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NanoDrop 8000 Spectrophotometer

V2.2 User Manual

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1. Overview

Instrument Description

The Thermo Scientific NanoDrop 8000 Spectrophotometer is a full-spectrum (220-750nm) instrument that accurately measures up to 8 individual 1 ul samples in one measurement cycle. The software allows the user to measure samples using either the full 8-position mode or a convenient single sample mode.

The NanoDrop 8000 utilizes the same patented sample retention technology employed on all NanoDrop™ instruments. The surface retention system holds the sample in place eliminating the need for cumbersome cuvettes and other sample containment devices. Clean-up is accomplished in seconds. In addition, the NanoDrop 8000 has the capability to measure highly concentrated samples without dilution (50X higher concentration than the samples measured by a standard cuvette spectrophotometer).

Applications

UV/VIS spectrophotometry is simple for samples as small as 1 ul using the NanoDrop 8000 Spectrophotometer. The small sample requirement and ease of use make the NanoDrop 8000 Spectrophotometer ideally suited for measuring:

- Nucleic acid concentration and purity of nucleic acid samples up to 3700 ng/ul (dsDNA) without dilution
- Fluorescent dye labeling density of nucleic acid microarray samples
- Purified protein analysis (A280 nm) up to 100 mg/ml (BSA)
- Expanded spectrum measurement and quantitation of fluorescent dye labeled proteins, conjugates, and metalloproteins
- Bradford Assay analysis of protein
- BCA Assay analysis of protein
- Lowry Assay analysis of protein
- Pierce Protein 660 nm analysis
- Cell density measurements
- General UV-Vis spectrophotometry
- Custom methods

Operation

Up to eight 1 ul samples are pipetted onto the sample pedestal using a low volume multi-channel pipettor.

Each position is actually the end of a fiber optic cable (the receiving fibers). A second set of fiber optic cables (the source fibers) are brought into contact with the liquid samples causing the liquid to bridge the gaps between the fiber optic ends. The pathlengths are automatically controlled to 1mm and 0.2 mm paths. Readings are acquired through sequential measurement across the 8 positions. A pulsed xenon flash lamp provides the light source and a spectrometer utilizing a linear CCD array is used to analyze the light that passes through the samples. The instrument is controlled by PC based software, and the data is logged in an archive file on the PC.

The NanoDrop 8000 is designed only for indoor use under the following conditions:

- Temperature: 40-100° F (4.4 - 37.8° C)
- Humidity: 10-90%

Safety

The NanoDrop 8000 is supplied with a 12V power supply. Use only the power supply provided with the instrument. The unit also comes with a grounded power cord. Plug this cord into a properly grounded outlet. Use of the instrument in a manner not specified by the manufacturer may impair the protection provided by the supplied power cord and power supply.

The power supply can remain plugged into the NanoDrop 8000 while the instrument is not in use. When the instrument is plugged in but not in use, the power consumption is ~5 W and the flash lamp is not energized. The instrument does not utilize a power switch. It is recommended that the instrument not be positioned in a way that makes it difficult to unplug the power supply from the unit or the wall.

WEEE Compliance

This product is required to comply with the European Union's Waste Electrical & Electronic Equipment (WEEE) Directive 2002/96/EC. If compliance is required, the instrument is marked with the following symbol:

We have contracted with one or more recycling/disposal companies in each EU Member State, and this product should be disposed of or recycled through them. Further information regarding our compliance with these directives, the recyclers in your country, and information on our products which may assist the detection of substances subject to the RoHS Directive are available at www.thermo.com/WEEERoHS.

Patents

The sample retention technology used in the NanoDrop 8000 is covered under US patents 6,628,382 and 6,809,826. Other patents are pending.

2. Initial Set Up

Computer Requirements

The operating software will only run on an IBM compatible PC meeting the below criteria. No Mac versions of the software are currently available.

- Microsoft Windows 2000, XP, or Vista (32 bit) and Windows 7 (32 and 64 bit)
- Windows Vista has also been tested successfully with the software
- The operating software is not compatible with Windows NT, 95, 98 or ME
- 800 MHz or higher processor
- CD ROM drive
- 128 MB or more of RAM
- 100 MB of free hard disk space
- Open USB port (the instrument can only be connected via the USB port)
- Microsoft Excel or other spreadsheet program to manipulate archived data (optional)

Unless otherwise specified, all screen shots have been generated using the Windows XP operating software.

Software Installation

IMPORTANT - PLEASE READ BEFORE INSTALLING SOFTWARE!

Note 1: The system software must be loaded onto the PC before the USB cable is connected.

Note 2: Uninstall all previous versions of NanoDrop 8000 software using Add/Remove Programs BEFORE installing this version. Current saved User Preferences will be preserved during the uninstall process.

Note 3: Administrative privileges are required to install this software.

Note 4: All users of this software must have read and write access to the folder C:\NANODROP DATA\ and all of its subfolders.

When attaching the USB cable, please wait at least 30 seconds for the USB devices and internal drivers to be installed and recognized.

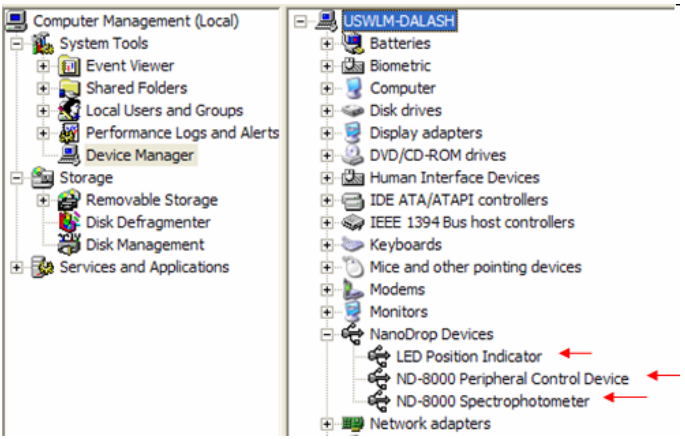
To properly install the operating software:

1. Close all programs and make sure that the USB cable is unplugged.

2. Insert the operating software CD in the CD drive of the PC. The software installation menu should appear automatically. If software menu does not appear, choose My Computer to view the contents of the CD. Double click on the file named **nd-8000…install.exe**.

3. After software installation, connect the USB cable to the instrument and the computer. The Found New Hardware Wizard should start.. Windows XP SP2 operating system will ask to allow it to search the internet for the proper software as shown - Select **No, not this time**. For other Windows operating systems, follow the prompts for automatic installation of the software.

4. Installation will require two cycles through the Found New Hardware Wizard, once for the NanoDrop 8000 Spectrophotometer and once for two devices internal to the instrument. For the NanoDrop 8000 to operate successfully a total of three USB devices need to install although only two cycles through the hardware wizard will be observed. To confirm installation, view the Windows Device Manager as shown below:



The NanoDrop 8000 Spectrophotometer should now be ready for operation. If the software does not start properly, refer to the Troubleshooting section for possible solutions.

Configuring the System Font
The software is designed to look best with the MS Sans Serif font, 8 point. To check that the system font is set to the proper selection:

1. Open the **Display Properties** by right clicking on the desktop and select Properties ÆAppearance. (Additional step for Windows XP: click on the **Advanced** button).
2. From item list select **icon**.
3. Select the **MS Sans Serif (western)** font and select **8 point** size.
4. Click **OK**.

Choosing an alternative font may result in some text being truncated in the operating software window.

Software Upgrades
Periodic upgrades are made to the operating software and are available for download. See our website for the latest available software version.

USB Flash Drive Port
Any standard PC USB flash drive may be used for exporting data. Note: When using the User Preferences Module to set-up a default automatic Export Report destination, keep in mind that the flash drive may not always be assigned the same removable device designation.

Cable Connections
To make measurements with the instrument, connect the USB cable to instrument and the PC, plug in the 12V power supply and connect to the power input at the back of the instrument.

Note: The NanoDrop 8000 Spectrophotometer is supplied with a 12V power supply. Use only the power supply provided with the kit. The unit also comes with a grounded power cord. Plug this cord ONLY into a properly grounded outlet. Use of the instrument in a manner not specified by the manufacturer may impair the protection provided by the supplied power cord and power supply.

The power supply can remain plugged into the NanoDrop 8000 Spectrophotometer while the instrument is not in use. When the instrument is plugged in but not in use, the power consumption is ~3 W and the flashlamp is not energized. Also, the instrument does not utilize

a power switch or give a visual indication of the operability of the 12V power supply.

Note: It is recommended that the instrument not be positioned in a way that makes it difficult to unplug the power supply from the unit or the wall.

Registering Your Instrument

Please register your product! We periodically update our software and add new features free of charge. We would like to keep our user list updated so that we may alert you to these updates. All information supplied is completely confidential. You can register your instrument on our website.

Lock Attachment Port

The NanoDrop 8000 is equipped with a lock slot that enables use of a standard locking cable typically used to secure a laptop PC.

3. General Operation

Loading samples on position A when operating within the Single Sample Mode.

Loading samples when operating within the 8 Sample Mode.

1) Position the instrument at an angle for optimal use of the pipette guide. With the sampling arm open, position the pipettor using the guide as shown above. Dispense the samples onto the lower measurement pedestal ensuring the samples “touch-off” (contact) the lower pedestal. If the tips splay or skew when touching the pedestal surfaces, please use an alternative brand or style with a more rigid tip structure.

2) Carefully withdraw the pipettor before releasing the pipettor’s dispensing mechanism. Visually verify all samples are correctly transferred to their respective pedestals. If some samples have not transferred adequately, it is recommended that the aliquots be wiped away with a lab wipe and fresh aliquots of all eight samples be reloaded to ensure consistent loading/measurement timing between samples.

3) Close the sampling arm and initiate a spectral measurement using the operating software on the PC. The sample columns are automatically drawn between the upper and lower measurement pedestals and the spectral measurement made.

4. When the measurement is complete, open the sampling arm and wipe the samples from both the upper and lower pedestals using a soft laboratory wipe.

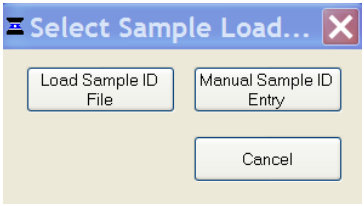
Escape Key (ESC)
The escape key is set to exit out of all screens. Hitting the **Escape** key twice will log the user out of an application module.

4. Sample ID Entry Options

Sample ID entry- Single Sample Mode

Selecting the Sample Loading Mode

After the instrument has completed the initialization process the following window will automatically display the options for plate setup:



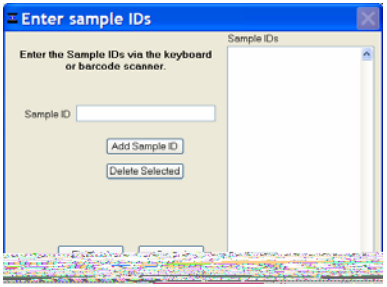
Load Sample ID File

The NanoDrop 8000 software enables the user to load a list of predefined sample IDs or names in either the 8 Sample or Single Sample mode.

The lists may be created in Excel or Notepad but all lists must be saved as a .txt file. It is recommended that the files be stored in the Plate Files folder at C:\ND-8000 Data. When creating a file, enter all sample names in a single file. Do not include a column header. A barcode reader can be used to scan in individual bar-coded sample names into the .txt file. The column format enables the user to predefine and load an unlimited number of sample IDs using just one file.

Manual Entry

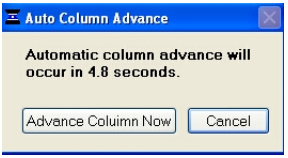
This option opens the Enter Sample IDs window enabling the user to manually enter samples IDs as prompted by the following screen:



Alternatively, a sample name may be entered directly into the sample ID box on the acquisition screen prior to each measurement.

- **Sample ID Required** - If selected, the sample ID field must be populated for each sample tested. Wells requiring a sample ID will appear red in the sample status color code (see below for description of this feature) and the following message will appear when the user attempts to make a sample measurement.

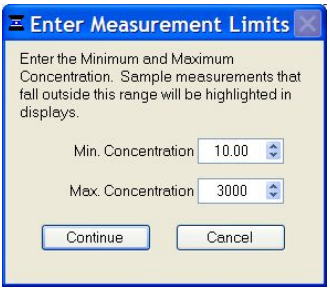
- **Auto Advance Columns** - If selected, there is a 5 second delay before the displayed spectra clear and the status code and Sample Position Illuminator (see below for description of these features) advance to the next column for sampling. This gives the user the option of canceling auto advance for that column. Auto advance will restart when the next column is measured. This feature can be set as a default function under the User Preferences application.



Note: All data is automatically archived and is accessible though the Data Viewer.

- **Prompt Close Data Viewer -** If selected, the user will be given the option of closing the Data Viewer when exiting the software module.

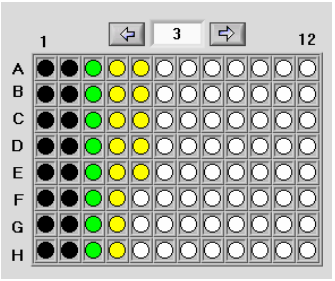
- **Measurement Limits** - Allows the user to set minimum and maximum concentration limits for samples to be measured. Additional information about setting measurement limits is included in each application module section.



x **Show Plate Summary** - Allows the user to review the results of the plate at any time during the measurement session. Once the entire plate has been read, this feature will allow the user the option of marking samples of interest for repeat testing

Sample Status Color Code

The 96 well plate schematic allows the user to monitor the position of the samples being measured. Black wells indicate that samples in the corresponding wells have been measured. Green wells indicate which positions are currently being measured while yellow represents well positions that are expected to be measured. Pre-loading a Sample ID file or manually entering in sample names will activate the respective wells. To select additional wells, use the Configuration drop down box and select Manual Plate Set-up. If Sample ID Required has been selected from the configuration drop down, any wells that do not have an ID assigned will appear red and a sample ID must be assigned before measurement can begin.



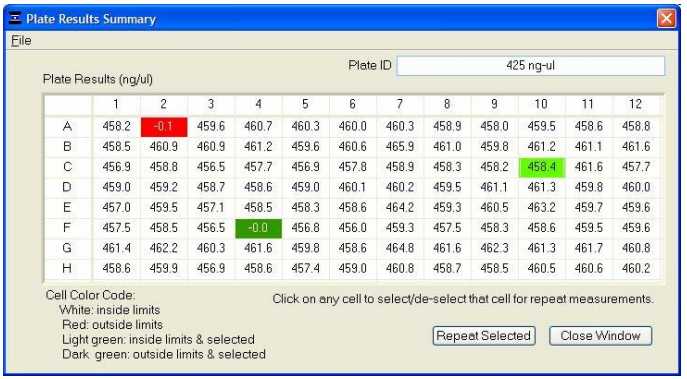
Sample Position Illuminator

This lighted guide allows the user to visualize the row of a standard 96-well micro titer plate that is to be sampled for measurement. The Sample Position Illuminator corresponds to the sample status color code displayed on the software screen and the pattern of illumination is determined by plate configuration at set up. If measurement limits have been defined, wells that are out of the defined range will flash on the

Sample Position Illuminator immediately after measurement. These positions will continue flashing until measurement of the current plate sample set is complete, the results have been reviewed and the Plate Results Summary window is closed.

Plate Review

The Plate Results Summary window will automatically appear if the auto advance column feature has been selected and measurement of the plate sample set is complete. Selecting Show Plate Summary from the configuration drop down menu will also open this window. From this window, sample wells of interest can be marked for repeat. If measurement limits were defined, sample measurements that are outside of the defined range will be indicated by a flashing light on the Sample Position Illuminator and the concentrations will appear in red when the plate summary is displayed. Once the plate summary has been reviewed, samples of interest marked for repeat, and the window closed, the Sample Position Illuminator will stop flashing.

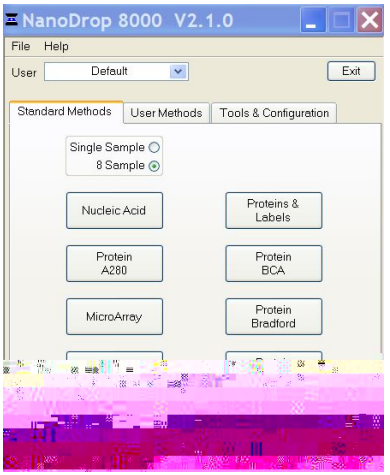


5. Standard Methods

Software Architecture and Features

Main Menu

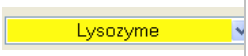
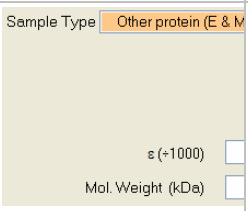
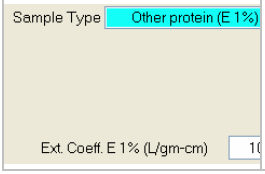
With the sampling arm in the down position, start the operating software by selecting the following path: Start Æ Programs ÆNanoDrop ÆND-8000 (version) The software opens to display three tabs including Standard Methods, User Methods and Tools & Configuration.



Applications

The operating software has been tailored to meet the life scientist's needs. It includes the following pre-configured application modules:

- **Nucleic Acid** – concentration and purity of nucleic acid
- **Protein A280** – concentration and purity of purified protein
- **MicroArray** – dye incorporation concentration and purity of nucleic acid
- **UV-Vis** – general UV-Vis measurements
- **Cell Cultures** – absorbance (light scattering) measurement of suspended microbial cells
- **Proteins & Labels** – concentration of dye-labeled proteins, conjugates, and metalloproteins
- ***Protein BCA –** protein concentration using the BCA assay
- ***Protein Bradford** – protein concentration using the Bradford assay
- ***Protein Lowry –** protein concentration using the Modified Lowry assay
- ***Protein Pierce 660 nm-** protein concentration using the new 660 nm assay

	Lysozyme reference. Unknown (sample) protein concentrations are calculated using the mass extinction coefficient of 26.4 at 280 nm for a 1% (10 mg/ml) Lysozyme solution.
	User-entered values for molar extinction coefficient (M^{-1} cm^{-1}) and molecular weight (MW) in kilo Daltons for their respective protein reference. Maximum value for e is 999 X 1000 and maximum value for M.W. is 9999 X 1000.
	User-entered mass extinction coefficient (L $gm^{-1}cm^{-1}$) for a 10 mg/ml (1%) solution of the respective reference protein.

- **nm 1 and nm 1 abs**: current value of the user-selectable wavelength cursor and corresponding 10mm equivalent normalized absorbance at the respective wavelength absorbance. The wavelength can be set by using the up/down arrows or typing in the desired wavelength. Note: The user selected wavelength and absorbance are not utilized in any calculations.

- **A280 10-mm Path**: 10 mm-equivalent absorbance at 280 nm for the protein sample measured.

- **A260/280**: ratio of sample absorbance at 260 nm and 280 nm.

- **Concentration (mg/ml):** sample concentration based on the absorbance at 280 nm and the selected analysis constant. The calculated concentration is displayed in the units selected via the units drop down box. The calculated concentration is displayed in the units selected via the units drop down box. The units will default to mg/ml each time the software is opened. See the “Concentration Calculation (Beer’s Law)” in the appendix for more details on this calculation.

- **Show Report:** formatted for 200 samples although the buffer size can be modified.

Spectrum Normalization

The baseline is automatically set to the absorbance value of the sample at 340 nm, which should be very nearly zero absorbance. All spectra are referenced off of this zero unless the user elects to turn off the normalization.

MicroArray

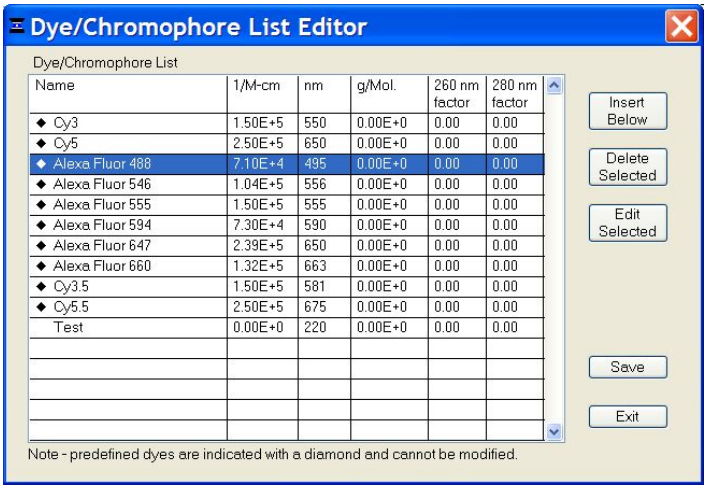
The capability to pre-select viable fluorescent-tagged hybridization probes for gene expression in micro-arrays can eliminate potentially flawed samples and improve research effectiveness. The NanoDrop 8000 Spectrophotometer measures the absorbance of up to 2 fluorescent dyes, allowing detection at dye concentrations as low as 0.2 picomoles per microliter.

Fluorescent Dye Selection

There are currently a number of fluorescent dyes that are hard-coded for use with the MicroArray module (see table below). Users can also enter & save fluorescent dyes not coded within the NanoDrop 8000 software using the Dye/Chromophore Editor button found in the main menu.

Dyes can be selected using the scroll arrows or by highlighting the Dye box. The respective absorbance wavelength, extinction coefficient, and 260 nm and 280 nm % corrections will be automatically utilized for measurement and concentration calculation. The default setting for Dye 1 is Cy3 and Dye 2 is Cy5. See User Preferences under the Tools & Configuration main page tab to designate alternative dyes as the defaults.

Note: Please refer to the dye manufacturer for the appropriate correction factors for user entered dyes.



Sample Volume Requirements
Field experience has indicated that 1 ul samples are sufficient to ensure accurate and reproducible results when measuring aqueous nucleic acid samples containing incorporated fluorescent dyes. However, if you are unsure about the surface tension properties of your sample or your pipettor accuracy, a 1.5-2 ul sample is recommended to ensure that the liquid sample column is formed and the light path is completely covered by sample.

Use an 8-channel pipettor when loading multiple samples to minimize evaporation due to delays in sample loading. It is recommended that spectrophotometric measurements be made immediately after pipetting samples onto the pedestals as delays can compromise accuracy.

Measurement Concentration Range
The NanoDrop 8000 Spectrophotometer will accurately measure fluorescent-dye and nucleic acid concentrations up to 100 pmols/ul (Cy3) and 750 ng/ul (DNA) respectively without dilution. A table of sample concentration ranges is listed below.

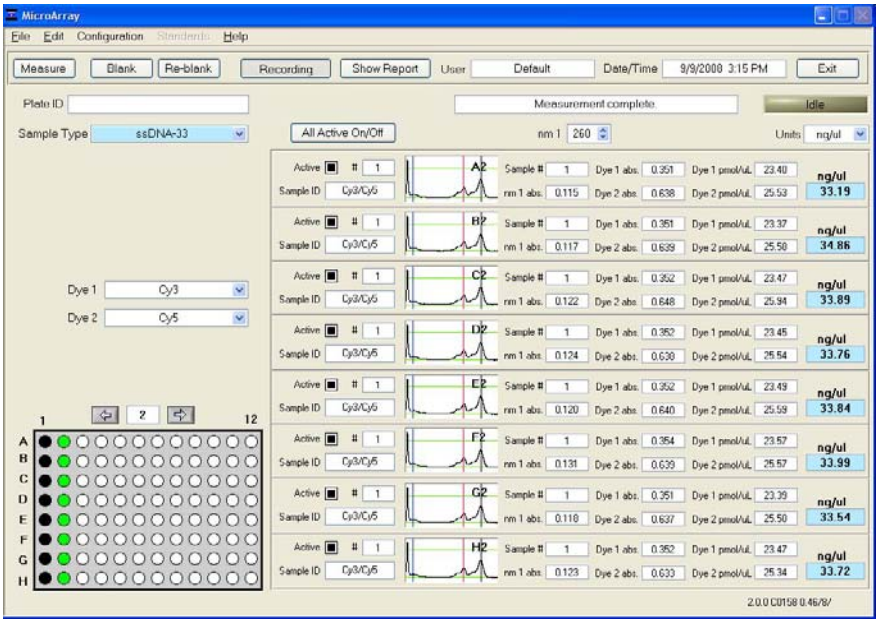
Sample Type	Detection Limit (pmol/ul)	Approx. Upper Limit (pmol/ul)	Typical Reproducibility (minimum 48 replicates) (SD= pmol/ul; CV= %)
Cy3, Cy3.5, Alexa Fluor 555 and Alexa Fluor 660	0.25	100	sample range 0.25-4 pmol/ul: r. 0.25 sample range >4.0 pmol/ul: r 2.5%
Cy5, Cy5.5 and Alexa Fluor 647	0.17	60	sample range 0.17-2.4 pmol/ul: r 0.17 sample range >2.4 pmol/ul: r 2.5%
Alexa Fluor 488 and Alexa Fluor 594	0.50	215	sample range 0.50-8.0 pmol/ul: r. 0.50 sample range >8.0 pmol/ul: r 2.5%
Alexa Fluor 546	0.42	145	sample range 0.42-6.0 pmol/ul: r. 0.42 sample range >6.0 pmol/ul: r 2.5%

By selecting Measurement Limits from the configuration drop down menu, minimum and maximum concentration limits can be set for the nucleic acid component as defined by the absorbance at 260 nm. These limits cannot be set as a default and must be defined each time the application module is opened. Nucleic acid measurements that are outside of the defined range will be indicated by a flashing light on the

Sample Position Illuminator. The sample concentrations will also appear in red when the plate summary is displayed.

Once the plate summary has been reviewed, samples of interest marked for repeat, and the window closed, the Sample Position Illuminator will stop flashing.

Unique Screen Features



- **Sample Type:** used to select the (color-keyed) type of nucleic acid being measured. The user can select 'DNA-50' for dsDNA, 'RNA-40' for RNA, ssDNA-33' for single-stranded DNA, or 'Other' for other nucleic acids. The default is ssDNA-33. If 'Other' is selected, the user can select an analysis constant between 15-150. When navigating amongst the three (3) general sample types within the MicroArray module, the last value of the constant entered within the Constant Sample Type will be retained. See "Concentration Calculation (Beer's Law)" in the appendix for more details on this calculation.

- **nm 1 and nm 1 abs:** current values of the user-selectable wavelength cursor and corresponding absorbance value for a 1 mm pathlength. The wavelength can be set by using the up/down arrows or typing in the desired wavelength. Note: The user selected wavelength and absorbance are not utilized in any calculations.

- **Dye 1:** user selected dye.

- **Dye 2:** user selected dye.

- **Dye 1 (or 2) pmol/ul:** concentration based upon selected dye's extinction coefficient. See "Concentration Calculation (Beer's Law)" in the appendix for more details on this calculation.

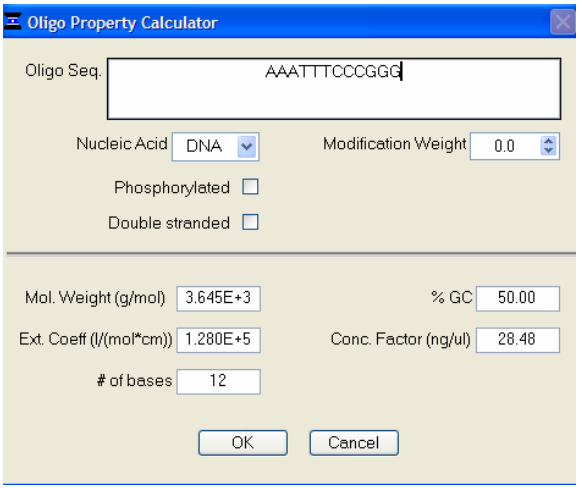
- **Concentration (ng/ul):** sample concentration based on the absorbance at 260 nm and the selected analysis constant. The calculated concentration is displayed in the units selected via the units drop down box. The calculated concentration is displayed in the units selected via the units drop down box. The units will default to ng/ul each time the software is opened. See the "Concentration Calculation (Beer's Law)" in the appendix for more details on this calculation.

- **Show Report:** formatted for 200 samples although the buffer size can be modified.

Oligo Calculator

The Oligo Calculator enables the user to type in a specific sequence and choose parameters associated with the oligo sequence.

When the Oligo Calc sample type option is first selected the following box will appear:



The calculator allows the user to define the sequence and include relevant information such as whether the oligo is phosphorylated or double stranded. The information boxes in the bottom of the screen automatically populated based about the sequence entered.

Baseline Calculation & Normalization

The software normalizes the visual spectrum display for all readings at 750 nm. Normalization for the fluorescent dyes is based upon a software determined slope between 400 and 750 nm for dye concentration calculations.

UV-VIS

The 'UV/VIS Absorbance' module allows the NanoDrop 8000 Spectrophotometer to function as a conventional spectrophotometer. Sample absorbance is displayed on the screen from 220 nm to 750 nm and cursors permit the measurement of individual peaks.

Sample Volume Requirements

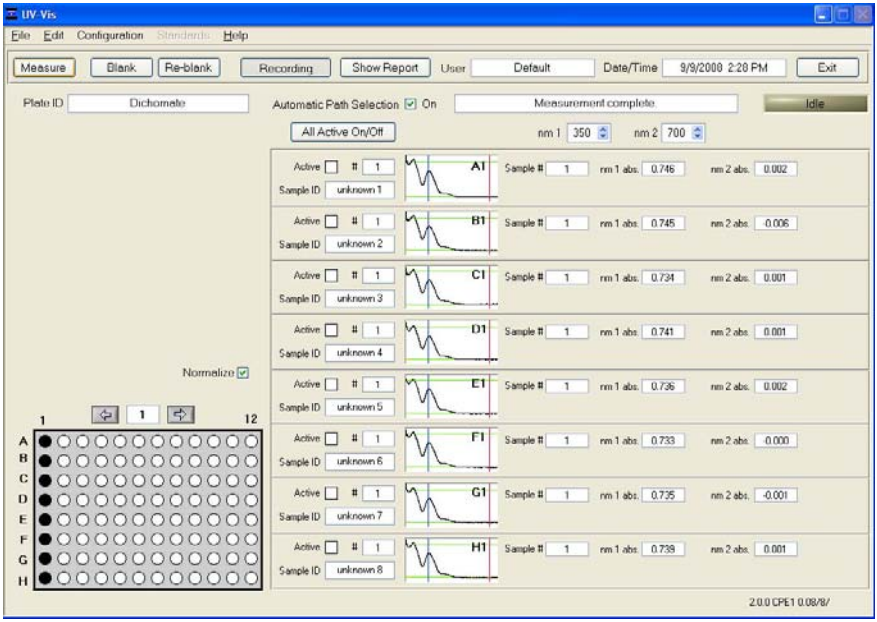
Field experience has indicated that 1 ul samples are sufficient to ensure accurate and reproducible results when measuring most aqueous samples. However, if you are unsure about the surface tension properties of your sample or your pipettor accuracy, a 1.5-2 ul sample is recommended to ensure that the liquid sample column is formed and the light path is completely covered by sample.

Use an 8-channel pipettor when loading multiple samples to minimize evaporation due to delays in sample loading. It is recommended that spectrophotometric measurements be made immediately after pipetting samples onto the pedestals as delays can compromise accuracy.

Measurement Concentration Range

The NanoDrop 8000 Spectrophotometer is configured to measure absorbance up to the 1 mm pathlength equivalent of 7.5 A when utilizing the 0.2 mm path via the automatic path selection feature. By selecting Measurement Limits from the configuration drop down menu, minimum and maximum absorbance limits can be set for the shorter of the two user selectable wavelengths. These limits cannot be set as a default and must be defined each time the application module is opened. Sample absorbances that are outside of the defined range will be indicated by a flashing light on the Sample Position Illuminator. The absorbances will also appear in red when the plate summary is displayed. Once the plate summary has been reviewed, samples of interest marked for repeat, and the window closed, the Sample Position Illuminator will stop flashing

Unique Screen Features



- **Automatic Path Selection:** If selected, the software will automatically switch from using the 1.0 mm pathlength to the 0.2 mm path when the absorbance value first reaches 1.25 for EITHER of the two wavelengths indicated with the two cursors.

  Note: It is important to pre-select a cursor position for the wavelength of interest before the measurement is taken. If the cursors are set for wavelengths with minimal absorbance, the 0.2 mm pathlength will not be utilized.

  Note: When the 0.2 mm pathlength is utilized, the data will be archived and displayed normalized to the 1.0 mm pathlength. The feature can be turned off using the UV/Vis tab in the Users Preferences module.

- **nm 1/abs1** and **nm 2/abs2:** current values of the user-selectable wavelength cursors and corresponding absorbencies for a 1 mm pathlength. The wavelengths can be set by using the up/down arrows or typing in the desired wavelength. The default wavelengths are 300 nm and 700 nm.

- **Normalize:** a user-selectable feature in this module**.** If selected, the software will automatically normalize the spectrum based on the lowest absorbance value in the range 400-700 nm.

- **Show Report:** formatted for 200 samples although the buffer size can be modified.

- Dyes can be selected using the scroll arrows or by highlighting the Dye box. The respective absorbance wavelength, extinction coefficient, and 260 nm and 280 nm % corrections will be automatically utilized for measurement and concentration calculation. The default setting for Dye 1 is Cy3 and Dye 2 is Cy5. See User Preferences under the Tools & Configuration main page tab to designate alternative dyes as the defaults.

- **Concentration (mg/ml):** sample concentration based on the absorbance at 280 nm and the selected analysis constant. The calculated concentration is displayed in the units selected via the units drop down box. The calculated concentration is displayed in the units selected via the units drop down box. The units will default to mg/ml each time the software is opened.

- **Show Report:** formatted for 200 samples although the buffer size can be modified.

Baseline Type

This application module has two user-selectable “Baseline Type” options. The default setting is set to normalize the display spectrum at 750 nm. Alternatively, the 400-750 Slope Baseline Type will normalize the display at 750 nm and accommodate any linear baseline offset across the 400 to 750 nm range. The 280 nm absorbance value is normalized at 340 nm unless the user elects to turn off the normalization.

Protein BCA

The BCA (Bicinchoninic Acid) Protein Assay is an alternative method for determining protein concentration. It is often used for more dilute protein solutions and/or in the presence of components that also have significant UV (280 nm) absorbance. Unlike the Protein A280 method, the BCA Assay requires that a standard curve be generated before unknown protein concentrations can be determined. The resulting Cu-BCA chelate formed in the presence of protein is measured at its wavelength maximum of 562 nm and normalized at 750 nm. Pre-formulated reagents of BCA and CuSO4, utilized in the assay, are available in kit form from numerous manufacturers. Follow the respective manufacturer's recommendations for all standards and samples (unknowns).

Sample Volume Requirements

The presence of surfactants or detergents in reagents can significantly alter the surface tension, resulting in difficulty forming and/or maintaining adequate columns for measurement. The column formation issue can be overcome without affecting the sample's absorbance by using a larger sample volume. **A 2 ul sample size is recommended for protein measurements.**

Use an 8-channel pipettor when loading multiple samples to minimize evaporation due to delays in sample loading. It is recommended that spectrophotometric measurements be made immediately after pipetting samples onto the pedestals as delays can compromise accuracy.

Pedestal Reconditioning

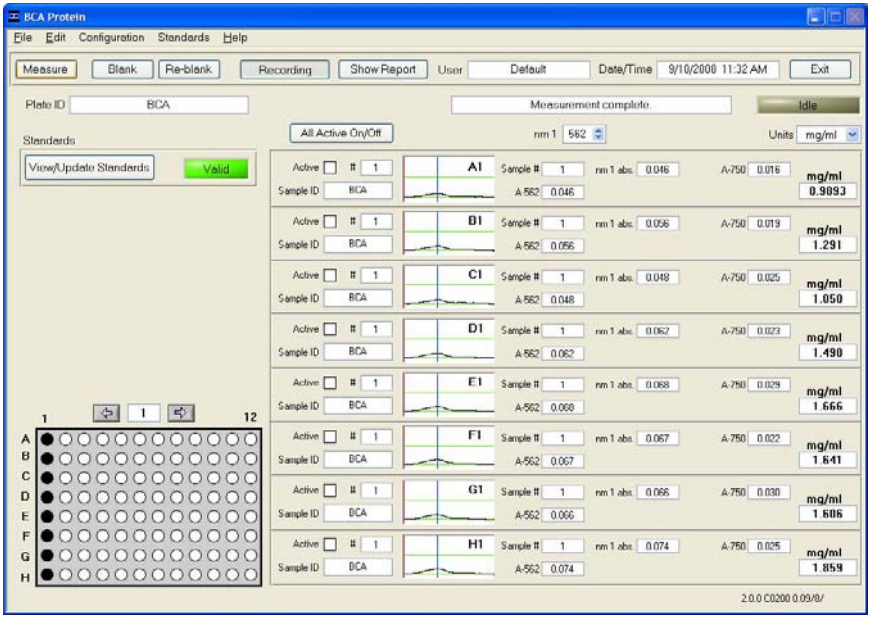
Solutions and reagents containing surfactants may "un-condition" the measurement pedestal surfaces so that the liquid column does not form properly. If this occurs, "buff" the measurement pedestal surfaces by rubbing each measurement surface aggressively with a dry laboratory wipe 30-40 times. This will "re-condition" the surface allowing the liquid sample column to form.

Alternatively, use the NanoDrop Pedestal Reconditioning Compound (PR-1) as a rapid means of reconditioning the pedestals when the surface properties have been compromised and liquid columns break during measurement. Additional information about the PR-1 kit may be found on our website.

Measurement Concentration Range
When using a 20:1 reagent to sample volume dilution, the BCA assay concentration range of detection is ~0.20 mg/ml to 8.0 mg/ml on the NanoDrop 8000. Using a 1:1 reagent to sample volume dilution the concentration range of detection is 0.01 mg/ml – 0.20 mg/ml.

By selecting Measurement Limits from the configuration drop down menu, minimum and maximum concentration limits can be set for protein (mg/ml) measured with this method at 562 nm. These limits cannot be set as a default and must be defined each time the application module is opened. Protein measurements that are outside of the defined range will be indicated by a flashing light on the Sample Position Illuminator. The sample concentrations will also appear in red when the plate summary is displayed. Once the plate summary has been reviewed, samples of interest marked for repeat, and the window closed, the Sample Position Illuminator will stop flashing.

Unique Screen Features



- **A 562nm:** the Cu-BCA complex's absorbance at 562 nm for the 1 mm pathlength.

- **nm 1 and nm 1 abs**: current value of the user-selectable wavelength cursor and corresponding absorbance value for a 1 mm

pathlength. The wavelength can be set by using the up/down arrows or typing in the desired wavelength. Note: The user selected wavelength and absorbance are not utilized in any calculations.

- **mg/mL:** the concentration of the sample (unknown). The calculated concentration is displayed in the units selected via the units drop down box.

- **Show Report:** formatted for 200 samples although the buffer size can be modified.

BCA Assay Sample Preparation

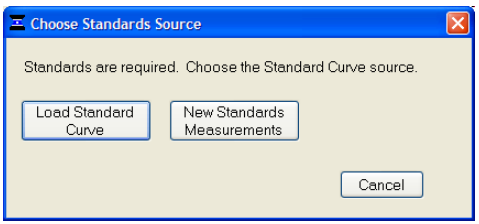
Follow the manufacturer's protocol for the assay including recommended incubation times and temperature.

In addition to the kit reagents, protein standards (BSA) for generating a standard curve for the BCA method are often provided by the manufacturer. Use the respective standard (e.g., BSA) and dilutions that cover the analytical range (mg/ml) of interest. Note: Since the NanoDrop 8000 can measure higher protein concentrations than a cuvette based spectrophotometer, you may need to supply your own protein standards at higher concentrations than routinely provided by the manufacturer.

Making BCA Measurements

A standard curve is required every time the BCA assay is run. Although curves can be saved and reloaded in the NanoDrop 8000 Spectrophotometer software, it is recommended that the user follow manufacturers' guidelines and generate fresh standard curves for each assay. Both single and multi-point standard curve generation are incorporated into the software. A standard curve can be developed using a reference (BCA reagent only – no protein) and a single replicate of one standard. The multi-point standard curve generator displays a maximum of 5 replicates for each of 7 different standards. There is no set order in which standards must be run.

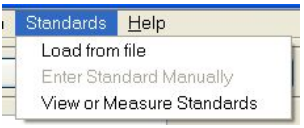
The following box will appear after the module initialization is complete:



The user may load a previously saved standard curve or generate a new curve. Selecting the New Standards Measurements button will bring up the dialogue box on the left, below:

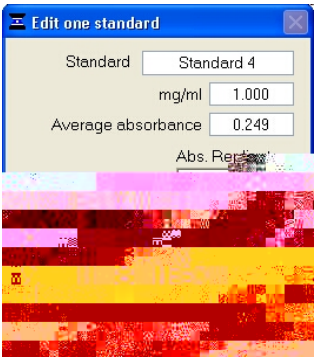
Clicking on the Yes button will allow the user to import just the Standard series without the respective measured values (See image on the right, above). This option is very useful when running a routine series of standards. Selecting 'No" enables the user to enter new concentrations values for standards 1-7. The reference should remain set at 0.00.

The Standards menu drop down may also be used to load a previously saved curve, generate a new standard curve, or view the current standard curve.



Then follow the steps below to either generate or modify the curve as needed:

- **Enter the concentration for each standard.**
  The user may either click on the Active/ Inactive box to the left of each standard or double click any where in the row of a particular standard to bring up the Edit Standard dialog box to enter in the concentrations for each standard. This box is also used to delete a single absorbance replicate value or reset the entire standard.



Alternatively, previously saved standard curves and standard curve concentration series may be loaded using the Standards menu bar drop-down options.

x **Measure Standards**
Up to 5 replicates of each standard will be displayed. The software will not allow measurement of samples until a minimum of either a reference and 1 standard or 2 standards – are measured. Polynomial curve fitting requires more standard points depending on the polynomial degree selected.

x **Measure Samples**
Once a minimum standard curve has been established, the standard curve indicator will change from gray (invalid) to green (valid), allowing the user to start measuring samples. The designation of "Valid" only indicates that the minimum requirement for a 2-point curve has been met. Sample concentrations are calculated by using

In addition to the kit reagents, protein standards (BSA) for generating a standard curve for the Bradford method are often provided by the manufacturer. Use the respective standard (e.g., BSA) and dilutions that cover the analytical range (mg/ml) of interest. Note: Since the NanoDrop 8000 can measure higher protein concentrations than a cuvette based spectrophotometer, you may need to supply your own protein standards at higher concentrations than routinely provided by the manufacturer.

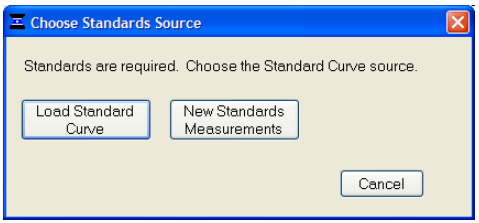
Variation Between Different Kits

When comparing Coomassie G-250 and the Coomassie Plus Protein Assay kit from Pierce, preliminary results show the Coomassie Plus Protein Assay produces better reproducibility amongst triplicate readings than the regular G-250 stain when reading the samples directly after the optimal incubation time.

Making Bradford Protein Measurements

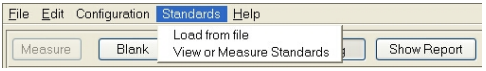
A standard curve is required every time the Bradford assay is run. Although curves can be saved and reloaded in the NanoDrop 8000 Spectrophotometer software, it is recommended that the user follow manufacturers' guidelines and generate fresh standard curves for each assay. Both single and multi-point standard curve generation is incorporated into the software. A standard curve can be developed using a reference (Bradford reagent only – no protein) and a single replicate of one standard. There is no set order in which standards must be run. The multi-point standard curve generator displays a maximum of 5 replicates for each of 7 different standards.

The following box will appear after the module initialization is complete:



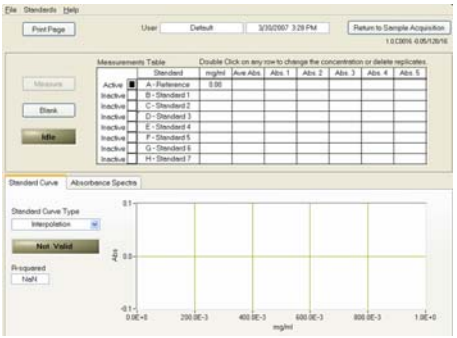
The user may load a previously saved standard curve or generate a new curve. Selecting the New Standards Measurements button will bring up the dialogue box on the left, below:

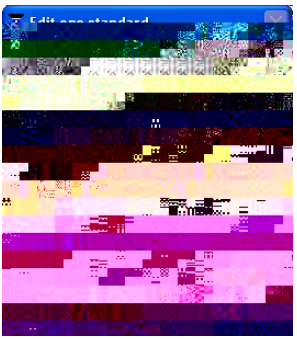
Clicking on the Yes button will allow the user to import just the Standard series without the respective measured values (See image on the right, above). This option is very useful when running a routine series of standards. Selecting 'No' enables the user to enter new concentrations values for standards 1-7. The reference should remain set at 0.00. The Standards menu drop down may also be used to load a previously saved curve, generate a new standard curve, or view the current standard curve.



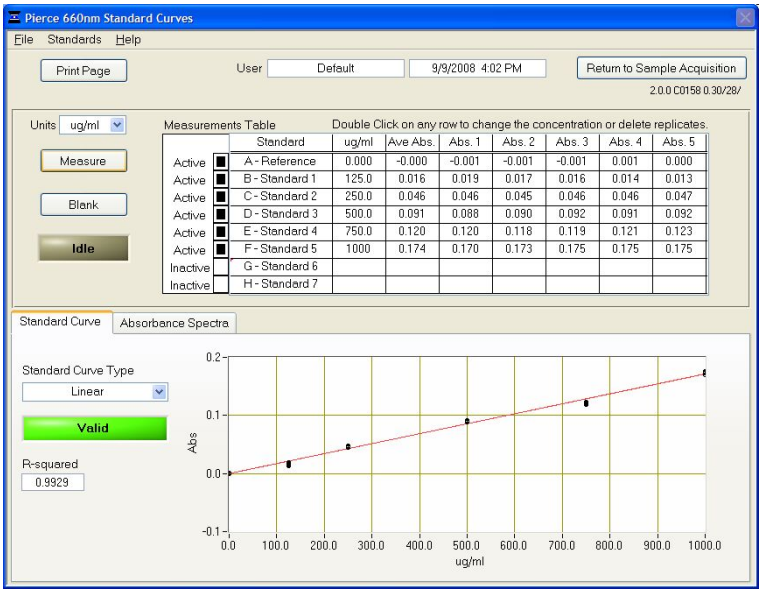
Then follow the steps below to either generate or modify the curve as needed:

- **Enter the concentration for each standard.**
  The user may either click on the Active/ Inactive box to the left of each standard or double click any where in the row of a particular standard to bring up the Edit Standard dialog box to enter in the concentrations for each standard. This box is also used to delete a single absorbance replicate value or reset the entire standard.





Alternatively, previously saved standard curves and standard curve concentration series may be loaded using the Standards menu bar drop-down options.



		Standard	ug/ml	Ave Abs.	Abs. 1	Abs. 2	Abs. 3	Abs. 4	Abs. 5
Active	■	A - Reference	0.000	-0.000	-0.001	-0.001	-0.001	0.001	0.000
Active	■	B - Standard 1	125.0	0.016	0.019	0.017	0.016	0.014	0.013
Active	■	C - Standard 2	250.0	0.046	0.046	0.045	0.046	0.046	0.047
Active	■	D - Standard 3	500.0	0.091	0.088	0.090	0.092	0.091	0.092
Active	■	E - Standard 4	750.0	0.120	0.120	0.118	0.119	0.121	0.123
Active	■	F - Standard 5	1000	0.174	0.170	0.173	0.175	0.175	0.175
Inactive		G - Standard 6							
Inactive		H - Standard 7							

A Pierce 660 nm assay using a 15:1 reagent to sample volume covers an approximate range of 50-2000 ug/ml

Exiting the Pierce 660 nm Module

It is recommended that you process all of the unknowns to be assayed before exiting the software module.

Cell Cultures

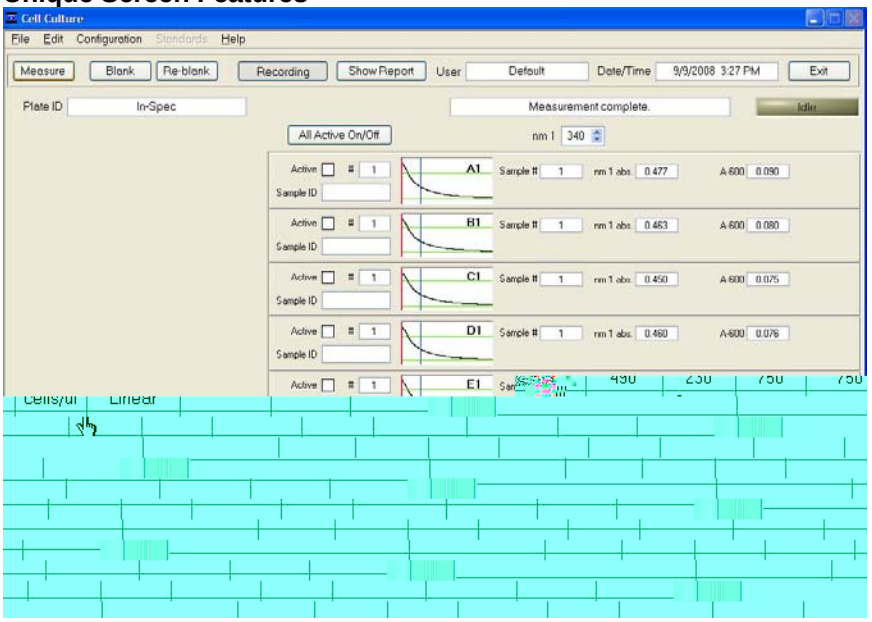
Using an absorbance spectrophotometer to monitor light scattered by non-absorbing suspended cells is common practice in life science laboratories. Such applications, more than any other, accentuate the differences between the optical systems of the numerous spectrophotometer designs.

Note: The most distinct difference between the NanoDrop 8000 Spectrophotometer “absorbance” values for cell microbial cultures and those observed using classical cuvette based systems will be attributable to the shorter pathlength (1 mm vs. 1 cm.) Values may not be exactly 10 fold different as readings are dependent on both the optics of a specific spectrophotometer as well as the cell type in suspension.

The Cell Cultures module displays the sample spectrum from 250 nm to 700 nm. The software will display the absorbance data for the frequently used wavelength for monitoring cell suspensions (600nm) in addition to displaying the value for a second wavelength of interest.

By selecting Measurement Limits from the configuration drop down menu, minimum and maximum absorbance limits can be set for the user selectable wavelength (cursor position). These limits cannot be set as a default and must be defined each time the application module is opened. Sample absorbances that are outside of the defined range will be indicated by a flashing light on the Sample Position Illuminator. The absorbance values will also appear in red when the plate summary is displayed. Once the plate summary has been reviewed, samples of interest marked for repeat, and the window closed, the Sample Position Illuminator will stop flashing.

Unique Screen Features



- **600nm Absorbance:** current value of the absorbance at the O1 cursor with the baseline absorbance subtracted. Note: The actual 1 mm absorbance is displayed.

- **nm 1:** current value of the user-selectable wavelength cursor and corresponding absorbance. The wavelength can be set by using the up/down arrows or typing in the desired wavelength.

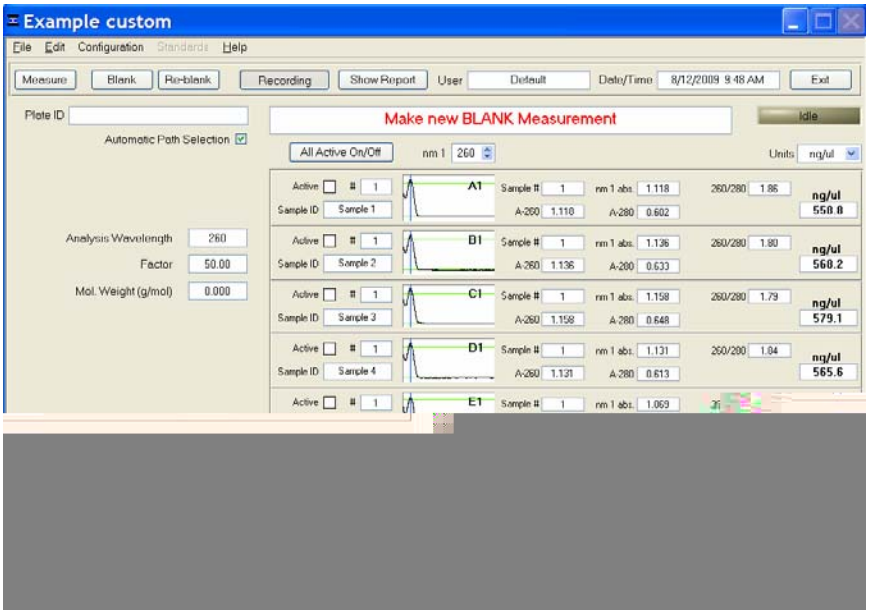
- **Show Report:** formatted for 200 samples although the buffer size can be modified.

Sample Size Requirements

Field experience has indicated that 1ul samples are sufficient to ensure accurate and reproducible results when measuring aqueous samples. However, if you are unsure about the surface tension properties of your sample or your pipettor accuracy, a 1.5-2 ul sample is recommended to ensure that the liquid sample column is formed and the light path is completely covered by sample.

Use an 8-channel pipettor when loading multiple samples to minimize evaporation due to delays in sample loading. It is recommended that spectrophotometric measurements be made immediately after pipetting samples onto the pedestals as delays can compromise accuracy.

User Method Acquisition Screen



The analysis wavelength and associated factors will be displayed on the acquisition screen when operating in either the Single or 8 Sample mode. The results of each additional formula will be displayed on the acquisition page when generated in the single sample mode but will not be displayed on the data 8 Sample mode. The additional formula results will be available in the data report and archived data for both operation modes.

Automatic Path Selection: If selected, the software will automatically switch from using the 1.0 mm pathlength to the 0.2 mm path when the absorbance value of the specified analysis wavelength reaches a threshold of 1.25.

7. Tools & Configuration

Archived Data

Sample data from all application modules is automatically stored in archive files and can be opened by either the integrated Data Viewer software program or spreadsheet programs such as MS Excel.

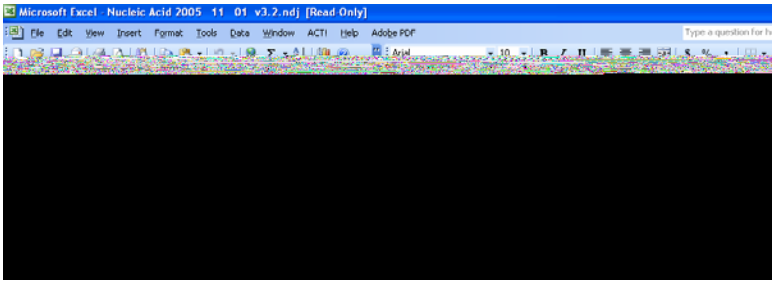
Archive File Creation

Every time an application module is started, an application-specific archive file is created for the user that is logged in. All measurements made by the user (in that application module) for a given calendar day are stored in a single archive file. These files bear the name of the respective application module with the date appended. For example, an archived file entitled "Nucleic Acid 2007 03 21.nd8" corresponds to Nucleic Acid data from the software session that began on March 21, 2007. A unique file extension (.nd8) has been given to these files to enable automatic startup with the Data Viewer (see the description of Data Viewer later in this section).

The data may be edited and/or reformatted and stored under names of the user's choice. The spectrum can be re-plotted from the wavelength data if needed for further analysis.

Absorbance data shown in archive files are represented as they are displayed on the screen. For Nucleic Acids, Protein A280, and Protein and Labels application modules, data is stored based on a 1.0 cm (10.0 mm) path. For MicroArray, UV-Vis, BCA Protein, Bradford, Lowry and Cell Culture application modules the data is normalized to a 1.0 mm (0.1 cm) path.

For data from all modules, a column entitled 'Measurement Type' is included. For each measurement, this column will contain 'Measure', 'Blank', or 'Reblank'. If the value is 'Measure', then the values in that row are from a normal measurement that has utilized the stored blank value. If the value is 'Blank', it indicates that the measurement is the initial blank recorded. If the value is 'Reblank', it is the re-analysis of the previous measurement with a new blank.



Data Storage Hierarchy
The hierarchy for archived files is as follows:
C:\ND-8000 Data ÆUser name ÆApplication Module (BCA Protein, Lowry, Bradford, Cell Culture, MicroArray, Nucleic Acid, Protein A-280, Proteins & Labels, UV-Vis).

All archived data files are stored in an application module folder that is within the User folder as shown below:

User-Defined Data File Export Location
In addition to the primary data storage, users may elect to export their data as anto an additional location. This option can be chosen under the Data Export Exporting tab in User Preferences from within the Tools & Configuration tab. Select the Automatic Data Export feature by enabling the On box. Select the data export destination using the icon next to the Data Export Folder dialog window. Save the alternative path by clicking on the 'Save and Exit' button before exiting the User Preferences window.

All data are written to the archive file immediately upon completion of the measurement. Inadvertent software or PC shutdowns should not affect the archive file.

Data Viewer
Data Viewer is a versatile data reporting software program incorporated into the operating software that offers the user the ability to customize

report structures, import stored data and re-plot data from previously generated data. Using the Data Viewer is the most expedient method to review data. This feature may be accessed during measurement sessions from the Show Report function found within each method module. It may also be accessed from the Main Menu page. A NanoDrop 8000 Spectrophotometer does not need to be connected to the PC to use the Data Viewer module.

Data Viewer Features
The Data Viewer is composed of two or three pages in a tabular form consisting of Plots, Reports and Standard Curves (where utilized). The user may access any page by clicking on the tabs.

The software opens to the Report page whether accessed through the Main Menu or Show Report. Note: Recording rather than Start Report must be selected in order to access the Data Viewer via Show Report.

Tool Bar Features common to all three pages include:

- **File:** Allows the user to define the page set up for printing out the spectra, the report and the standard curve. This drop down also allows the user to save the window as a jpg.

- **Configuration:** Options controlled by this tool bar function include 'Auto Scale', 'Include graph in printout' and 'Include standards in printout'.

- **Data:** Includes options to import data, rename samples and delete sample data. Note: After deleting all samples, it is important to exit out of the Data Viewer module and re-enter if importing data for a different application type.

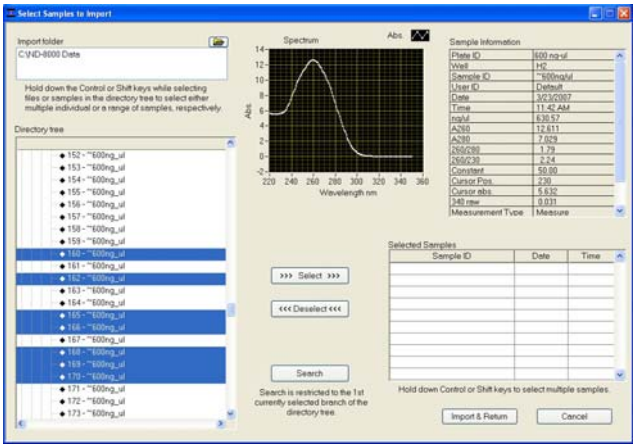
- **Reports:** This tool bar function allows the user to select columns of interest to be included in a report. See following section on Reports Page for details on additional drop down box options.

- **Print Window:** The current Plot, Report, or Standards screen may be printed by selecting 'Print Window' or 'CTL +P'.

- **Save Window:** Saves files as .JPGs.

Import Page

To select samples for viewing, select 'Import Samples' from the Data menu bar drop down options from either the Plots or Report pages within the Data Viewer software. This will bring up a new window with an Import Folder box and a Directory Tree as shown below.



Features include:

- **Import folder:** Used to select folder where data is to be imported from. Folder selection must be at the level of user or higher--may not select an application or method folder within a user in this activity box.

- **Directory tree:** Used to select specific data to be imported. Clicking on the square to the left of each file name will provide further detail to each level. Users may choose to select either individual samples within a file or the entire file. All import selections must be of the same application or method type.

- **Select or Deselect:** Used to move the highlighted sample choices to or from the Selected Samples box. Note: The software defaults to a buffer size of 1000 samples.

- **Search:** Function allows the user to locate specific data by searching through sample ID names.

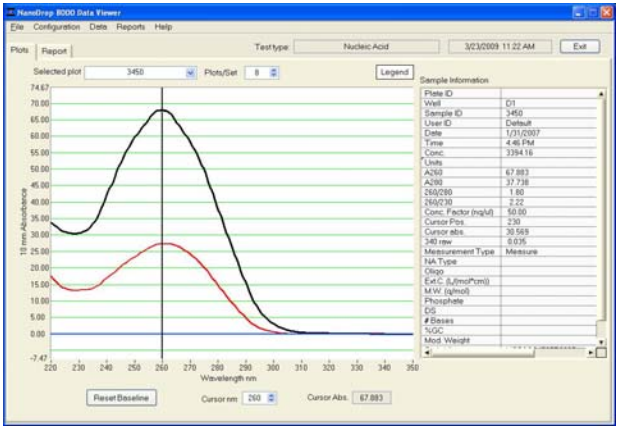
- **Sample Information and Spectrum:** Are populated with the information associated with the most recently highlighted sample.

- **Import and Return:** Uses selected sample data to populate Plots and Reports windows. Note: Holding down the shift or control PC

function keys will allow the user to select multiple samples and/or files for importing. The keys can also be used to deselect multiple samples.

Plots Page

The Plots page displays selected sample spectra.



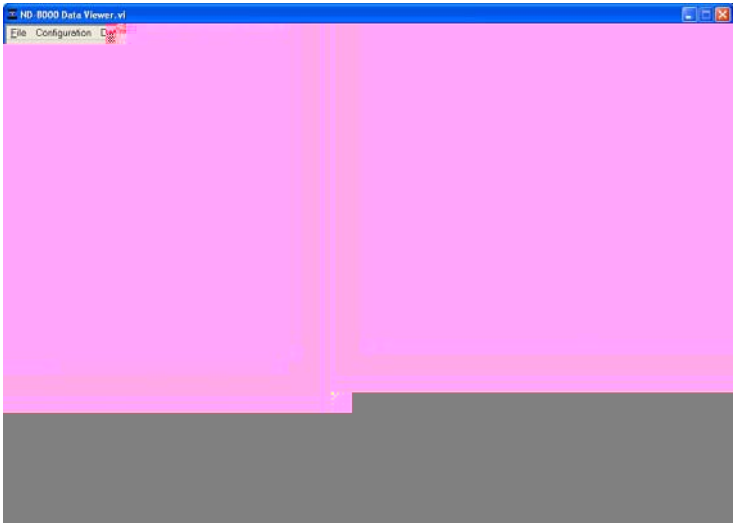
Features include:

- **Test Type:** Auto fills in module name.
- **Date:** Auto fills in date and time of report.
- **Selected Plot:** There are two methods of selecting or highlighting individual sample data. The user may simply move the cursor over the plot of interest and click or use the 'Selected Plot' drop down box (which will also display the legend). The selected sample will show up as a bold plot line.
- **Plots/Sets:** Users may select the maximum number of individual plots (up to 20) graphed per page. Since a report can hold data for many samples and a graph page is limited to 20 plots, additional sample spectra are displayed on new pages. Each page is then referred to as a set.
- **Legend:** Positioning the cursor over the legend box will bring up a visual display matching the sample name to a plot color. The user is not able to select or highlight a sample from the legend.
- **Sample information:** Automatically populates with data associated with selected sample. Data displayed is appropriate for data type chosen. Note: Information is based on data collected at the time the sample was measured and is not modified by a change in cursor position on the Data Viewer real time display.

- **Movable x and y axis:** Available for all data types. If the cursor is out of view in either direction- rescale the axis by typing over one of the outer limit numbers. The cursor absorbance information displayed at the bottom of the page is determined by the position of the movable cursors. The movable X determines the baseline from which the peak of the Y position is calculated. Reset Baseline will reposition the x axis back to zero.

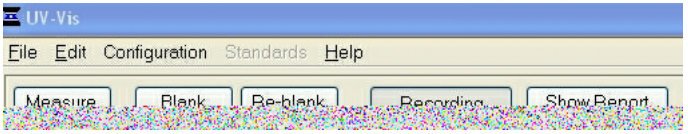
Report Page

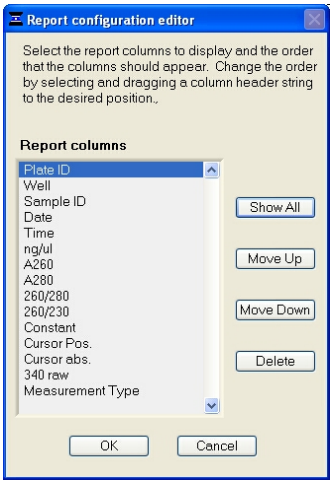
The Report page displays the data for selected samples in a table format. The user may modify column configurations for each method type and save multiple customized formats.



Start Report / Recording

All data is automatically archived. The user can log measurement results in an active report table as the data is accumulating by using the Start Report / Recording feature in the acquisition module. The default setting has the Recording feature activated for all modules. If **Start Report** is displayed, the accumulating data will still be archived but will not be shown in the active report.





Selecting **OK** will return the user to the Report page displaying only the columns of interest.

Additional options include:

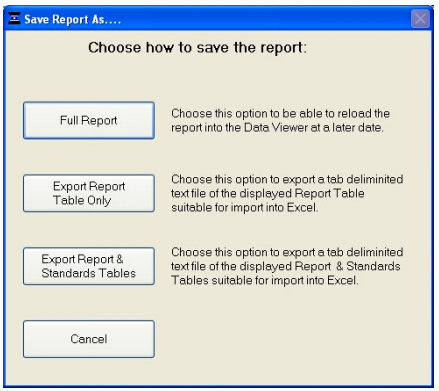
- **Sort:** Allows users to sort data by column (example-by date or sample name) and by either ascending or descending order.

- **Save Report Format:** Saves the current report format as an .nr8 file for retrieval and future use. To designate a saved report format as the default format, exit to the Main Menu, choose Users Preferences and click **Reports**. Use the Select Default Report Format to see the list of saved formats available for the specific method type.

- **Load Report Format:** Allows saved report formats to be loaded either before or after data is imported.

- **Print Report:** Will print out only the Report page by default. Users may choose whether or not to print out the standards or plots pages by selecting these options under the Configuration drop down on the tool bar.

- **Save Report and Load Report:** There are several options for this feature as seen in the following window:



Using the Full Report option will allow the user to use the Data Viewer to reload the report at a later date. The saved report may be recalled using the pull down Load Report. If using the Load Report feature- the report will be displayed with the default column configuration. Note: Access the User Preferences module on the main menu to modify and save preferred default configurations. Reports are saved in an .nr8 format. The user may select specific default report configurations for each pre-defined method. Only one default report formula is available for all user defined methods. Use the drop down Load Report Format to utilize a different saved configuration when running a custom method.

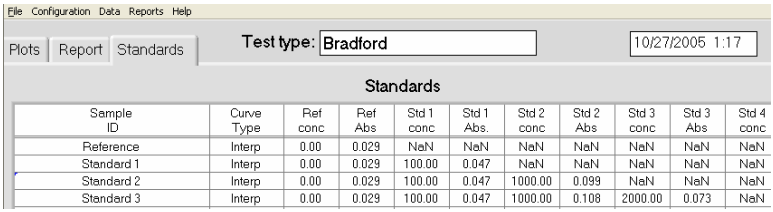
The other two options are meant for reports that are expected to be opened in Excel type spreadsheets. To open these reports, go to the C:\ND-8000 Data\Reports folder and right click on the file of interest.

Additional features of the Report page:

- **Method:** Automatically populated with data method type.
- **Date and Time:** Automatically populated when report is generated.
- **Report Name:** User defined designation for the current report
- **Report Full mode:** Drop down box defining options for managing reports.
  The user may elect to Print, Save, or Print and Save a report at any time by using the Report Full Mode drop down box shown below. The default setting of 1000 samples per report may be modified by highlighting the box and typing in the desired number. Choosing 'Ignore' from the drop-down will allow the user to include an unlimited number of samples in a report.
- **Max Report Size:** Default number is set at 1000.

Standards Page

The Standards page will display the actual reference standards applied to each particular sample at the time of measurement. Note: This page is only available for software modules utilizing a Standard Curve.



Sample ID	Curve Type	Ref conc	Ref Abs	Std 1 conc	Std 1 Abs.	Std 2 conc	Std 2 Abs	Std 3 conc	Std 3 Abs	Std 4 conc
Reference	Interp	0.00	0.029	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Standard 1	Interp	0.00	0.029	100.00	0.047	NaN	NaN	NaN	NaN	NaN
Standard 2	Interp	0.00	0.029	100.00	0.047	1000.00	0.099	NaN	NaN	NaN
Standard 3	Interp	0.00	0.029	100.00	0.047	1000.00	0.108	2000.00	0.073	NaN

Opening Archived Data with Spreadsheet Programs

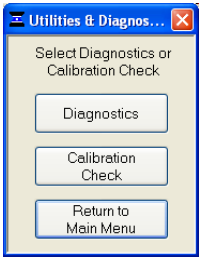
The archived files are in tab-delimited format and can be opened in Microsoft Excel or an equivalent spreadsheet program. To open these reports, go to the C:\ND-8000 Data\Reports folder and right click on the file of interest.

Note: Save and rename files before making any changes if opened with Excel type of programs to ensure that the original archived data is available for importing using the Data Viewer function.

Diagnostics and Utilities

Calibration Check

The Calibration Check is found within the Utilities and Diagnostics module and is accessed through the Main Menu. It is used to confirm that both pathlengths are within calibration specifications.



A CF-8 kit is required to run the calibration check procedure. The kit includes 8-well PCR strip tubes and two ampoules of an aqueous potassium dichromate ($K_2Cr_2O_7$) solution (CF-1) for use in confirming calibration of NanoDrop 8000 Spectrophotometers

The Thermo Scientific NanoDrop 8000 Calibration Check diagnostic utilizes five measurements on each of the 8 positions to verify the pathlength calibration. It is important to pay careful attention to technique when performing this procedure, as a single outlier caused by user error can result in a failed calibration check on one or more pedestals.

Calibration Check Best Practices

- Do not open the vial of CF-1 until ready to perform the calibration check.
- Position the instrument at an angle that will allow for optimal use of the pipette guide.
- Ensure the NanoDrop 8000 is not situated near an air vent or an exhaust fan from a nearby instrument.

- Aliquot 60 uL of CF-1 into each of the 8 tubes in the PCR strip. A volume of 60 ul in each PCR tube is required to reduce the effects of evaporation and potential fluid concentration.

- Use a small-volume (0.5-10 uL) multi-channel pipettor and well fitting low retention tips. If using an electronic pipettor do not draw up large volumes to dispense multiple aliquots. The CF-1 reserve stored in the tips may begin to concentrate, affecting the quality of results. Draw and dispense individual 1.5 uL aliquots for each measurement cycle.

- Ensure that adequate volumes of CF-1 are being pipetted onto the center of each pedestal. If tips are not fitted properly on each channel of the multi-channel pipettor, individual channels may not properly draw up, or dispense an adequate volume onto each pedestal. Columns that are too thin, or shifted off to one side may not completely cover the fiber-optic center of each pedestal.

- Always use fresh aliquots for each replicate set of measurements.

Required Materials

- CF-8 Calibration Kit (Cat # CHEM-CF-8)
- low volume, 8-channel pipettor with the appropriate tips
- dH_20
- low lint lab wipes

Preparation

Follow the cleaning and reconditioning steps prior to beginning the calibration check procedure:

1. Open the vial containing PR-1 and use the applicator provided in the kit to remove a pin-head sized amount of the compound.

2. Apply a very thin, even layer of PR-1 to the surface of the upper and lower pedestals.

3. Wait 30 seconds for the PR-1 to dry.

4. Fold a clean, dry laboratory wipe into quarters and remove the PR-1 by aggressively rubbing the surface of the upper and lower pedestals until all compound residue is removed

Note: The black appearance of the removed residue is normal and is not indicative of surface dirt.

5. Ensure the measurement pedestals are clean and that a 1.5 ul water sample “beads” up on each of the lower pedestals. Repeat reconditioning procedure if a water sample droplet flattens out and covers the surface of any pedestal.

NOote: CF-1 is supplied in two single use vials and both ampoules must be used within 30 minutes of opening. Prolonged exposure to the environment may cause a significant concentration change.

Calibration Check Procedure

1. Position the instrument at an angle that will allow for optimal use of the tip guide.

2. Select the Calibration Check: Tools & Configuration Tab > Utilities & Diagnostics>Calibration Check

3. Enter the Target Absorbance of the CF-1 in the pop-up box “Target absorbance @350 nm, 1 mm pathlength.”

   Note: The target absorbance is located on the ampoule label and is lot specific.

4. Add 60 ul of dH_20 to each well of one of the 8-well strips provided.

5. Use an 8-channel pipettor to simultaneously pipette 1.5uL of water to each pedestal position, lower the arm and click the **Blank** button. At the end of the measurement cycle, use a lab wipe to remove the water aliquots from the upper and lower pedestals and change tips.

6. Thoroughly mix CF-1 Calibration Fluid by vigorously shaking ampoule and ensure all solution is collected in the bottom portion of the vial.

7. Carefully break the neck of ampoule to open the CF-1 Calibration Fluid and aliquot 60 ul into each of well of the second 8-well strip.

8. **Use an 8-channel pipettor** to simultaneously pipette 1.5uL of CF-1 fluid onto each pedestal, lower the arm, and click the **Measure** button.

9. At the end of each measurement cycle, use a lab wipe to remove the CF-1 aliquots from the upper and lower pedestals.

10. **Change pipette tips**, then repeat step 8. Measure a total of 5 separate sets of replicates.

Calibration Check Results

After the 5th measurement, the results will be displayed on-screen.

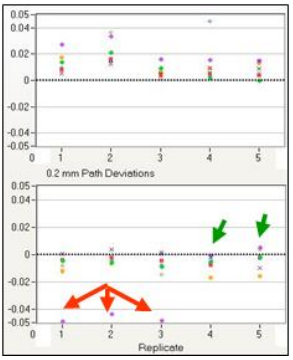
When the instrument passes the check procedure, a pop up box will indicate that the instrument works within specifications and the results will be saved as both a JPG and a .TXT file in the ND-8000 Data\Calib check folder on the local drive.

If the calibration check results in a failure or conditional pass, please review each series of data points looking at trends associated with individual positions. Choose the "Take No Action" option to review the data before exiting the diagnostic module. Refer to the Common Technique Issues section below for troubleshooting information.

If the instrument needs to be recalibrated, contact your local distributor or Technical Support for assistance.

Common Technique Issues

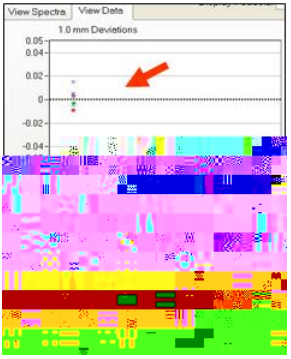
Improper Blank
When individual positions appear to have very low absorbance values as shown by the red arrows in the figure below, it often indicates an improper blank was measured. The green arrows in the same figure illustrate the difference in measurements after a new blank was measured.



When this occurs, reset the calibration check and ensure all pedestals are clean before making a new blank measurement.

Multiple Measurements with Same Aliquot

Measuring the same aliquots for subsequent measurements often results in most or all of the 1.0 mm data points moving off the reported scale. In the image below- note that the 1.0 mm data is off the scale while the 0.2 mm data for replicate 2 is within the accepted deviation.



When this occurs, reset the calibration check and ensure fresh aliquots are used for each replicate.

Using Single Channel Pipettor

Loading samples with a single channel pipettor often results in most or all of the 1.0 mm measurements being reported as more concentrated than would be expected.

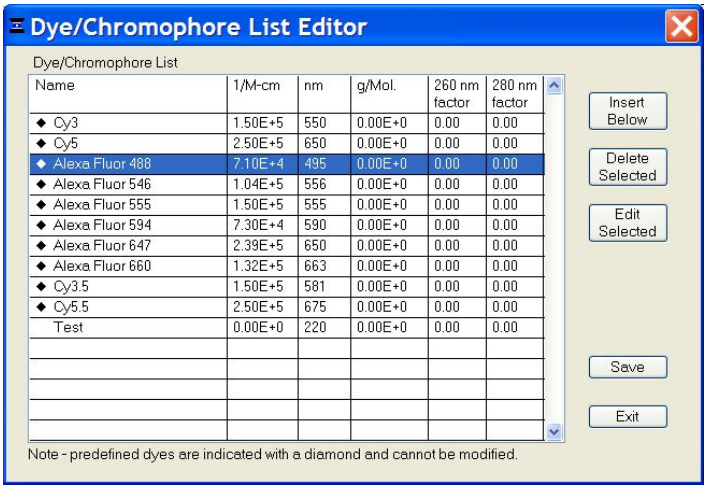
Auto Reporting
Users may choose to select the Auto Reporting option for any of the application modules. The auto reporting option allows data to automatically be saved to the report for all samples. Users may choose this option under the Reports tab by selecting the corresponding box next to the modules listed under Auto Reporting. Save the auto reporting functions by clicking on the Save & Exit button before exiting the User Preferences window.

Note: User preferences are stored in a '.log' file. When upgrading to a newer version of the software, this file should be preserved. If the user preferences do not appear correctly after upgrading to a new software version, the .log file should be manually copied to the proper directory. This file contains the User ID & password for all accounts and is readable only by the software. It can be found in the c:\ND-8000 Data\log files folder. It is strongly recommended that each time a new user account is added or a password is changed, the administrator make a **copy** of the updated file and store it in the c:\ND-8000 Data\log files folder. If the administrator's account becomes locked, the up-to-date copy can be renamed and used as the password.log file.

Dye/Chromophore Editor

The Dye/Chromophore Editor gives the user the ability to add additional dyes or chromophores to the list of predefined fluorescent dyes available for use with the MicroArray and Proteins & Labels modules. Predefined dye methods are indicated by a diamond and cannot be modified.

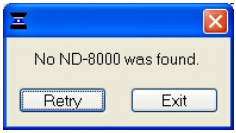
Absorbance contribution at 260nm and 280nm from the respective dye can be corrected by entering the appropriate decimal correction in the respective field when adding a new dye to the list. Please refer to the dye manufacturer for the appropriate correction factors for user-entered dyes.



8. Troubleshooting

Error Codes

Instrument Not Found

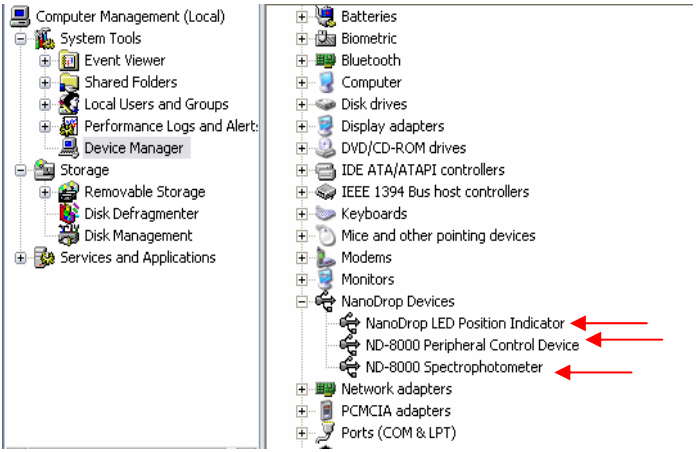


This error might appear upon software startup and usually indicates that either the power supply or the USB cable is not properly connected or the software is not loaded properly. To troubleshoot, do the following:

1. Check that the power supply is connected to the instrument. Confirm that the instrument is getting power by observing that light can be seen through the USB opening on the rear of the instrument.

2. Confirm that the USB cable is connected to both the PC and the instrument. Note: There are internal USB drivers in addition to the USB cable. When attaching the USB cable, please wait at least 30 seconds for the multiple USB devices to be installed and recognized before opening the software.

3. If the cable is connected properly but the Instrument recognition error persists, open the Windows Device Manager by either right clicking on the **My Computer** icon on the desk top or selecting Start Æ My Computer (right click) ÆManage ÆDevice Manager Æ NanoDrop Devices.



4. If an unknown device, a yellow exclamation point or a question mark appears next to one of three expected NanoDrop devices, manually uninstall the device by right clicking and selecting **Uninstall** from the options displayed.

5. Disconnect the USB cable first and then disconnect the power supply from the NanoDrop 8000.

6. Reconnect the power supply, wait 5 seconds and then reconnect the USB cable. At this point you may or may not see the Found New Hardware Wizard. If the wizard appears, follow the prompts for automatic installation of the software. Windows XP SP2 operating system will ask to allow it to search the internet for the proper software as shown - Select **No, not this time**.

Intro Page: Windows XP- SP2

Other Windows Operating Systems

Note: If the Found New Hardware Wizard appears, installation will require two cycles through the Wizard, once for the spectrometer

This error occurs when the user does not have “Write” access to one of the report format files located at c:\ND-8000 Data\custom report formats or the file has been moved from this folder. This error is similar to Error Code 8 (see above). Contact your PC administrator to give all users Read and Write access to this folder. Replace the files if they have been removed. If the file cannot be located, reinstall the software.

Other Software Error Messages

- **Source Error…**
  This error indicates that there is insufficient light getting through to make good absorbance measurements. Check that the sampling arm is in the down position and the power is connected.

- **No Active Samples for Measurement…**
  This error indicates that there are not any sample positions currently selected for measurement. The user may click either ‘All Active’ or select individual positions for the next measurement.

- **Error 8005**
  This error occurs when trying to load a plate file that is not in a .txt format.

- **Error 9000**
  This error occurs when the passwords.log file is missing or corrupt. Reinstall the operating software and "overwrite" the existing copy when prompted." A new copy of the passwords.log file should appear in the C:\ND-8000 Data\Log Files folder.

- **Error 9003**
  This error indicates that the monitor resolution is below the 1024x768 required. Check the computer settings. Be sure that the Start menu tool bar is set to the bottom and not along the side.

- **Low Detector Bias…**
  This occurs when the software has identified a problem with the detector. Contact your local distributor or Technical Support if you encounter this error.

Driver X Configuration Failed- You Must Manually Edit the Registry

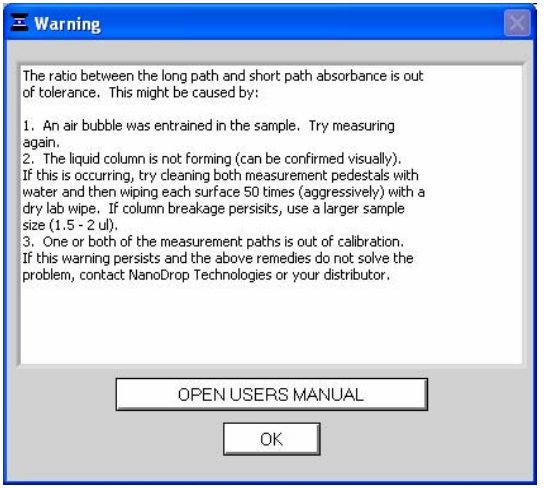
This error message (or others with similar wording) occurs when attempting to install the operating software on a computer running

Windows 2000 or XP. It occurs because the user does not have the necessary authorization to install the software. Contact your system administrator if this occurs.

Insufficient Memory…

This error message (or others with similar wording) occurs when attempting to install the operating software on a computer that does not have at least 100 MB of free hard disk space.

Liquid Column Breakage



This warning occurs when a possible problem with the column is detected. The software compares the long path and short path absorbances and issues a warning to the user if the short path is not 20% of the long path absorbance, within a tolerance. The most common explanation is that the column is not forming properly due to the pedestal being “unconditioned”.

When a pedestal becomes unconditioned, sample droplets applied to the bottom pedestal will 'flatten-out' and cover the entire pedestal surface rather than 'bead up'. Buffers containing detergents and various other reagents may cause the pedestal surfaces to become unconditioned. We have noted that routine use of the Bradford reagent may result in difficulty forming columns with 1 ul samples.

Pedestal Reconditioning

Use the NanoDrop Pedestal Reconditioning Compound (PR-1) as a rapid means of reconditioning the pedestals when the surface properties have been compromised and liquid columns break during measurement.

1. Open the vial containing PR-1 and use the applicator provided in the kit to remove a pin-head sized amount of the compound.,

2. Apply a very thin, even layer of PR-1 to the surface of the upper and lower pedestals

3. Wait 30 seconds for the PR-1 to dry

4. Fold a clean, dry laboratory wipe into quarters and remove the PR-1 by aggressively rubbing the surface of the upper and lower pedestals until all compound residue is removed. Note: The black appearance of the removed residue is normal.

The reconditioning process is complete once the laboratory wipe shows no more black residue. To check the effectiveness of the reconditioning, load a 1 ul aliquot of dH_20 onto the lower measurement pedestals and visually verify that the water “beads” up.

As an alternative to using the PR-1 Kit, the pedestals may be reconditioned us follows:

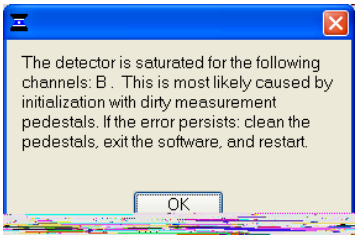
1. Fold a clean dry lab wipe over several times to increase its thickness.

2. Press the lab wipe firmly down on the lower pedestals and "buff/rub" very aggressively at least 50 times - the lab wipe will rip during this procedure and will have to be refolded several times throughout the procedure. The upper pedestals may also be buffed but care should be taken not to put too much force on the upper arm.

To check the effectiveness of the reconditioning, load a 1 ul aliquot of dH_20 onto the lower measurement pedestals and visually verify that the water “beads” up.

If the warning persists and the user visually confirms that the liquid column is forming, contact your local distributor or Technical Support for assistance.

Saturated Detector



This error message can occur when the software calculates high integration times for particular positions during initialization. This is most likely due to the presence of an air bubble or a dried sample left on the measurement surface. Cleaning both the top and bottom pedestals with de-ionized water and exiting out of the software module to the main menu should alleviate the problem. It is not necessary to close the software completely as each module is re-initialized when it is opened. If the error persists, contact your local distributor or Technical Support for assistance.

Unusual Spectrum

A sample that exhibits jagged “cuts” out of the spectrum, but an otherwise normal shape, may be the result of detector saturation. This can be caused by the software selecting too high of an integration time due to a dirty sample pedestal upon startup. Try cleaning lower and upper sample pedestals thoroughly and restarting the software. For reference, examples of spectra generated with a saturated detector are shown below.

Detector saturation- nucleic acid measurement

Detector saturation- Bradford measurement

A spectrum that is very “un-smooth” or “ragged” can be caused by insufficient light intensity reaching the spectrometer. If you suspect that this is occurring, contact your local distributor or Technical Support for assistance.