compatible cuvettes, see [Measuring a Sample using a Cuvette](#).

**Note** Clean and dry cuvettes after each measurement. Use cuvettes that are free of scratches and avoid fingerprints which may affect results.

**NOTICE** Do not use a squirt or spray bottle on or near the instrument as liquids will flow into the instrument and may cause permanent damage.

### To maintain the cuvette sampling system

- Keep the instrument arm closed when the instrument is not in use.
- Use canned air to remove any dust from the cuvette holder.
- Clean up any spills inside the cuvette holder with a new laboratory wipe.

To clean and maintain cuvettes, follow the recommendations of the cuvette manufacturer.

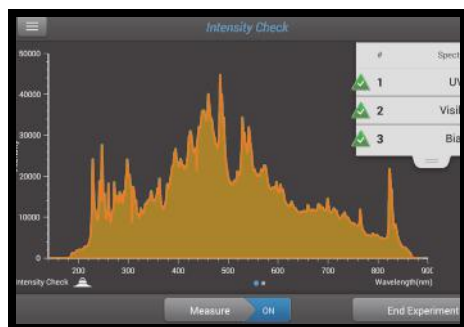


### Related Topics

- [Measure Cuvette Sample](#)
- [Best Practices for Cuvette Measurements](#)

## Instrument Diagnostics

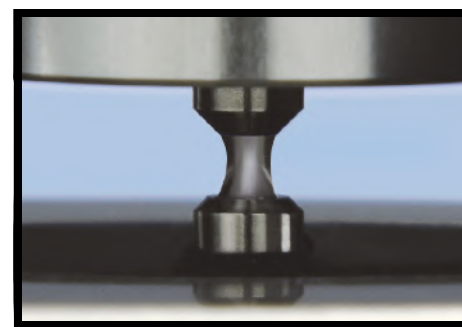
Every 6 months, run the following performance and quality checks to verify instrument operation.



Intensity Check



Performance Verification



Pedestal Image Check


### Intensity Check

Run Intensity Check every 6 months to verify operation of the instrument's internal components. The test measures the intensity of light from the xenon source through the instrument to verify that throughput, wavelength accuracy, and bias are within specifications. If the instrument has a cuvette holder (NanoDrop One<sup>C</sup> model only), the test is automatically repeated using the cuvette optical path.

#### Supplies needed

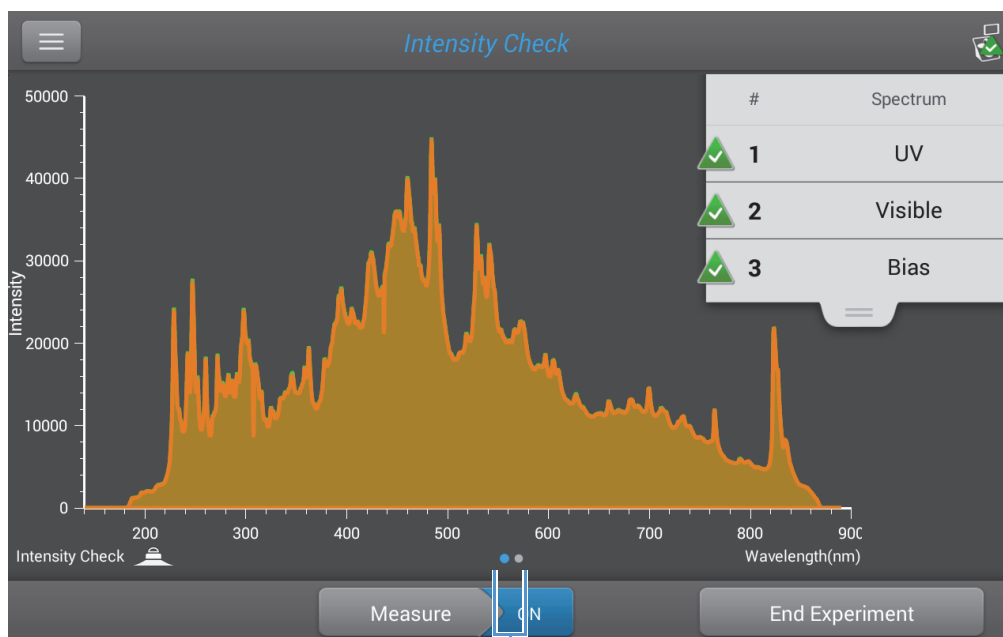
- lint-free laboratory wipes

### To run intensity check

1. Lift the instrument arm and clean the upper and lower pedestal with a new laboratory wipe.
2. For the NanoDrop One<sup>C</sup> model instrument, remove any cuvette from the cuvette holder.
3. Lower the arm.
4. From the instrument home screen, tap  (Diagnostics) and then tap **Intensity Check**.

5. Tap **Measure** and wait for the measurements to complete.

Here is an example of a typical intensity check result screen.



**Swipe screen left** to view detailed results

6. To rerun the intensity check, tap **Measure**.
7. When finished, tap **End Experiment**.

After the test is completed, the results are available from the Data Viewer (see example below). See [Manage identifiers on the instrument](#) for details.

The screenshot shows the 'Data Viewer' interface. At the top, it says '2 experiments found'. Below, there is a list of experiments:

Date	Measurement Count
Thursday, August 20, 2015	1 experiment found
Thursday, August 13, 2015	1 experiment found
Intensity Check_08/13/2015 14:24:48	1 measurement

## To interpret intensity check results

If one of these indicators:

- UV
- Visible
- Bias

has an adjacent yellow triangle instead of the green check marks shown above, [clean the pedestals with deionized water](#) and then repeat the Intensity Check.

If a yellow triangle appears next to the Bias indicator, make sure the room is within the temperature specifications for the instrument.

If the Intensity Check fails again, [contact us](#).

### Related Topics

- [Performance Verification](#)
- [Pedestal Image Check](#)

## Performance Verification

Run Performance Verification every 6 months to confirm pathlength accuracy is within specifications.

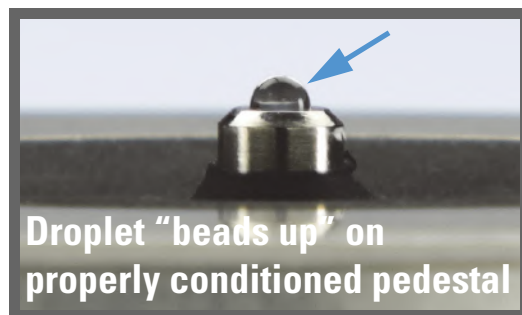
### Supplies needed

- lint-free laboratory wipes
- deionized water (DI H<sub>2</sub>O)
- calibrated precision pipettor (0–2 µL)
- [PV-1 performance verification solution](#) (liquid photometric standard available only from us or a local distributor)
- laboratory gloves


**Note** The PV-1 solution comes in a single-use ampoule. Before you open the ampoule, shake it vigorously and then allow the liquid to collect in the bottom portion of the ampoule. After the ampoule is opened, its contents must be used within one hour. Pipette directly from the ampoule; do not transfer the solution.

## Before you begin

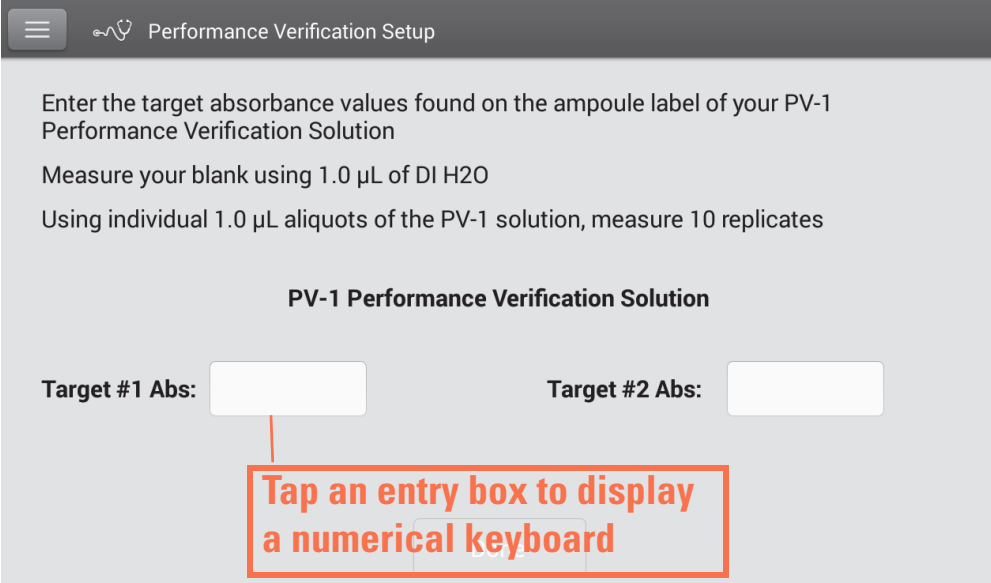
First make sure the pedestals are properly conditioned. To test pedestal conditioning, clean the pedestals with a new laboratory wipe, then pipette 1  $\mu\text{L}$  DI  $\text{H}_2\text{O}$  onto the lower pedestal. The droplet should “bead up” as shown below. If it does not, [recondition both pedestals](#).




## To run performance verification

1. From the instrument home screen, tap  (Diagnostics) and then tap **Performance Verification**.

A message asks for target absorbance values.



☰  Performance Verification Setup

Enter the target absorbance values found on the ampoule label of your PV-1 Performance Verification Solution

Measure your blank using 1.0  $\mu\text{L}$  of DI  $\text{H}_2\text{O}$

Using individual 1.0  $\mu\text{L}$  aliquots of the PV-1 solution, measure 10 replicates

**PV-1 Performance Verification Solution**

Target #1 Abs:  Target #2 Abs:

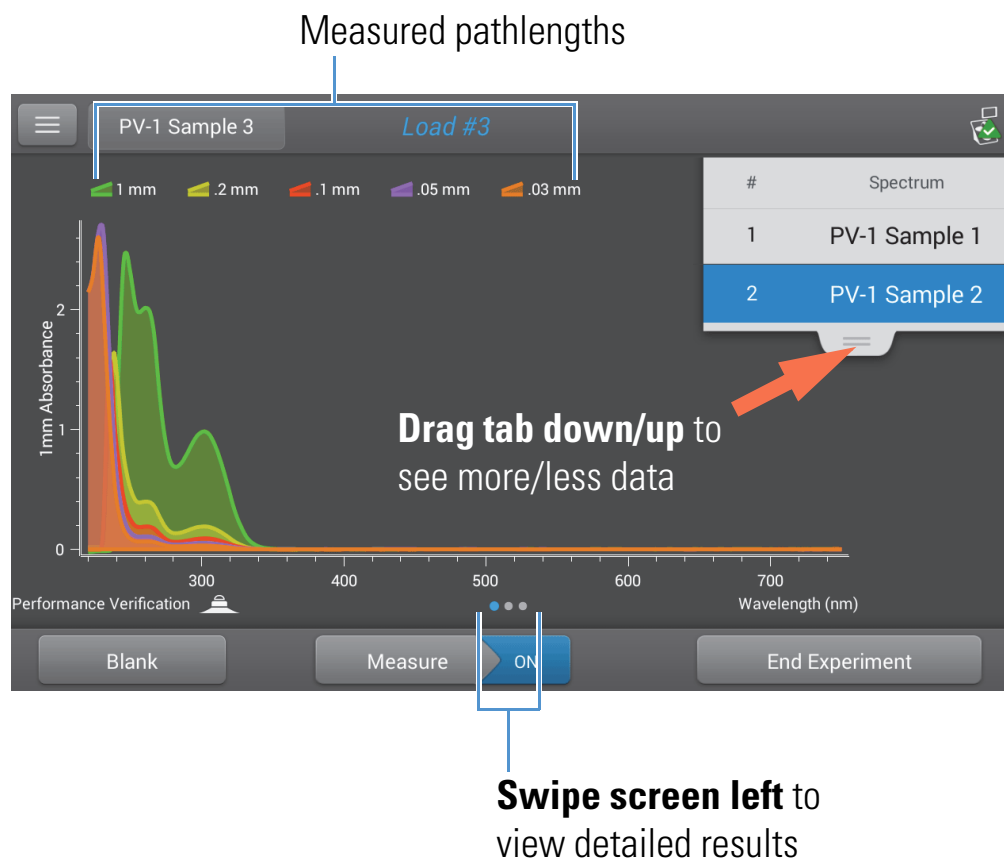
Tap an entry box to display a numerical keyboard

2. Enter each lot-specific target absorbance value from the label on the PV-1 ampoule in its associated entry box and then tap **Done**.
3. Lift the instrument arm and clean the upper and lower pedestal with a new laboratory wipe.
4. Pipette 1  $\mu\text{L}$  DI  $\text{H}_2\text{O}$  onto the lower pedestal, lower the arm and tap **Blank**.
5. Lift the arm and clean both pedestals with a new wipe.

**Note** Vigorously shake the ampoule of PV-1 solution, allow the liquid to collect in the bottom portion of the ampoule and then follow standard practices to open it.

6. Pipette 1  $\mu\text{L}$  PV-1 solution onto the lower pedestal and start the sample measurement:
  - If **Auto-Measure** is On, lower arm
  - If Auto-Measure is off, lower arm and tap **Measure**

After the measurement, the software displays the results. Here is an example of the performance verification result screen.



7. Repeat step 6 to measure the PV-1 solution nine more times using a new 1  $\mu\text{L}$  aliquot for each measurement and cleaning both pedestals after each measurement.

After each measurement, a new sample result is added to the display. Swipe the screen left to see a summary of the 10 sample results.



Swipe left again to see additional measurement details, along with the overall test result.

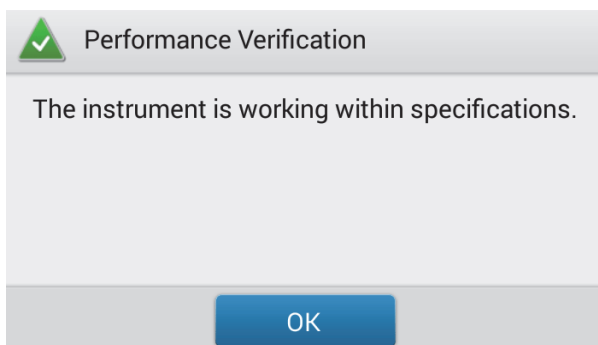
	1 mm	0.2 mm	0.1 mm	0.05 mm	0.03 mm
Target Absorbance	0.96740	0.19348	0.09674	0.09935	0.05961
Current Absorbance	0.983	0.194	0.092	0.113	0.071
Average Absorbance	0.982	0.194	0.092	0.109	0.068
% Error	1.5	0.1	5.3	9.8	13.9
Standard Deviation	0.004	0.002	0.001	0.002	0.002
Measurement Wavelength (nm)	302	302	302	260	260
Correction Wavelength (nm)	600	600	600	600	600
Integration Time (ms)	40	40	40	40	40

Pass: The instrument is working within specifications.

Performance test result



After the tenth measurement, a message indicates whether the instrument passed or failed performance verification:



8. If the instrument failed, immediately repeat step 6 using ten 2  $\mu\text{L}$  aliquots of the PV-1 solution.
9. When finished, tap **End Experiment** and [clean the pedestals with 3–5  \$\mu\text{L}\$  DI  \$\text{H}\_2\text{O}\$](#) .

After the test is completed, the results are available from the Data Viewer (see example below). See [Manage identifiers on the instrument](#) for details.



## To interpret performance verification results

If your instrument failed performance verification and you repeated ten measurements using 2  $\mu\text{L}$  aliquots, [contact us](#).

### Related Topics

- [PV-1 Performance Verification Solution](#)
- [Intensity Check](#)
- [Pedestal Image Check](#)


### Pedestal Image Check

Run the Pedestal Image Check periodically to verify the instrument's column sensor which monitors for possible errors such as an empty column or bubbles in a sample. The Pedestal Image Check can be used for routine quality control purposes. It also provides important diagnostic information if a detection system component fails.

#### Supplies needed

- lint-free laboratory wipes

#### To run pedestal image check

1. Lift the instrument arm and clean the upper and lower pedestal with a new laboratory wipe.
2. Lower the arm.
3. From the instrument home screen, tap  (Diagnostics) and then tap **Pedestal Image Check**.
4. Tap **Measure**.

The instrument runs a series of tests to check pedestal position and image quality. After the measurements are completed, the results are displayed. A green check mark indicates the instrument passed the Pedestal Image Check.

5. When finished, tap **End Experiment**.

#### To interpret pedestal image check results

If the Pedestal Image Check displays a yellow triangle instead of the green check mark, follow the on-screen instructions to fix any possible problems. Then rerun the Pedestal Image Check. If the instrument fails again, [contact us](#).

#### Related Topics

- [Performance Verification](#)
- [Intensity Check](#)

## Safety and Operating Precautions



**Safety Information**



**Operating Precautions**



**NOTICE** Be sure that all persons operating this system read the safety manual first.

# Operating Precautions



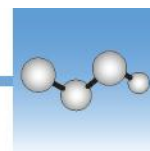
**CAUTION** Do not remove the instrument cover. Removing the cover exposes the operator to sharp edges and delicate fiber optic cables. The instrument warranty is void if the cover has been removed.

NanoDrop One spectrophotometers are designed to operate indoors in an environment that meets our specifications. For details, see the site preparation guide for your instrument.

Follow these precautions to avoid damaging your NanoDrop spectrophotometer during use:

- Use a grounded power cord appropriate for your electrical service. If the supplied power cord is incompatible or if it becomes damaged, [contact us](#).
- Do not remove the instrument cover.
- The plate below the arm assembly is made of heat tempered glass. The LCD display uses heat treated, chemical tempered glass. Both are rugged and difficult to break. However, should either the plate or display become cracked or broken, contact us for replacement.
- Use solvents that are compatible with the instrument (see [Hazardous Materials](#))
- Do not use hydrofluoric acid (HF) on the pedestals. Fluoride ions will permanently damage the quartz fiber optic cables.
- To prevent damage from spills, keep containers of liquids away from the instrument.
- Do not use a squirt or spray bottle on or near the instrument as liquids will flow into the instrument and may cause permanent damage.
- Do not attempt to remove the diaphragm around the lower pedestal as it is permanently affixed to the instrument.
- Do not allow HCl, alcohol, bleach, acetone or any other solvent to remain on the diaphragm for more than one minute or it may loosen the seals. If the diaphragm becomes loose, [contact us](#).





## Safety Information

Before operating a NanoDrop One instrument, please read the safety information and follow its recommendations for the system.

### Safety and Special Notices

In many cases, safety information is displayed on the instrument itself. The symbol indicates that there is additional safety information in the documentation and failure to heed the safety precautions could result in injury.



**WARNING** Indicates a hazardous situation which, if not avoided, could result in death or serious injury.



















**CAUTION** Indicates a hazardous situation which, if not avoided, could result in minor or moderate injury.

**NOTICE** Follow instructions with this label to avoid damaging the system hardware or losing data.

**Note** Contains helpful supplementary information.

The following table lists some of the safety symbols and their indications that may appear in the user documentation.

Symbols	Indication
	This is a mandatory action symbol. It is used to indicate that an action shall be taken to avoid a hazard.
	This is a prohibition symbol. The graphic in this symbol is used to alert the user to actions that shall not be taken or shall be stopped.
	This is the general warning sign. Failure to heed the safety precautions could result in personal injury.
	<b>Avoid shock hazard.</b> If you see either of these symbols, there is a risk of electrical shock in the vicinity. Only qualified persons shall perform the related procedures.
	<b>Avoid fire hazard.</b> Do not test flammable or explosive samples. Read and follow the associated instructions carefully.
	<b>Avoid eye injury.</b> If you see these symbols, there is a risk of exposure to ultraviolet light, which can harm your eyes if safety glasses are not worn.
	<b>Avoid Biohazard.</b> This icon informs of a biological hazard in the area. Read and follow the associated instructions carefully.
	<b>Avoid chemical burns.</b> This symbol alerts you to possible skin irritation. Wear gloves when handling toxic, carcinogenic, mutagenic, or corrosive or irritant chemicals. Use approved containers and proper procedures to dispose of waste.

Symbol	Description
	Alternating current
	Earth terminal or ground
	Direct current
	Protective conductor terminal
	Frame or chassis terminal
	Fuse
	Power on
	Power off

## When the System Arrives



**WARNING** Avoid personal injury. If this equipment is used in a manner not specified in the accompanying documentation, the protection provided by the equipment may be impaired.



**CAUTION** Avoid personal injury. Perform *only* those procedures described in the documentation. If there are other problems, contact us. Any other service must be performed by trained personnel.



**CAUTION** Avoid shock hazard. Do not remove the cover of the instrument. All service to the instrument must be performed by trained personnel.

When the instrument arrives, check the exterior of the shipping box for signs of damage. If damage is apparent, contact us or your local distributor for instructions.

- Move the shipping box to the installation location at least 24 hours before installation.

### NOTICE

- Inside the shipping box, the instrument is sealed in a plastic bag to keep the unit dry.
- Allow 24 hours for the instrument to reach room temperature before opening the bag. If the bag is opened before the instrument reaches room temperature, moisture could condense on the optical components and cause permanent damage.

- Keep the instrument upright at all times.

The warranty will not cover:

- Damage due to improper moving techniques.
- Damage due to removing the sealed plastic bag before the instrument has come to room temperature.

**Note** It is important to have all system utilities installed before the instrument arrives. Utility installations must comply with all local building and safety codes.

## Lifting or Moving the Instrument

To avoid risk of injury, use proper lifting techniques when lifting or moving the instrument or other system components.

## Electrical Requirements and Safety

Power supplied to the system must be from dedicated, uninterrupted sources. Power must be free of voltage dropouts, transient spikes, frequency shifts, and other line disturbances that impair reliable performance.

If you suspect power quality problems at your site, or if your system will be installed in a heavy industrial environment, we recommend a power quality audit before installation. Contact us or your local electrical authority for more information.



### **CAUTION** Avoid shock hazard.

- Only a qualified person using the appropriate measuring device shall check the line voltage, current and frequency.
- Only our trained and certified service representatives shall attempt to service a component that carries this symbol.
- If a protective cover on a system component appears damaged, turn off the system and secure it against any unintended operation. Always examine the protective cover for transport stresses after shipping.
- Even after this instrument has been disconnected from all voltage sources, capacitors may remain charged for up to 30 seconds and can cause an electrical shock.
- Do not allow liquid to run over or into any surface where it may gain entry into the instrument.
- Do not attempt to remove the cover of the instrument.

### **Grounding**



**CAUTION** Avoid shock hazard. Each wall outlet used must be equipped with a ground. The ground must be a noncurrent-carrying wire connected to earth ground at the main distribution box.



## Power Cords

Be sure to use an appropriate grounded power cord for your electrical service. If the power cord received is not appropriate for the electrical system in your location, or if the power cord becomes damaged, contact us.

### Power Line Conditioning Accessories

A UPS reduces the probability of a system shutdown if power is lost elsewhere in the building. Power line conditioners (which ensure that your service is free from sags, surges or other line disturbances) also are available in the U.S.A. from us for 120 volt operation. Line conditioners for 220 volt operation can be purchased locally. Contact technical support for information about power conditioners and UPS.

### Electrical Service Specifications

The following table lists the specifications for electrical service. Contact our service representative in your area if you have questions about the requirements.

Requirements	Specifications
Input current	5.0 A (max.)
Input voltage	100-240 VAC
Line frequency	50-60 Hz
Line disturbances	Sags, surges or other line disturbances must not exceed 10% of input voltage (even for a half cycle).
Noise	< 2 V (common mode) < 20 V (normal mode)

### Power Consumption

Generally, 50% more power should be available than the entire system (including accessories) typically uses. Maximum power consumption and heat dissipation specifications for the spectrometer and accessories are shown below. The values are approximate.

Item	Power Consumption	Max. Heat Dissipation
instrument	60 W	205 Btu/hr

## Fire Safety and Burn Hazards

**NOTICE** Do not position the instrument so that it is difficult to operate the power switch or access the power supply and power cord.

To avoid a burn injury and the risk of fire or explosion:

- Use caution when testing flammable or explosive samples (see the “Hazardous Materials” section)
- Never block any of the vents on the instrument or its power supply
- Only use exact replacement power supplies from us

## Optical Safety

This instrument was designed with a protective housing to prevent user exposure to ultraviolet light.



**WARNING** Avoid personal injury. Never look at the lamp while illuminated.

## Hazardous Materials

Many standard spectroscopy methods are based on the use of solvents. Others involve corrosive samples or pressurized samples in a gaseous state.

### Volatile Solvents and Flammable Samples



**CAUTION** Avoid personal injury. Do not leave solvents or flammable samples near the instrument. Be sure that the workspace is properly ventilated.

### Compatible Solvents

Most solvents typically used in life science laboratories are compatible with the fiber optic pedestals of all NanoDrop spectrophotometers. However, the high vapor pressure properties of some solvents may not be conducive to small volume measurements when using the pedestal for measurements on any of the NanoDrop instruments. If you are measuring samples with high vapor pressures, use an instrument with provision for measuring samples in cuvettes.

The following solvents are compatible for use on the **pedestals** of all NanoDrop instruments.

**NOTICE** Spillage of these solvents on surfaces other than the pedestals may damage the instrument.

- methanol
- isopropanol
- ether
- DMSO
- THF
- benzene
- dilute HCl
- ethanol
- butanol
- chloroform
- DMF
- toluene
- sodium hydroxide
- dilute HNO<sub>3</sub>
- n-propanol
- acetone
- carbon tetrachloride
- acetonitrile
- hexane
- sodium hypochlorite (bleach)
- dilute acetic acid

It is recommended that all corrosive solvents be wiped from the pedestal immediately upon completion of a measurement. It is also recommended that the user end a series of measurements with a dH<sub>2</sub>O sample to ensure that solvents are not inadvertently left on the pedestal.

The diaphragm around the pedestal of the NanoDrop is permanently affixed to the instrument. Do not attempt to remove the diaphragm or break the seal. Avoid prolonged exposure of the diaphragm to HCl, alcohol, bleach, acetone or other solvents as the adhesive securing the seal may be affected. If the seal comes loose please contact us.

**NOTICE** All forms of Hydrofluoric Acid (HF) are incompatible as the fluoride ion will etch the fiber optic cable.

### **Biohazard or Radioactive Materials and Infectious Agents**

Biological samples such as tissues, body fluids, infectious agents, and blood of humans and other animals have the potential to transmit infectious diseases. Wear appropriate protective equipment. Individuals should be trained according to applicable regulatory and organization requirements before working with potentially infectious materials. Follow your organization's Biosafety Program protocols for working with and/or handling potentially infectious materials.



**WARNING** Reduce the risk associated with potentially infectious samples:

- Do not spill samples on any of the instrument components.
- If spill occurs, disinfect the external surfaces immediately following your laboratory protocols.

Instruments, accessories, components or other associated materials should not be disposed of and may not be returned to us or other accessory manufacturers if they are contaminated with biohazard or radioactive materials, infectious agents, or any other materials and/or conditions that could constitute a health or injury hazard to employees. Contact us if you have questions about decontamination requirements.

## About this Help System

### Conventions Used

Safety precautions and other important information use the following format:



**CAUTION** Indicates a hazardous situation which, if not avoided, could result in minor or moderate injury.

**NOTICE** Follow instructions with this label to avoid damaging the system hardware or losing data.

**Note** Contains helpful supplementary information.

**Tip** Provides helpful information that can make a task easier.

### Trademark Information

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## Contact Technical Support

### For U.S./Canada Technical Support, please contact:

Thermo Fisher Scientific  
3411 Silverside Road  
Bancroft Building, Suite 100  
Wilmington, DE 19810 U.S.A.

**Telephone:** 302 479 7707  
**Toll Free:** 1 877 724 7690 (U.S. & Canada only)  
**Fax:** 302 792 7155  
**E-mail:** [nanodrop@thermofisher.com](mailto:nanodrop@thermofisher.com)  
**Website:** [www.thermoscientific.com/nanodrop](http://www.thermoscientific.com/nanodrop)



### For International Support, please contact:

Contact your local distributor. For contact information go to:

**<http://www.nanodrop.com/Order.aspx>**

If you are experiencing an issue with your system, refer to the troubleshooting information. If the issue persists, contact us. If you are outside the U.S.A. and Canada, please contact your local distributor.

If your instrument requires maintenance or repair, contact us or your local distributor.

