
GeneQuant™ 1300

USER MANUAL



Declaration of Conformity

This is to certify that the GeneQuant™ 1300 UV/Visible Spectrophotometers part numbers:

80-2120-00/01/02/03/04/05/06/07/08 are manufactured by Biochrom Ltd. conform to the requirements of the following Directives:-

73/23/EEC & 89/336/EEC& IVD


Standards to which conformity is declared

EN 61010-1: 2001 Safety requirements for electrical equipment for measurement, control and laboratory use.

EN 61326-2.3: 1998 Electromagnetic compatibility - generic emission standard Electrical equipment for measurement, control and laboratory use.

EN 61000-4-6: 1992 Electromagnetic compatibility - generic immunity standard part 1. Residential, commercial and light industry.

2002/96/EC This appliance is marked according to the European directive 2002/96/EC on Waste Electrical and Electronic Equipment (WEEE). By ensuring this product is disposed of correctly, you will help prevent potential negative consequences for the environment and human health, which could otherwise be caused by inappropriate waste handling of this product.

The symbol  on the product, or on the documents accompanying the product, indicates that this appliance may not be treated as household waste. Instead it shall be handed over to the applicable collection point for the recycling of electrical and electronic equipment. Disposal must be carried out in accordance with local environmental regulations for waste disposal.

RoHS Statement

EU: This device is currently exempt from the European RoHS requirements as it falls under category 9 of the Directive

China: This device does NOT fall under any categories detailed in the Chinese EIP classification list dated 16/3/2006 but for informational purposes currently is non-compliant with Chinese RoHS requirements as it contains lead based solders, but is safe for 20 years of use.

It is intended that lead free solder processes will be implemented as soon as possible

Signed:



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ESSENTIAL SAFETY NOTES

There are a number of warning labels and symbols on your instrument. These are there to inform you where potential danger exists or particular caution is required. Before commencing installation, please take time to familiarise yourself with these symbols and their meaning.



Caution (refer to accompanying documents).
Background colour yellow, symbol and outline black.

Unpacking, Positioning and Installation

- Inspect the instrument for any signs of damage caused in transit. If any damage is discovered, inform your supplier immediately.
- Ensure your proposed installation site conforms to the environmental conditions for safe operation:
 - Indoor use only.
 - Temperature range 5°C to 35°C. Note that if you use the instrument in a room subjected to extremes of temperature change during the day, it may be necessary to recalibrate (by switching off and then on again) once thermal equilibrium has been established (2-3 hours). A temperature of no more than 4°C/hour is recommended.
 - Maximum relative humidity of 80% up to 31°C decreasing linearly to 50% at 40°C
- The instrument must be placed on a stable, level bench or table that can take its weight (< 4.5 kg) so that air can circulate freely around the instrument.
- This equipment must be connected to the power supply with the power adaptor supplied. The adaptor can be used on 90 – 240 V, 50-60 Hz supplies.
- If the instrument has just been unpacked or has been stored in a cold environment, it should be allowed to come to thermal equilibrium for 2-3 hours in the laboratory before switching on. This will prevent calibration failure as a result of internal condensation.
- Switch on the instrument via the keypad () after it has been plugged in. The instrument will perform a series of self-diagnostic checks.
- Please read through this user manual prior to use.
- Please contact your original supplier in the first instance if you experience technical or sample handling difficulties.

If this equipment is used in a manner not specified or in environmental conditions not appropriate for safe operation, the protection provided by the equipment may be impaired and instrument warranty withdrawn.

INTRODUCTION

Your spectrophotometer

Your spectrophotometer is a simple-to-use UV/Visible instrument with twin CCD array detectors (1024 pixels). It has no moving parts, which is the basis of the rapid scanning operating system.

The user interface is built around folders which are displayed on the home page when the instrument is switched on. After switch on and calibration, the default home page is "GeneQuant™ 1300" offering the choice of:

| | |
|--------------|--|
| Life Science | Standard Life Science methods such as nucleic acid assays, protein assays and cell counting |
| Applications | General spectroscopic methods |
| Favourites | A folder to store your more frequently used configured methods |
| Methods | Contains nine folders that can store less frequently used configured methods (nine methods per folder) |
| Utilities | Instrument set up (date, time, language, etc) and games |

The instrument is supplied with a program PVC (Print via Computer) on the accompanying CD. When used with a USB cable to connect to a PC onto which the software has been installed, it enables the user to "print through" the PC directly to the printer that is connected to it. The data may also be stored as an Excel spreadsheet, as an EMF graphics file, a comma delimited (csv) data file, a tab delimited (txt) data file or in native PVC format for later access

Alternatively, results may be sent to the PC via a Bluetooth accessory; this can either be supplied pre-installed or is available as an optional accessory if the need for its use arises after installation of the product. PVC works in a similar way.

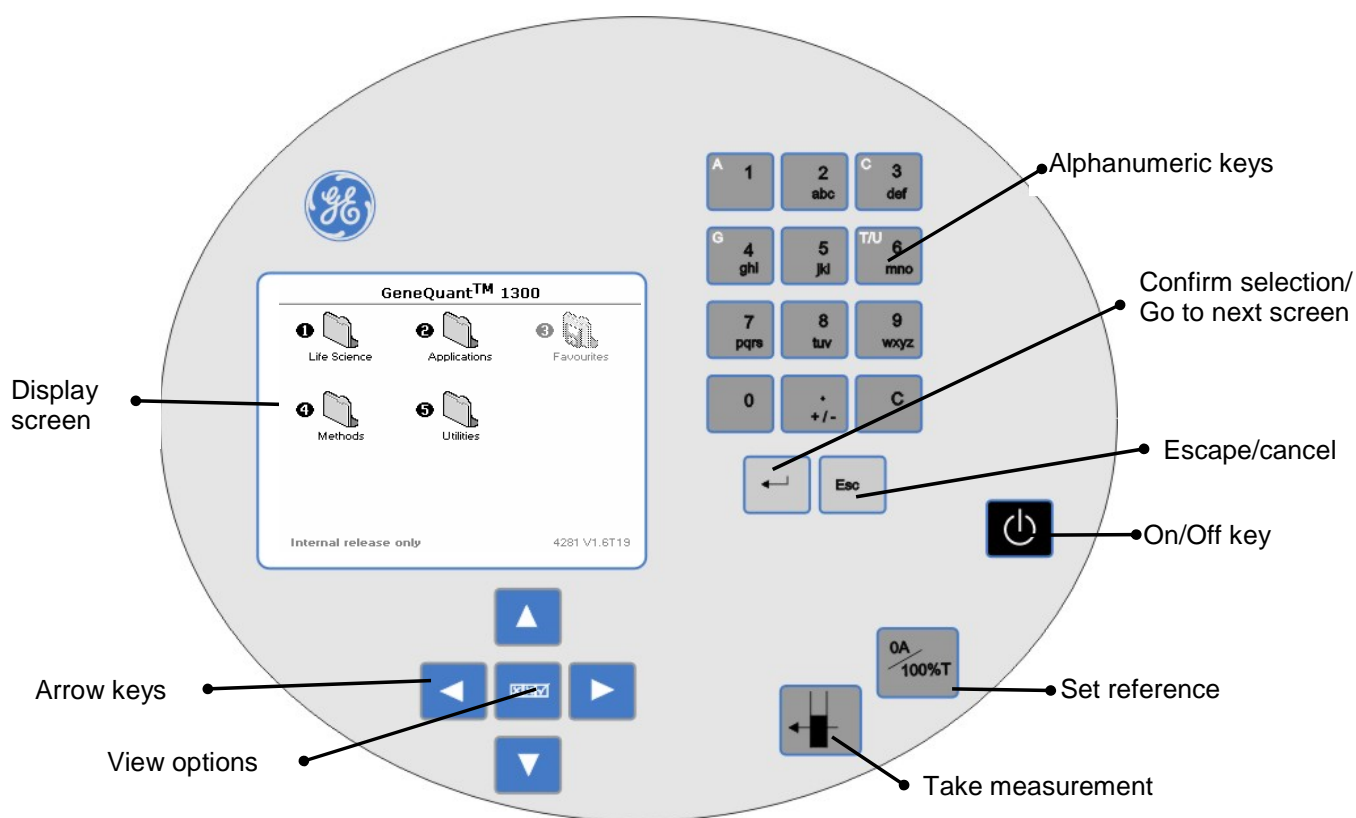
A printer is available for the instrument; this may either be supplied pre-installed or is available as an optional accessory if the need for its use arises after installation of the product.

Sample handling tips

- Note that the light beam is directed from RIGHT to LEFT through the cell chamber; therefore please ensure the cell is inserted in the correct alignment.
- The cell holder supplied with the instrument accepts standard 10 mm pathlength quartz, glass or plastic cells.
- The optical height is 15 mm, and the minimum volume that can be used is approx. 10µl in a Quartz ultra-micro cell.
- 12 mm test tubes may be used (e.g. for cell cultures), however they are not recommended as higher quality data is produced by using disposable cuvettes for the analysis. If used, align the indicator line on 12 mm test tubes in the same direction to ensure reproducible positioning of the tube. Note that test tubes do not last forever, and that the surface becomes scratched and blemished through repetitive use; if this is the case they should be replaced.

Keypad and display

The back-lit liquid crystal display is very easy to navigate around using the alphanumeric entry and navigation arrow keys on the hard wearing, spill proof membrane keypad.



Key

Action

On/off key

Turns the instrument on/off

Arrow keys

Use the four arrow keys to navigate around the display and select the required setting from the active (highlighted) option.

View Options:   

View options for that application mode. Some of these are common to all applications and described below. Options unique to an application are described in the relevant section.

Alphanumeric keys

Use these to enter parameters and to write text descriptions where appropriate, or required. Use repeated key presses to cycle through lower case, number and upper case. Leave for 1 second before entering next character. Use C button to backspace and 1 to enter a space.

Escape

Escape from a selection and return to the previous folder.

Set Reference: 0A/100%T

Set reference to 0.000 A or 100%T on a reference solution at the current wavelength in the mode selected. When in scan mode, make a reference scan.

OK/Next: 

Enter or confirm a selection.



Take a measurement.



Options (select using key pad numbers)

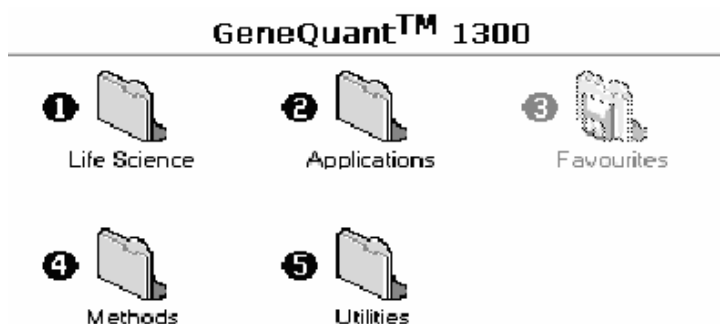
1. View parameters for the experiment.
2. Print the results.
- 3,4,5,6 Described in the application.
7. Define the sample number you wish to start from.
8. Save the parameters as a method to a defined folder name with a defined method name.
9. Toggle auto-print on/off. Default is off.

Exit options by pressing Esc, or wait.






Experienced operators can use the numeric keys as a shortcut to the option required without needing to enter the Options menu.

Software style

The user interface is built around having folders of files which are displayed on the home page when the instrument is switched on. Different folders are numbered and opened by using the associated number key on the keypad.

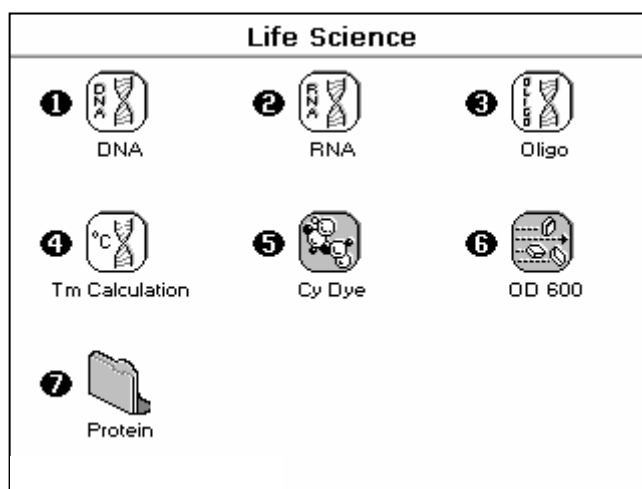


4281 V1.6T19

| Summary Function | Keypad number | Description |
|---|---------------|---|
|  Life Science | 1 | Nucleic acids, Proteins and Cell counting |
|  Applications | 2 | Single wavelength, Concentration, Wavelength scan, Kinetics, Standard Curve, Multiple wavelengths and Ratio |
|  Favourites | 3 | Sub-folder for favourite user selected and configured methods |
|  Methods | 4 | Nine further sub-folders for configured methods |
|  Utilities | 5 | Instrument set up (date, time, language, etc) and games |

LIFE SCIENCE FOLDER

This contains seven applications/subfolders. Contents of these applications/subfolders are detailed below:



| Application | Keypad number | Function |
|----------------|---------------|--|
| DNA | 1 | Concentration and purity check for DNA samples |
| RNA | 2 | Concentration and purity check for RNA samples |
| Oligo | 3 | Concentration and purity check for Oligo samples |
| TM Calculation | 4 | DNA melting point calculator |
| CyDye | 5 | Labeling efficiency measurement |
| OD 600 | 6 | Cell culture OD600 with correction factor |
| Protein | 7 | Folder containing 5 methods of protein determination |

DNA, RNA and oligonucleotide characterisation

Nucleic Acid Quantification (NAQ)

- Nucleic acids can be quantified at 260 nm because it is well established that a solution of DNA in a 10 mm pathlength cell with an optical density of 1.0 has a concentration of 50, or 40 µg/ml in the case of RNA. Oligonucleotides have a corresponding factor of 33 µg/ml, although this does vary with base composition; this can be calculated if the base sequence is known.
Concentration = Abs₂₆₀ * Factor

- The instrument uses factors 50, 40 and 33 as defaults for DNA, RNA and oligonucleotides, respectively, and compensates for dilution and use of cells which do not have 10 mm pathlength; dilution factor and cell pathlength can be entered.

•

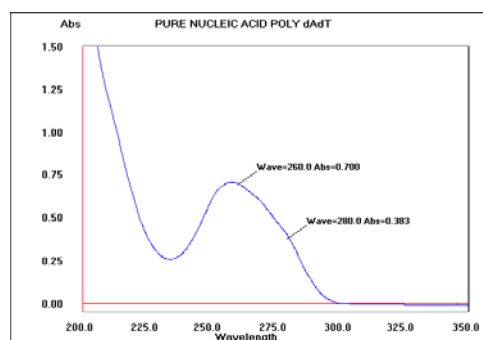
Nucleic Acid Purity Checks

- Nucleic acids extracted from cells are accompanied by protein, and extensive purification is required to separate the protein impurity. The 260/280 ratio gives an indication of purity; it is only an indication, however, and not a definitive assessment. Pure DNA and RNA preparations have expected ratios of ≥ 1.8 and ≥ 2.0 , respectively; deviations from this indicate the presence of impurity in the sample, but care must be taken in interpretation of results.
- The 260 nm reading is taken near the top of a broad peak in the absorbance spectrum for nucleic acids, whereas the 280 nm reading is taken on a steep slope (i.e. small changes in wavelength cause large changes in absorbance). Consequently, small variations in wavelength at 280 nm will have a greater effect on the 260/280 ratio than variations will at 260 nm. Thus different instruments of the same and different types may give slightly different ratios due to variations in wavelength accuracy. But each instrument will give consistent results within itself.
- Concentration also affects 260/280 readings. If a solution is too dilute, the readings will be at the instrument's detection limit, and results may vary as there is less distinction of the 260 peak and 280 slope from the background absorbance. This is one reason why the Abs₂₆₀ value should be greater than 0.1 for accurate measurements.
- An elevated absorbance at 230 nm can indicate the presence of impurities as well; 230 nm is near the absorbance maximum of peptide bonds and also indicates buffer contamination since This, EDTA and other buffer salts absorb at this wavelength. When measuring RNA samples, the 260/230 ratio should be > 2.0 ; a ratio lower than this is generally indicative of contamination with guanidinium thiocyanate, a reagent commonly used in RNA purification and which absorbs over the 230 - 260 nm range. A wavelength scan of the nucleic acid is particularly useful for RNA samples.
- The instrument can display 260/280 and 260/230 ratios, and compensates for dilution and use of cells that do not have 10 mm pathlength; dilution factor and cell pathlength can be entered.

Use of Background Correction

- Background correction at a wavelength totally separate from the nucleic acid and protein peaks at 260 and 280 nm, respectively, is sometimes used to compensate for the effects of background absorbance. The wavelength used is 320 nm and it can allow for the effects of turbidity, high absorbance buffer solution and the use of reduced aperture cells. The instrument can use background correction.
- If it is used, there will be different results from those when unused, because Abs₃₂₀ is subtracted from Abs₂₆₀ and Abs₂₈₀ prior to use in equations:
Concentration = (Abs 260 - Abs 320) * Factor
Abs ratio = (Abs 260 - Abs 320) / (Abs 280 - Abs 320)
Abs ratio = (Abs 260 - Abs 320) / (Abs 230 - Abs 320)
- If your laboratory has not used background correction before, set this option to NO.
- The use of background correction can remove variability due to handling effects of low volume disposable cells.

Spectral scan of nucleic acid



Note:

- absorbance maximum near 260 nm and absorbance minimum near 230 nm
- flat peak near 260 nm and steep slope at 280 nm
- very little absorbance at 320 nm

Operation of the instrument for Nucleic Acid measurements is described in the following sections

DNA and RNA are very similar, whilst in Oligo it is possible to calculate the factor from the composite bases by entering the proportions of the 4 bases.

1: DNA

The procedure is as follows:

DNA - Parameters

| | |
|-----------------|--------|
| Pathlength | Units |
| 10 mm | µg/ml |
| Dilution Factor | Factor |
| 1.000 | 50.0 |
| Background | |
| Off | |
| OK | Cancel |

DNA - Parameters

Dilution Factor

| | |
|--------|---------|
| Volume | Diluent |
| 1.000 | 0.000 |
| OK | Cancel |

DNA

| | | | |
|-----------|---------|---------------|-------|
| A230 | 0.089 A | Sample | 1 |
| A260 | 0.258 A | | |
| A280 | 0.167 A | | |
| A260/A280 | | Concentration | 12,9 |
| 1.54 | | | |
| A260/A230 | | Units | µg/ml |
| 2.90 | | | |

Step 1

Press 1 to select DNA mode.

Step 2

Select path length using the left and right arrows. Options are 5 or 10 mm.

Press the down arrow.

Step 3 (dilution factor known)

Enter the dilution factor using the keypad numbers. Range 1.00 to 9999. Use the C button to backspace and clear the last digit entered.

OR

Step 3 (calculate dilution factor)

Press to enter the dilution factor screen (see second parameter screen to the left).

Enter the volume of the sample using the keypad numbers. Range 0.01 to 9999.

Press the down arrow.

Enter the volume of the diluent using the keypad numbers. Range 0.01 to 9999.

Press OK to calculate the dilution factor and return to the Parameters screen.

OR Press Cancel to cancel the selections and return to the Parameters screen.

Step 4

Select whether the background correction at 320 nm is used or not with the left and right arrows.

Press the down arrow.

Step 5

Select the units of measurement using the left and right arrows. Options: µg/ml, ng/µl, µg/µl.

Press the down arrow.

Step 6

Enter the factor using the keypad numbers. Default value is 50, range is 0.01 to 9999.

Step 7

Press OK to enter the Results screen and begin taking measurements.

OR to return to the Life Science folder.

Results Screen

Step 8

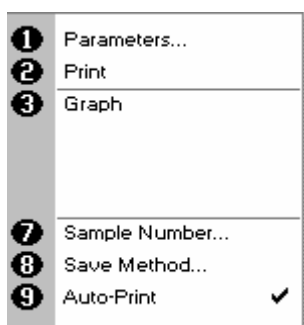
Insert the reference sample. Press 0A/100%T Key. This will be used for all subsequent samples until changed.

Step 9


Insert sample and press . This measures at the selected wavelengths and displays the results. The ratio of wavelengths 1 and 2 absorbencies are calculated (both corrected by the background wavelength value if selected). Gives concentration based on absorbance at wavelength 1. Repeat step 9 for all samples.

Press to return to the Life Science folder.

Press to display available Options which are described below.



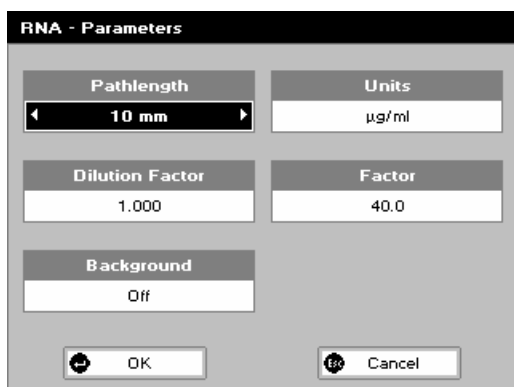
Options (select using key pad numbers)

1. Return to parameters screen (step 1 above).
2. Print result via selected method.
3. Toggle graph on/off. The graph shows a wavescan plot across the range 220 nm to 320 nm with cursors denoting 230, 260, 280 and (if background correction selected) 320 nm.
7. Sample number – add a prefix to the sample number and reset the incrementing number to the desired value.
8. Save method – use the alpha-numeric keys to enter a name for the method and press Save .
9. Auto-print – toggles auto-print on/off.

Exit options by pressing  or wait.

2: RNA

The procedure is as follows:



The 'RNA - Parameters' screen displays several settings. At the top, 'Pathlength' is set to '10 mm' with left and right arrow buttons. To its right, 'Units' is set to 'µg/ml'. Below 'Pathlength', 'Dilution Factor' is set to '1.000'. To its right, 'Factor' is set to '40.0'. Below 'Dilution Factor', 'Background' is set to 'Off'. At the bottom, there are 'OK' and 'Cancel' buttons.

Step 1

Press 2 to select RNA mode.

Step 2

Select path length using the left and right arrows. Options are 5 or 10 mm.


Press the down arrow.

Step 3 (dilution factor known)

Enter the dilution factor using the keypad numbers. Range 1.00 to 9999. Use the C button to backspace and clear the last digit entered.

OR


Step 3 (calculate dilution factor)


Press  to enter the dilution factor screen (see second image to the left).

Enter the volume of the sample using the keypad numbers. Range 0.01 to 9999.

Press the down arrow.

Enter the volume of the diluent using the keypad numbers. Range 0.01 to 9999.

Press OK  to calculate the dilution factor and return to the Parameters screen.

OR Press  to cancel the selections and return to the Parameters screen.

Step 4

Select whether the background correction at 320 nm is used or not with the left and right arrows.

Press the down arrow.

Step 5


Select the units of measurement using the left and right arrows. Options: µg/ml, ng/µl, µg/µl.


Press the down arrow.

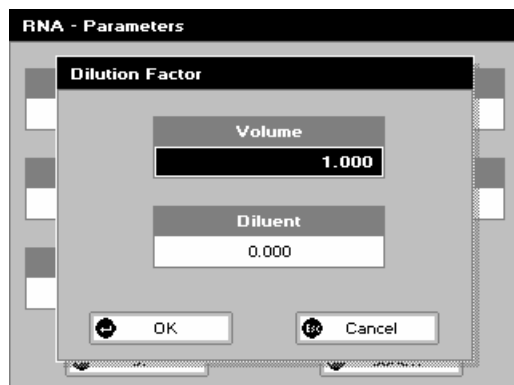
Step 6

Enter the factor using the keypad numbers. Default value is 40, range is 0.01 to 9999.

Step 7

Press OK  to enter the Results screen and start taking measurements

OR  to return to the Life Science folder.




The 'Dilution Factor' screen is a sub-screen of the RNA parameters. It has a 'Volume' field set to '1.000' and a 'Diluent' field set to '0.000'. At the bottom, there are 'OK' and 'Cancel' buttons.


Results Screen


Step 8

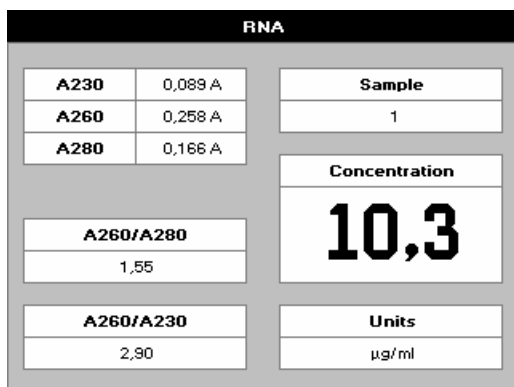
Insert the reference sample. Press 0A/100%T Key. This will be used for all subsequent samples until changed.

Step 9

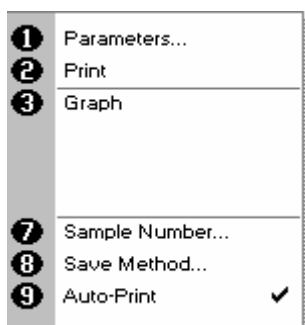
Insert sample and press . This measures at the selected wavelengths and displays the results. The ratio of wavelengths 1 and 2 absorbencies are calculated (both corrected by the background wavelength value if selected). Gives concentration based on absorbance at wavelength 1. Repeat step 9 for all samples.

Press  to return to the Life Science folder.


Press  to display available Options which are described below.




The 'RNA' results screen displays a table of absorbance readings. The table has two columns: Wavelength (A230, A260, A280) and Absorbance (0.089 A, 0.258 A, 0.166 A). To the right of the table is a 'Sample' field set to '1'. Below the table is a 'Concentration' field set to '10.3'. At the bottom, there are 'A260/A280' and 'A260/A230' ratio fields set to '1.55' and '2.90' respectively, and a 'Units' field set to 'µg/ml'.



Options (select using key pad numbers)

1. Return to parameters screen (step 1 above).
2. Print result via selected method.
3. Toggle graph on/off. The graph shows a wavescan plot across the range 220 nm to 320 nm with cursors denoting 230, 260, 280 and (if background correction selected) 320 nm.
7. Sample number – add a prefix to the sample number and reset the incrementing number to the desired value.
8. Save method – use the alpha-numeric keys to enter a name for the method and press Save .
9. Auto-print – toggles auto-print on/off.

Exit options by pressing , or wait.

3: Oligo

The procedure is as follows:

Step 1

Press 3 to select Oligo mode.

Step 2

Select path length using the left and right arrows. Options are 5 or 10 mm.

Press the down arrow.

Step 3 (dilution factor known)

Enter the dilution factor using the keypad numbers. Range 1.00 to 9999. Use the C button to backspace and clear the last digit entered.

OR

Step 3 (calculate dilution factor)

Press $\boxtimes\boxtimes\boxtimes$ to enter the dilution factor screen.

Enter the volume of the sample using the keypad numbers. Range 0.01 to 9999.

Press the down arrow.

Enter the volume of the diluent using the keypad numbers.

Range 0.01 to 9999.

Press OK \leftarrow to calculate the dilution factor and return to the Parameters screen.

OR Press **Esc** to cancel the selections and return to the Parameters screen.

Step 4

Select whether the background correction at 320 nm is used or not with the left and right arrows.

Press the down arrow.

Step 5

Select the units of measurement using the left and right arrows. Options: $\mu\text{g/ml}$, $\text{ng}/\mu\text{l}$, $\mu\text{g}/\mu\text{l}$ and $\text{pmol}/\mu\text{l}$. If $\text{pmol}/\mu\text{l}$ is selected the factor changes to a selection table denoting the ratios of the 4 bases in the structure.

Press the down arrow.

Step 6 (units not $\text{pmol}/\mu\text{l}$)

Enter the factor using the keypad numbers. Default value is 33, range is 0.01 to 9999.

OR

Step 6 (units $\text{pmol}/\mu\text{l}$)

Enter the proportions of bases present using the keypad numbers and up and down arrows to move between boxes. Default is 10 for each, range is 0 to 9999.

Step 7

Press OK \leftarrow to enter the Results screen and start taking measurements

OR

Esc to return to the Life Science folder.

| Oligo | | |
|-----------|---------|------------------------------|
| A230 | 0,089 A | Sample 1 |
| A260 | 0,258 A | |
| A280 | 0,167 A | |
| A260/A280 | | Concentration 0,60 |
| 1,54 | | |
| A260/A230 | | Units pmol/μl |
| 2,90 | | |

Results Screen

Step 8

Insert the reference sample. Press 0A/100%T Key. This will be used for all subsequent samples until changed.

Step 9



Insert sample and press . This measures at the selected wavelengths and displays the results. The ratio of wavelengths 1 and 2 absorbencies are calculated (both corrected by the background wavelength value if selected). Gives concentration based on absorbance at wavelength 1.

Repeat step 9 for all samples.

Press to return to the Life Science folder

Press to display available Options which are described below.

| | |
|---|------------------|
| 1 | Parameters... |
| 2 | Print |
| 3 | Graph |
| | |
| 7 | Sample Number... |
| 8 | Save Method... |
| 9 | Auto-Print |

Options (select using key pad numbers)

1. Return to parameters screen (step 1 above).
2. Print result via selected method.
3. Toggle graph on/off. The graph shows a wavescan plot across the range 220 nm to 320 nm with cursors denoting 230, 260, 280 and (if background correction selected) 320 nm.
7. Sample number – add a prefix to the sample number and reset the incrementing number to the desired value.
8. Save method – use the alpha-numeric keys to enter a name for the method and press Save .
9. Auto-print – toggles auto-print on/off.

Exit options by pressing , or wait.

4. *T_m* Calculation

This utility calculates the theoretical melting point from the base sequence of a primer. It is done using nearest neighbour thermodynamic data for each base in the nucleotide chain in relation to its neighbour (Breslauer et al, Proc.Natl. Acad. Sci. USA Vol 83, p3746 1986). The data obtained are useful both in characterization of oligonucleotides and in calculating *T_m* for primers used in PCR experiments.

The ACGT/U sequence entered into the utility is used to calculate the theoretical *T_m*, the theoretical absorbance (Absorption units/μmol) and the conversion factor (μg/ml). This is because the stability of a bent and twisted sequence of bases such as an oligonucleotide is dependent on the actual base sequence; the calculated thermodynamic interactions between adjacent base pairs have been shown to correlate well with experimental observations.

This utility uses matrices of known, published thermodynamic values and extinction coefficients to calculate *T_m* and the theoretical absorbance/factor respectively of an entered base sequence.

T_m

This is calculated using the equation:-

$$T_m = \frac{\Delta H \times 100}{\Delta S + [1.987 \times \log_e(c/4 + 53.0822)]} - 273.15 + 16.6 \log [\text{salt}]$$

where *ΔH* and *ΔS* are the enthalpy and entropy values summed from respective 2x4x4 nearest neighbour matrices

c is the Primer concentration of oligonucleotide (pmoles/μl) in the calculated *T_m* or the measured concentration in measured *T_m*. In the latter case concentration is obtained from the equation:

$$c = \frac{\text{Abs}(260\text{nm}) \times \text{calculated factor} \times \text{pathlength multiplier} \times 10000}{\text{Calculated MW}}$$

Calculated factor and MW are defined below

[salt] is the buffer molarity plus total molarity of salts in the hybridization solution (moles/l)

Weights for *ΔS* are indexed by adjacent paired bases.

A similar equation applies to Weights for *ΔH*, again indexed by adjacent bases.

Note that bivalent salts may need normalizing using a multiplying factor of 100 because of their greater binding power

Theoretical Absorbance

The Theoretical Absorbance is based on a calculation as follows:

For each adjacent pair of bases (nearest neighbours) an extinction coefficient weight is accumulated using a 4x4 table (one for either DNA or RNA). This total weight is then doubled. Then for each internal base a counterweight is subtracted using another 1x 4 table. The end bases are excluded from the latter summation

That is:

$$\text{Total Extinction Coefficient } E = \sum (2 \times aTable[\text{base_type}][\text{base}(n)][\text{base}(n+1)]) - \sum (tTable[\text{base_type}][\text{base}(n)])$$

Conversion factor

The Conversion Factor is given by
$$= \frac{\text{Molecular weight}_{ABCDE}}{\sum E_{ABCDE}}$$

where

$$E_{ABCDE} = [2 \times (E_{AB} + E_{BC} + E_{CD} + E_{DE}) - E_B - E_C - E_D]$$

- The molecular weight (MW) of a DNA oligonucleotide is calculated from:

- $$\text{MW (g/mole)} = [(dA \times 312.2) + (dC \times 288.2) + (dG \times 328.2) + (dT \times 303.2)] + [(\text{MW counter-ion}) \times (\text{length of oligo in bases})]$$

(for RNA oligonucleotide, (dT x 303.2) is replaced by (dU x 298.2))

The MW calculated using this equation must be adjusted for the contribution of the atoms at the 5' and 3' ends of the oligo.

For phosphorylated oligos: add: [17 + (2 x MW of the counter-ion)]

For non-phosphorylated oligos: subtract: [61 + (MW of the counter-ion)]

The MW (g/mole) of the most common oligo counter-ions are

| | |
|-------------------------|-------|
| Na (sodium) | 23.0 |
| K (potassium) | 39.1 |
| TEA (triethylammonium), | 102.2 |
| Other | 1 |

Calculated molecular weight: a weight is added for each base looked up from a table. The weight of the counter ion is added for every base from a small table for the known ions. If phosphorylated then the system adds 17.0 plus two counter ions otherwise it subtracts 61.0 and one ion.

Theoretical Absorbance: For each adjacent pair of bases (nearest neighbours) a weight is accumulated using a table. For each internal base a weight is subtracted using another table. Separate tables are used for DNA and RNA.

Calculated factor: This is just the calculated molecular weight divided by the theoretical absorbance.

Tm Calculation - Parameters

| | |
|-----------------------|--------------------------|
| Base Type DNA | Buffer Molarity 0.100 |
| Phosphorylated No | Counter Ion Na |
| Primer Conc. 1.000 | |

Next Cancel

Tm Calculation - Parameters

| | |
|-----------------------|--------------------------|
| Base Type DNA | Buffer Molarity 0.100 |
| Phosphorylated No | Counter Ion Other |
| Primer Conc. 1.000 | Other MW 1.0 |

Next Cancel

Tm Calculation - Base Sequence

Pathlength
10 mm

Base Sequence

OK Back

Tm Calculation - Base Sequence

Pathlength
10 mm

Base Sequence
AGC,AAG,ACT

OK Back

Step 1

Press 4 to enter the Tm Calculation parameters screen.

Step 2

Select the base type: DNA or RNA.

Press the down arrow.

Step 3

Select whether the sample is phosphorylated or not: yes or no.

Press the down arrow

Step 4

Enter the primer concentration using the keypad numbers.

Range 0.000 to 99.9

Press the down arrow.

Step 5

Enter the buffer molarity using the keypad numbers.

Range 0.000 to 10

Press the down arrow.


Step 6

Select the counter ion: Na, K, TEA or Other.

Step 7 (if Other selected)

Enter the molecular weight of the counter ion used.

Step 8

Press Next  to select these parameters and go on to the Base Sequence screen

OR

Press Cancel  to return to the Life Science folder.

Step 9


Select the pathlength of the sample cells: 5 or 10 mm.

Press the down arrow


Step 10

Enter the known base sequence triplets using the number keys:
1 for A, 3 for C, 4 for G and 6 for T or U.

Step 11

Press OK  to select these parameters and start to measure Tm

OR

Press Cancel  to return to the Parameters screen.


| Tm Calculation | |
|--------------------------|----------------------|
| 260 nm | Sample |
| 0.130 A | 1 |
| Theoretical Abs | Measured Tm |
| 115.1 | 44.1 |
| Calculated MW | |
| 3887.4 | |
| Calculated Factor | Calculated Tm |
| 33.8 | 44.4 °C |

Results Screen


Step 12


Insert the reference sample. Press 0A/100%T Key. This will be used for all subsequent samples until changed.


Step 13

Insert sample and press . The unit measures the absorbance and uses this information to calculate the Measured Tm.


Repeat step 13 for all samples.


Press  to return to the Life Science folder

Press  to display available Options which are described below.

| | |
|----------|--|
| 1 | Parameters... |
| 2 | Print |
| <hr/> | |
| 7 | Sample Number... |
| 8 | Save Method... |
| 9 | Auto-Print  |

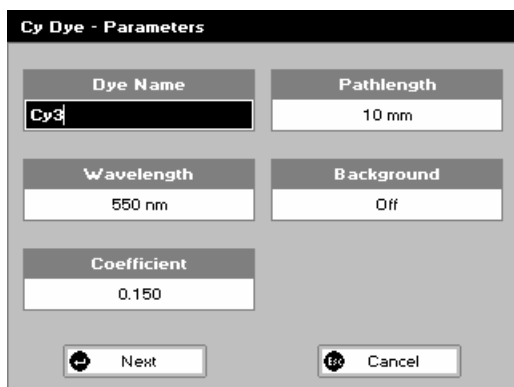
Options (select using key pad numbers)

1. Return to parameters screen (step 1 above).
2. Print result via selected method.
7. Sample number – add a prefix to the sample number and reset the incrementing number to the desired value.
8. Save method – use the alpha-numeric keys to enter a name for the method and press Save .
9. Auto-print – toggles auto-print on/off.

Exit options by pressing , or wait.

5. Cy dye

Measurement of the labelling efficiency of fluorescently labelled cDNA probes before 2-colour microarray hybridisation ensures that there is sufficient amount of each probe to give satisfactory hybridisation signals. These data also provides an opportunity to balance the relative intensities of each fluorescent dye by adjusting the concentration of each probe before hybridisation. The cDNA yield is measured at 260 nm while the incorporation of fluorescein, Cy3 and Cy5 are measured at their absorption peaks. This method may also be useful for measuring the yields and brightness of fluorescently labelled *in-situ* hybridisation probes.



Step 1

Press 5 to enter the Cy dye parameter screen

Step 2

Enter the name of the dye being used, the default is Cy3, but others may be generated using the Clear key C and the alphanumeric keypad

Press the down arrow

Step 3

Enter the wavelength of the dye peak absorbance.

Press the down arrow

Step 4

Enter the dye coefficient of extinction.

Press the down arrow

Step 5

Enter the pathlength of the sample cell: 5 or 10 mm.

Press the down arrow

Step 6

Select whether background correction is on or off.

Step 7

Press Next  to enter the settings screen

OR




Press Cancel  to return to the Life Sciences folder.


Step 8 (dilution factor known)


Enter the dilution factor using the keypad numbers. Range 1.00 to 9999. Use the C button to backspace and clear the last digit entered.

OR

Step 8 (calculate dilution factor)

Press    to enter the dilution factor screen (see second image to the left). Enter the volume of the sample using the keypad numbers. Range 0.01 to 9999. Press the down arrow. Enter the volume of the diluent using the keypad numbers. Range 0.01 to 9999.

Press OK  to calculate the dilution factor and return to the Parameters screen.

OR Press  to cancel the selections and return to the Parameters screen.

Step 9

Enter the conversion factor using the keypad numbers. Press the down arrow

Step 10

Enter the volume of the probe in μ l

Press the down arrow


Step 11


Enter the amount of starting RNA in ng. Maximum 99999 ng.

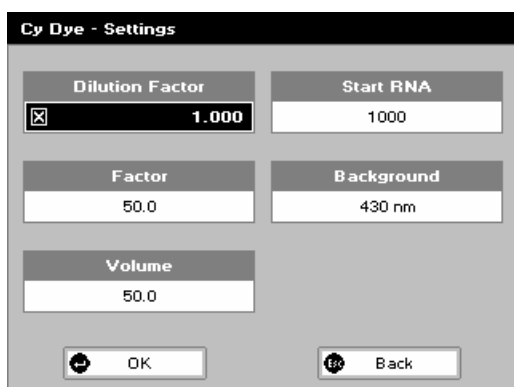
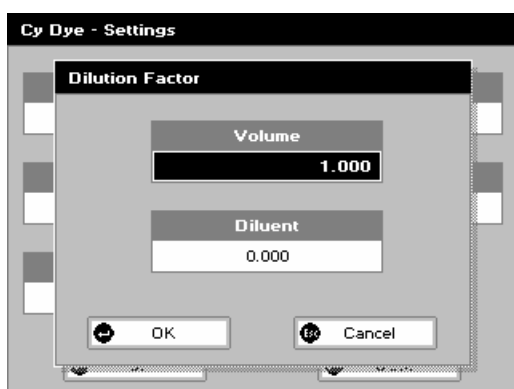
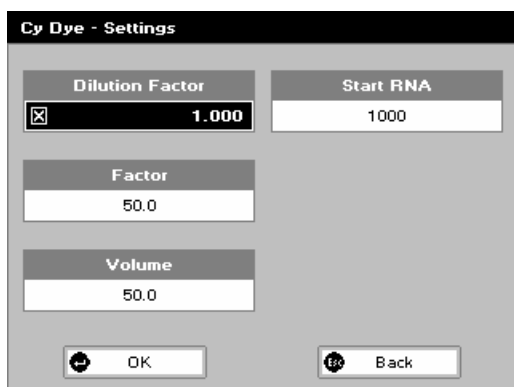
Step 12 (if background correction is on)

Enter the background correction wavelength if required

Step 13

Press OK  to select these settings and start to measure

OR Press Cancel  to cancel the settings and return to the parameters screen.



| Cy Dye | | |
|---|---------|-------------------------------|
| A230 | 0.045 A | Sample 1 |
| A260 | 0.130 A | |
| A280 | 0.084 A | |
| Adye | 0.136 A | |
| A260/A230 2.889 A260/A280 1.548 Adye/A260 1.046 | | Concentration 6.500 |
| | | Units ng/μl |

Results Screen

Step 14


Insert the reference sample. Press 0A/100%T Key. This will be used for all subsequent samples until changed.


Step 15

Insert sample and press . The system returns the dye concentration.


Repeat step 15 for all samples.

Press **Esc** to return to the Life Science folder

Press  to display available Options which are described below.

| | |
|---|---|
| 1 | Parameters... |
| 2 | Print |
| 3 | Graph |
| 4 | Results  |
| 7 | Sample Number... |
| 8 | Save Method... |
| 9 | Auto-Print |

Options (select using key pad numbers)

- Return to parameters screen (step 1 above).
- Print result via selected method.
- Toggle graph on/off. The graph shows the spectral scan of the dye sample over the wavelength range of interest
- Toggle results on/off. When off the results screen shows the absorbance values and absorbance ratios. When on the results screen shows the total DNA, DNA Yield, nucleotides and number of dyes/probe. This only functions if the graph display is off (see below)
- Sample number – add a prefix to the sample number and reset the incrementing number to the desired value.
- Save method – use the alpha-numeric keys to enter a name for the method and press Save .
- Auto-print – toggles auto-print on/off.

Exit options by pressing **Esc**, or wait.

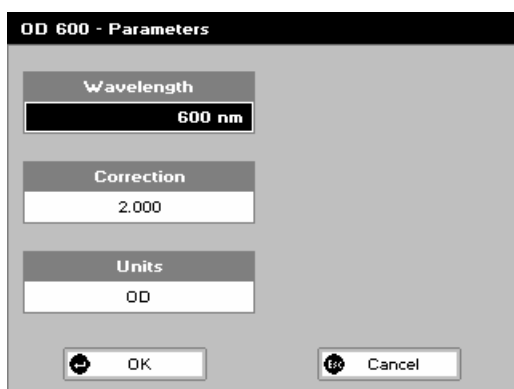
| Cy Dye | |
|------------------------|------------------------------|
| Total DNA 645 | Sample 2 |
| DNA Yield 64.5 | Concentration 12.9 |
| Nucleotides 22.2 | |
| Dye Per Probe 1.793 | Units ng/μl |

Results screen with option 4 On

6. Bacterial Cell Culture Measurement (OD600)

- Bacterial cell cultures are routinely grown until the absorbance at 600 nm (known as OD600) reaches approximately 0.4 prior to induction or harvesting. A linear relationship exists between cell number (density) and OD 600 up to approx. 0.6.
- It is important to note that for turbid samples such as cell cultures, the absorbance measured is due to light scattering, and **not** the result of molecular absorption. The amount of scatter is affected by the optics of the system (distance between the cell holder and instrument exit slit, geometry of this slit and the monochromator optics). Different spectrophotometer types therefore give different responses for the same turbid sample; to compare results, they must be normalised using calibration curves.
- A calibration curve can be determined by comparing measured OD 600 to expected OD 600. Expected OD 600 is determined by counting cell number using an alternative technique (for example microscope slide method) and converting to OD 600 using the rule of thumb that 1 OD 600 = 8×10^8 cells/ml for E. Coli.
- Your GeneQuant instrument has much smaller optics than most conventional spectrophotometers, and more light is transmitted through to the detector resulting in lower than expected OD 600 values. Results obtained by comparing measured OD 600 with expected OD 600 (see above) indicate that a correction factor of 2.0 is required to make the data comparable to larger instruments; this factor is included as a default value in set up.
- The use of 10 mm pathlength disposable cells is recommended for optical density measurements of cell culture solutions; to prevent the suspension settling too quickly and giving an OD that changes with time, glycerol should be added to the sample.

The procedure is as follows



Step 1

Press 6 to select OD600 mode.

Step 2

Select the wavelength using either arrow or alphanumeric keys. Default value is 600 nm.

Press the down arrow.

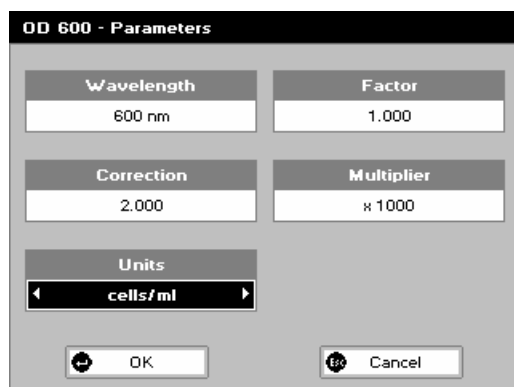
Step 3

Enter the correction factor to compensate for different optical configurations between this and other instruments. Default value is 2.

Press the down arrow.

Step 4

Select the units. Options are OD or cells/ml. If cells/ml is selected two further parameters are displayed.



Step 5 (if cells/ml selected)

Enter the factor using the keypad numbers. Range 0.00 to 9999. C button backspaces and clears the last digit entered.

Press the down arrow.


Step 6 (if cells/ml selected)

Select the multiplier using the left and right arrows. Options are 1000 or 1,000,000.

Step 7

Press OK  to enter the Results screen

OR

Press Cancel  to cancel selections and return to the Life Science folder.

| OD 600 | |
|------------------------------|--------------------------------|
| Wavelength 600 nm | Sample 1 |
| Absorbance 0,002 A | cells/ml 1,40 |
| Multiplier x 1000 | |

Results Screen

Step 8


Insert the reference and press the 0A/100%T key. This will be used for all subsequent samples until changed.




Step 9


Insert the sample and press .

The wavelength, absorbance and OD600 value is displayed.


Repeat step 9 for all samples.


Press  to return to the Life Science folder.

Press    to display available Options which are described below.

| | |
|----------|--|
| 1 | Parameters... |
| 2 | Print |
| <hr/> | |
| 7 | Sample Number... |
| 8 | Save Method... |
| 9 | Auto-Print  |

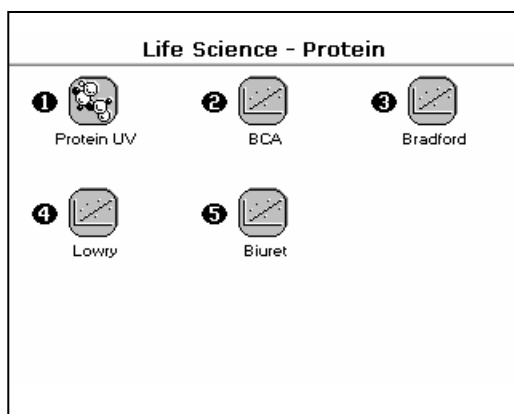
Options (select using key pad numbers)

1. Return to parameters screen (step 1 above).
2. Print result via selected method.
7. Sample number – add a prefix to the sample number and reset the incrementing number to the desired value.
8. Save method – use the alpha-numeric keys to enter a name for the method and press Save .
9. Auto-print – toggles auto-print on/off.

Exit options by pressing , or wait.

7. Protein Determination

The GeneQuant™ 1300 includes five methods for assaying proteins. Press 7 to enter the protein folder.



Protein Determination at 280 nm

Protein can be determined in the near UV at 280 nm due to absorption by tyrosine, tryptophan and phenylalanine amino acids; Abs 280 varies greatly for different proteins due to their amino acid content, and consequently the specific absorption value for a particular protein must be determined.

- The presence of nucleic acid in the protein solution can have a significant effect due to strong nucleotide absorbance at 280 nm. This can be compensated by measuring Abs 260, and applying the equation of Christian and Warburg for the protein crystalline yeast enolase (Biochemische Zeitung 310, 384 (1941)):
$$\text{Protein (mg/ml)} = 1.55 * \text{Abs 280} - 0.76 * \text{Abs 260}$$

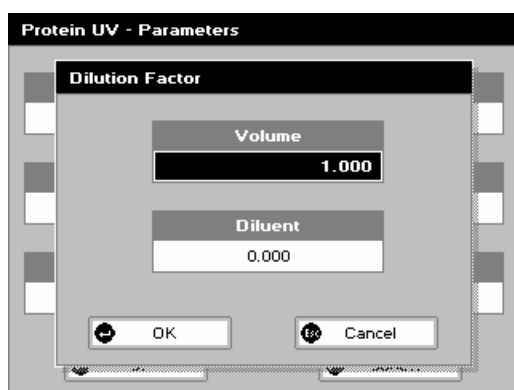
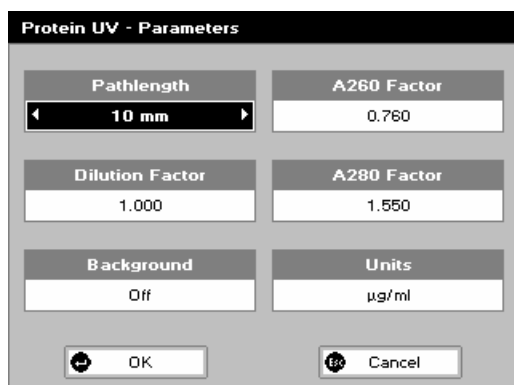
or, Protein conc. = (Factor 1 * Abs 280) - (Factor 2 * Abs 260)
- This equation can be applied to other proteins if the corresponding factors are known. The instrument can determine protein concentration at 280 nm and uses the above equation as default; the factors can be changed, and the use of background correction at 320 nm is optional.
- To customise the equation for a particular protein, the absorbance values at 260 and 280 nm should be determined at known protein concentrations to generate simple simultaneous equations; solving these provides the two coefficients. In cases where Factor 2 is found to be negative, it should be set to zero since it means there is no contribution to the protein concentration due to absorbance at 260 nm.
- Set Factor 2 = 0.00 for direct λ_{280} UV protein measurement; Factor 1 is based on the extinction coefficient of the protein. If BSA (bovine serum albumin) is an acceptable standard, setting Factor 1 = 1.115 will give linear results from 0 to 0.8 mg/ml protein.
$$\text{Protein (mg/ml)} = 1.115 * \text{Abs 280}$$
- Rapid measurements such as this at Abs 280 are particularly useful after isolation of proteins and peptides from mixtures using spin and HiTrap columns by centrifuge and gravity, respectively.

Protein Determination at 595, 546, 562 and 750 nm

- The Bradford method depends on quantitating the binding of a dye, Coomassie Brilliant Blue, to an unknown protein and comparing this binding to that of different, known concentrations of a standard protein at 595 nm; this is usually BSA, bovine serum albumin.
- The Biuret method depends on reaction between Cupric ions and peptide bonds in an alkali solution, resulting in the formation of a complex absorbing at 546 nm.
- The BCA method also depends on reaction between cupric ions and peptide bonds, but in addition combines this reaction with the detection of cuprous ions using bicinchoninic acid (BCA), giving an absorbance maximum at 562 nm. The BCA process is less sensitive to the presence of detergents used to break down cell walls.
- The Lowry method depends on quantifying the colour obtained from the reaction of Folin-Ciocalteu phenol reagent with the tyrosyl residues of an unknown protein and comparing with those derived from a standard curve of a standard protein at 750 nm; this is usually BSA, bovine serum albumin
- Detailed protocols are supplied with these assay kits, and must be closely followed to ensure accurate results are obtained.
- The use of plastic disposable cells is recommended. To use a zero concentration standard include it in the number of standards to be entered and enter 0.00 for concentration; use this when required to enter standard 1.
- A linear regression analysis of the calibration standard data points is calculated; the result, together with the correlation coefficient, can be printed out. A correlation coefficient of between 0.95 and 1.00 indicates a good straight line.

1: Protein UV

This is the Christian and Warburg assay discussed above. The procedure is as follows:



Step 1

Press 1 to select Protein UV mode.

Step 2

Select path length using the left and right arrows. Options are 5 or 10 mm.



Press the down arrow.

Step 3 (dilution factor known)

Enter the dilution factor using the keypad numbers. Range 1.00 to 9999. Use the C button to backspace and clear the last digit entered.

OR

Step 3 (calculate dilution factor)

Press   to enter the dilution factor screen, shown to the left.


Enter the volume of the sample using the keypad numbers.


Range 0.01 to 9999.

Press the down arrow.

Enter the volume of the diluent using the keypad numbers.

Range 0.01 to 9999.

Press OK  to calculate the dilution factor and return to the Parameters screen.

OR Press  to cancel the selections and return to the Parameters screen.

Step 4

Select whether the background correction at 320 nm is used or not with the left and right arrows.

Press the down arrow.

Step 5

Enter the coefficient value at 260 nm using the keypad numbers (see method described in introduction). Default value is 0.76, range is 0 to 9999.

Press the down arrow.

Step 6


Enter the coefficient value at 280 nm using the keypad numbers (see method described in introduction). Default value is 1.55, range is 1 to 9999.

Press the down arrow.


Step 7

Select the units of measurement using the left and right arrows. Options: µg/ml, ng/µl and µg/µl.

Step 8

Press OK  to enter the Results screen

OR

Cancel  to return to the Protein folder

| Protein UV | |
|-------------|---------------|
| A260 | Sample |
| 0,258 A | 1 |
| A280 | Result |
| 0,167 A | 0,06 |
| | Units |
| | µg/ml |

Results Screen

Step 9

Insert the reference sample. Press 0A/100%T Key. This will be used for all subsequent samples until changed.

Step 10



Insert a sample and press . This measures at both 260 and 280 nm wavelengths and displays the result. Protein concentration is calculated (corrected by background wavelength value if selected).

Repeat step 10 for all samples.

Press to return to the Protein folder.

Press to display available Options which are described below.

| | |
|----------|------------------|
| 1 | Parameters... |
| 2 | Print |
| 3 | Graph |
| <hr/> | |
| 7 | Sample Number... |
| 8 | Save Method... |
| 9 | Auto-Print |

Options (select using key pad numbers)

1. Return to parameters screen (step 1 above).
2. Print result via selected method.
3. Toggle graph on/off. The graph shows a wavescan plot across the range 220 nm to 330 nm with cursors denoting 230, 260, 280 and (if background correction selected) 320 nm.
7. Sample number – add a prefix to the sample number and reset the incrementing number to the desired value.
8. Save method – use the alpha-numeric keys to enter a name for the method and press .
9. Auto-print – toggles auto-print on/off.

Exit options by pressing , or wait.

2: BCA

The procedure is as follows:

BCA - Parameters

| | | | |
|------------|--------|-------------|------------|
| Wavelength | 562 nm | Curve Fit | Regression |
| Standards | 6 | Calibration | Standards |
| Units | µg/ml | Replicates | Off |

Next Cancel

Units

Units

DP

Auto

OK Cancel

BCA - Parameters

| | | | |
|------------|--------|-------------|------------|
| Wavelength | 562 nm | Curve Fit | Regression |
| Standards | 6 | Calibration | Standards |
| Units | µg/ml | Replicates | Off |

Next Cancel

BCA - Standards

| | | | |
|--------|-------|--------|-------|
| Std. 1 | 0.200 | Std. 4 | 0.800 |
| Std. 2 | 0.400 | Std. 5 | 1.000 |
| Std. 3 | 0.600 | Std. 6 | 1.400 |

Next Back

Step 1

Press 2 to select BCA mode.

Step 2

The wavelength for this method is set at 562 nm.

Step 3

Enter the number of standard concentration points (1-9) to be used in the curve using the keypad numbers or left and right arrows.

Press the down arrow.

Step 4

Units: The user can enter a text string up to 8 characters long. To access a list of pre-defined units press the Options key and then use the left/right arrows (µg/ml, µg/µl, pmol/µl, mg/dl, mmol/l, µmol/l, g/l, mg/l, µg/l, U/l, %, ppm, ppb, conc or none). These units can also be edited once OK is pressed.

This screen also allows the number of displayed decimal points (DP) to be selected, from 0 to 2. Note that the result will always be fixed to 5 significant figures regardless of how many decimal points are selected (so 98768.2 will display as 98768 even with 1 decimal point selected).

Press OK to store the chosen parameters or Cancel

Esc

Step 5

Enter the type of curve fit. Options are straight line regression, zero regression (forces the straight line through the origin), interpolated or cubic spline.

Press the down arrow.

Step 6

Select the calibration mode, either standards (measure prepared standards) or manual (keypad data entry, go to step 9)

Step 7 (standards selected)

Select the number of replicates using the left and right arrows. This determines the number of standards to be measured and averaged at each standard concentration point. Can be OFF (1), 2 or 3.

Step 8 (standards selected)

Press Next to enter the Standards screen

OR

Press Cancel Esc to cancel selections and return to the Protein folder.

Standards Screen

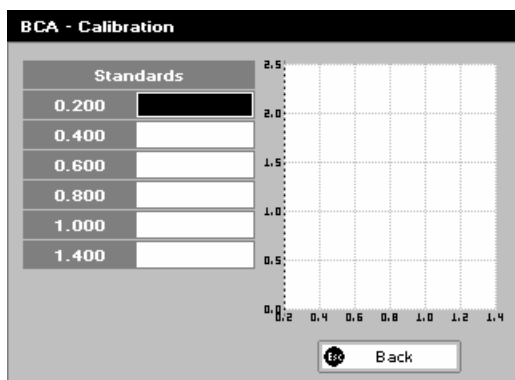
Step 9 (standards/manual selected)

Enter the concentration values by using the keypad numbers and the up and down arrows to move between the different standard boxes. Range 0.001 to 9999. C button backspaces and clears the last digit entered.

Step 10 (standards/manual selected)

Press Next to enter the Calibration screen. If there are duplicate or non-monotonic (increasing) entries the unit will beep and highlight the incorrect entry.

OR Press Back Esc to return to the Parameter screen.



Calibration Screen (replicates off)

This shows the calibration values and allows standards to be measured or entered using the keypad numbers (if calibration mode is manual).


Step 11 (standards selected)

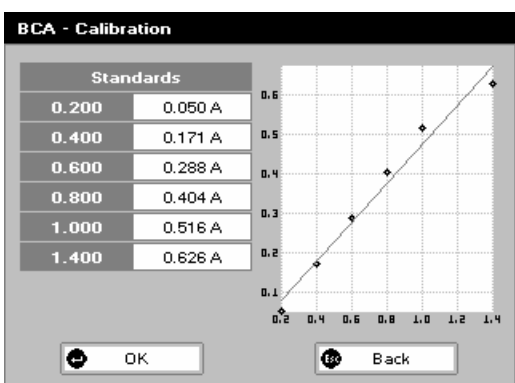
Insert the reference sample. Press 0A/100% key.

This will be used for all subsequent samples until changed.

Step 12 (standards selected)

Insert the standard (use C to clear previously stored results before measuring)

Press  to measure the standard and store the result.




Repeat step 12 for all standards. A graph will display the results and the fitted curve as the measurements are made.


Use the up and down arrows to select a standard to be repeated if a poor reading has been obtained. Use C to clear the previous reading.

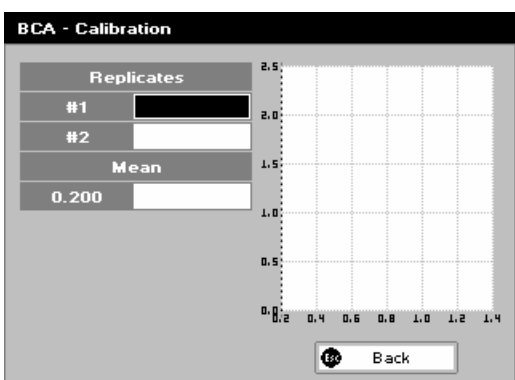
Step 13 (standards/manual selected)

When all standards are measured the OK box appears. Press

OK  to accept the calibration and go to the Results screen (see below)

OR

Press Back  to cancel selections and return to the Standards screen.



Calibration Screen (replicates on)


This shows the calibration values and allows standards to be measured.


Step 11 (standards selected)

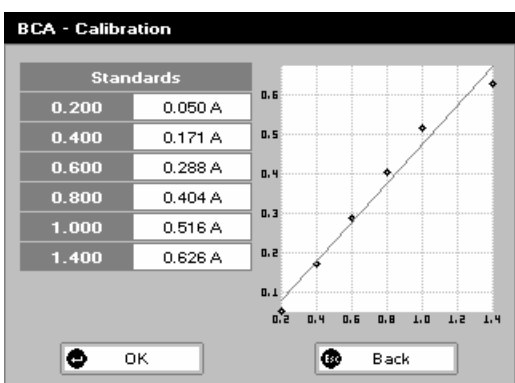
Insert the reference sample. Press 0A/100% key.


This will be used for all subsequent samples until changed.

Step 12 (standards selected)

Press Replicates  to display the replicate entry boxes. Use C to clear previously stored results before measuring.

Insert the standard and press  to measure the standard and store the result.




Repeat for all replicates and standards. Use Next  to bring up fields for the next standard.


A graph will display the results and the fitted curve as the measurements are input.

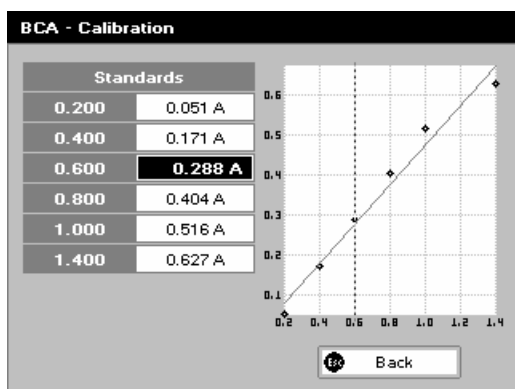
Use the up and down arrows to select a standard to be repeated if a poor reading has been obtained. Use C to clear the previous reading.

Step 13 (standards/manual selected)

Press OK  to accept the calibration and go to the Results screen (see below)

OR

Press Back  to return to the Standards screen.



Calibration (Manual entry)

Shows previously entered calibration values and allows values to be entered via the keypad.

The highlighted box can be edited in order to enter an absorbance value corresponding to a given concentration value using the keypad numbers. Range 0.001 to 9999. Use C to backspace and clear the last digit entered and the up and down arrows to move between boxes. Pressing the down arrow from the last standard will bring up the OK box.

Press OK to accept the calibration and go to the Results screen (see below)

OR

Press Back to return to the Standards screen.

BCA

| | |
|--------------------------------|-------------------------------------|
| Wavelength 562 nm | Sample 1 |
| Absorbance 0.288 A | Concentration 0,62 |
| Curve Fit Regression | Units μg/μl |

Results screen

Step 14

Insert the reference sample and press the 0A/100%T key. This will be used for all subsequent samples until changed.

Step 15

Insert the sample and press .

The concentration of the sample is taken and displayed. Repeat step 15 for all samples.

Press to return to the Protein Folder.

Press to display available Options which are described below.

| | |
|---|------------------|
| 1 | Parameters... |
| 2 | Print |
| 3 | Graph |
| 7 | Sample Number... |
| 8 | Save Method... |
| 9 | Auto-Print |

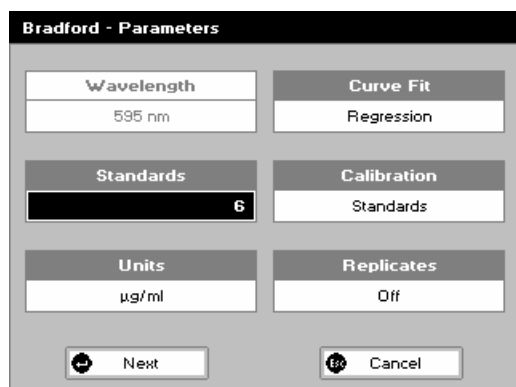
Options (select using keypad numbers)

1. Return to parameters screen (step 1 above).
2. Print result via selected method.
3. Toggle graph on/off. Displays the calibration graph, cursors give values for last measured sample.
7. Sample number – add a prefix to the sample number and reset the incrementing number to the desired value.
8. Save method – use the alpha-numeric keys to enter a name for the method and press Save .
9. Auto-print – toggles auto-print on/off.

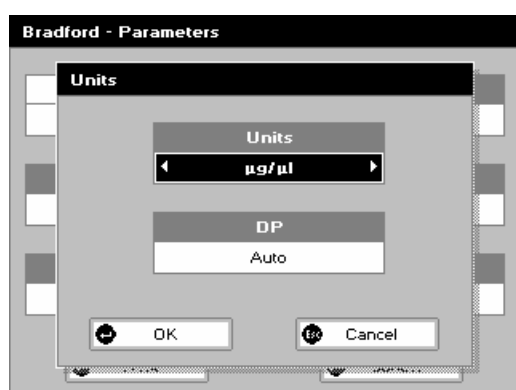
Exit options by pressing , or wait.

3: Bradford

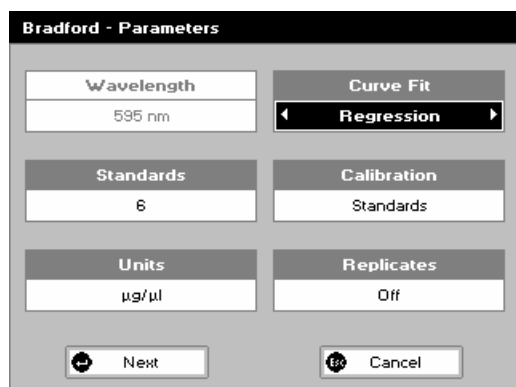
The procedure is as follows:



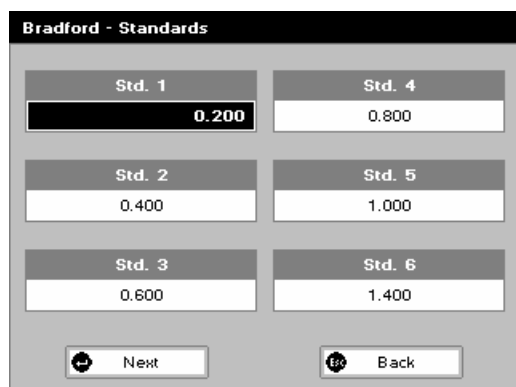
The 'Bradford - Parameters' screen displays several settings in a grid. The 'Wavelength' is set to 595 nm. 'Curve Fit' is set to Regression. 'Standards' is set to 6. 'Calibration' is set to Standards. 'Units' is set to µg/ml. 'Replicates' is set to Off. At the bottom, there are 'Next' and 'Cancel' buttons.



A dialog box titled 'Units' is shown over the 'Bradford - Parameters' screen. It contains a 'Units' dropdown menu with 'µg/µl' selected, a 'DP' dropdown menu with 'Auto' selected, and 'OK' and 'Cancel' buttons at the bottom.



The 'Bradford - Parameters' screen is shown again, but the 'Curve Fit' dropdown menu is now open, showing 'Regression' as the selected option. The other settings remain the same.



The 'Bradford - Standards' screen displays six standard concentration boxes. 'Std. 1' is 0.200, 'Std. 2' is 0.400, 'Std. 3' is 0.600, 'Std. 4' is 0.800, 'Std. 5' is 1.000, and 'Std. 6' is 1.400. At the bottom, there are 'Next' and 'Back' buttons.

Step 1

Press 3 to select Bradford method.

Step 2

The wavelength for this method is set at 595 nm.


Step 3

Enter the number of standard concentration points (1-9) to be used in the curve using the keypad numbers or left and right arrows.



Press the down arrow.

Step 4

Units: The user can enter a text string up to 8 characters long.

To access a list of pre-defined units press the Options key  and then use the left/right arrows (µg/ml, µg/µl, pmol/µl, mg/dl, mmol/l, µmol/l, g/l, mg/l, µg/l, U/l, %, ppm, ppb, conc or none). These units can also be edited once OK is pressed.

This screen also allows the number of displayed decimal points (DP) to be selected, from 0 to 2. Note that the result will always be fixed to 5 significant figures regardless of how many decimal points are selected (so 98768.2 will display as 98768 even with 1 decimal point selected).

Press OK  to store the chosen parameters or Cancel .

Step 5

Enter the type of curve fit. Options are: straight line regression, zero regression (forces the straight line through the origin), interpolated or cubic spline.

Press the down arrow.


Step 6


Select the calibration mode, either standards (measure prepared standards) or manual (keypad data entry, go to step 9)

Step 7 (standards selected)

Select the number of replicates using the left and right arrows. This determines the number of standards to be measured and averaged at each standard concentration point. Can be OFF (1), 2 or 3.

Step 8 (standards selected)

Press Next  to enter the Standards screen


OR Press Cancel  to cancel selections and return to the Protein folder.

Standards Screen


Step 9 (standards/manual selected)

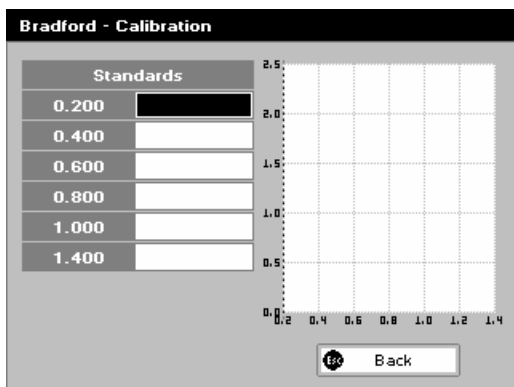
Enter the concentration values by using the keypad numbers and the up and down arrows to move between the different standard boxes. Range 0.001 to 9999. C button backspaces and clears the last digit entered.

Step 10 (standards/manual selected)

Press Next  to enter the Calibration screen. If there are duplicate or non-monotonic (increasing) entries the unit will beep and highlight the incorrect entry.

OR

Press Back  to return to the Parameters screen



Calibration Screen (replicates off)

This shows the calibration values and allows standards to be measured or entered using the keypad numbers (if calibration mode is manual).


Step 11 (standards selected)

Insert the reference sample. Press 0A/100% key.

This will be used for all subsequent samples until changed.

Step 12 (standards selected)

Insert the standard (use C to clear previously stored results before measuring)


Press  to measure the standard and store the result.


Repeat step 12 for all standards. A graph will display the results and the fitted curve as the measurements are made.

Use the up and down arrows to select a standard to be repeated if a poor reading has been obtained. Use C to clear the previous reading.

Step 13 (standards/manual selected)

When all standards are measured the OK box appears. Press

OK  to accept the calibration and go to the Results screen (see below)

OR Press Back  to cancel selections and return to the Standards screen.

Calibration Screen (replicates on)


This shows the calibration values and allows standards to be measured.

Step 11 (standards selected)


Insert the reference sample. Press 0A/100% key.

This will be used for all subsequent samples until changed.

Step 12 (standards selected)

Press replicates  to display the replicate entry boxes. Use C to clear previously stored results before measuring.


Insert the standard and press  to measure the standard and store the result.

Repeat for all replicates and standards. Press Next  to move from replicates of one standard to replicates of the next standard.


A graph will display the results and the fitted curve as the measurements are input.

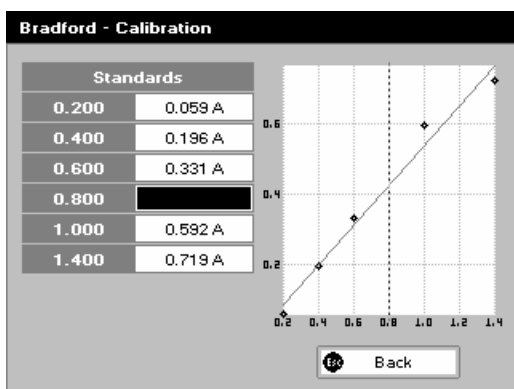
Use the up and down arrows to select a standard to be repeated if a poor reading has been obtained. Use C to clear the previous reading.

Step 13 (standards/manual selected)

Press OK  to accept the calibration and go to the Results screen (see below)

OR

Press Back  to return to the Standards screen.



Calibration (Manual entry)

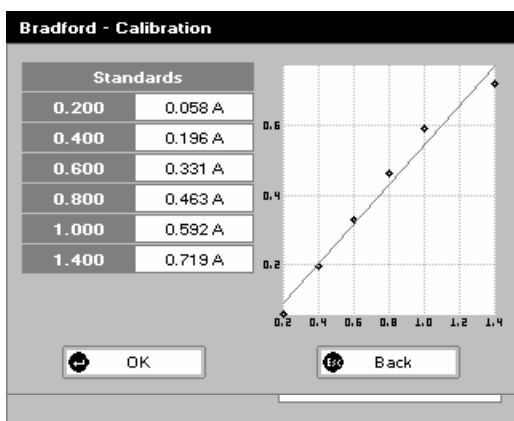
Shows previously entered calibration values and allows values to be entered via the keypad.

The highlighted box can be edited in order to enter an absorbance value corresponding to a given concentration value using the keypad numbers. Range 0.001 to 9999. Use C to backspace and clear the last digit entered and the up and down arrows to move between boxes. Pressing the down arrow from the last standard will bring up the OK box.

Press OK to accept the calibration and go to the Results screen (see below)

OR

Press Back to return to the Standards screen.



Results screen

Step 14

Insert the reference sample and press the 0A/100%T key. This will be used for all subsequent samples until changed.

Step 15

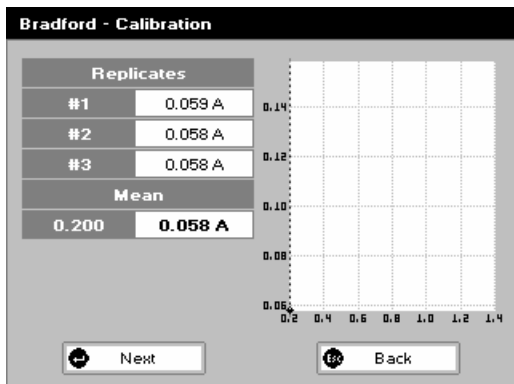
Insert the sample and press .

The concentration of the sample is taken and displayed.

Repeat step 15 for all samples.

Press **Esc** to return to the Protein Folder.

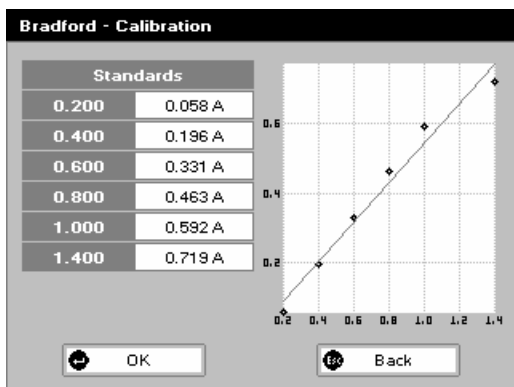
Press to display available Options which are described below.



Options (select using key pad numbers)

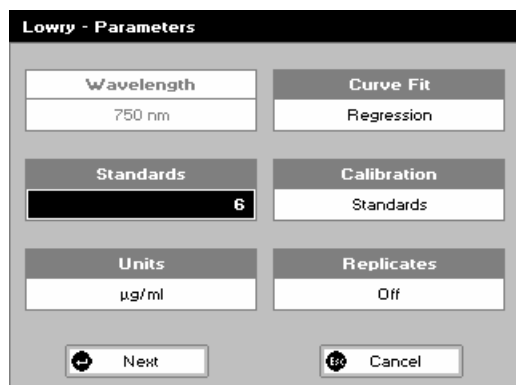
1. Return to parameters screen (step 1 above).
2. Print result via selected method.
3. Toggle graph on/off. Displays the calibration graph, cursors give values for last measured sample.
7. Sample number – add a prefix to the sample number and reset the incrementing number to the desired value.
8. Save method – use the alpha-numeric keys to enter a name for the method and press Save .
9. Auto-print – toggles auto-print on/off.

Exit options by pressing , or wait.



4: Lowry

The procedure is as follows:



Lowry - Parameters

| | |
|----------------------|--------------------------|
| Wavelength 750 nm | Curve Fit Regression |
| Standards 6 | Calibration Standards |
| Units µg/ml | Replicates Off |
| Next | Cancel |

Step 1

Press 4 to select Lowry method.

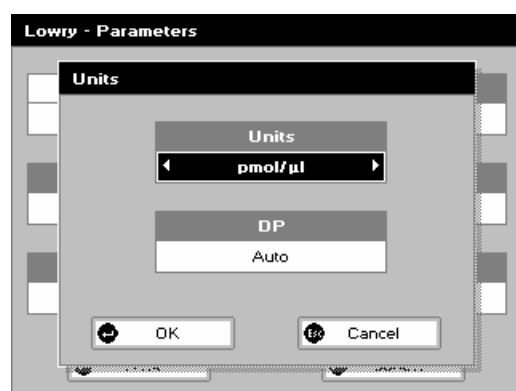
Step 2

The wavelength for this method is set at 750 nm.

Step 3

Enter the number of standard concentration points (1-9) to be used in the curve using the keypad numbers or left and right arrows.

Press the down arrow.



Lowry - Parameters

Units


Units
pmol/µl

DP
Auto

OK Cancel


Step 4

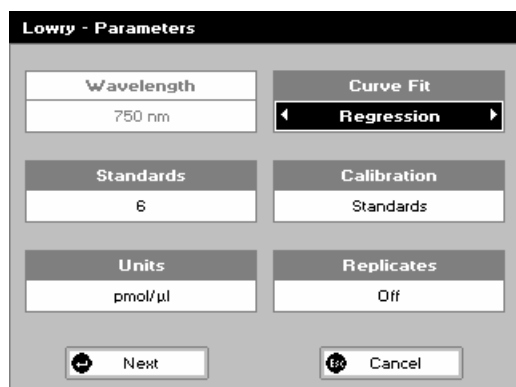
Units: The user can enter a text string up to 8 characters long.

To access a list of pre-defined units press the Options key  and then use the left/right arrows (µg/ml, µg/µl, pmol/µl, mg/dl, mmol/l, µmol/l, g/l, mg/l, µg/l, U/l, %, ppm, ppb, conc or none).

These units can also be edited once OK is pressed.

This screen also allows the number of displayed decimal points (DP) to be selected, from 0 to 2. Note that the result will always be fixed to 5 significant figures regardless of how many decimal points are selected (so 98768.2 will display as 98768 even with 1 decimal point selected).

Press OK  to store the chosen parameters or Cancel .



Lowry - Parameters

| | |
|----------------------|--------------------------|
| Wavelength 750 nm | Curve Fit Regression |
| Standards 6 | Calibration Standards |
| Units pmol/µl | Replicates Off |
| Next | Cancel |

Step 5

Enter the type of curve fit. Options are straight line regression, zero regression (forces the straight line through the origin), interpolated or cubic spline.

Press the down arrow.

Step 6


Select the calibration mode, either standards (measure prepared standards) or manual (keypad data entry, go to step 9)

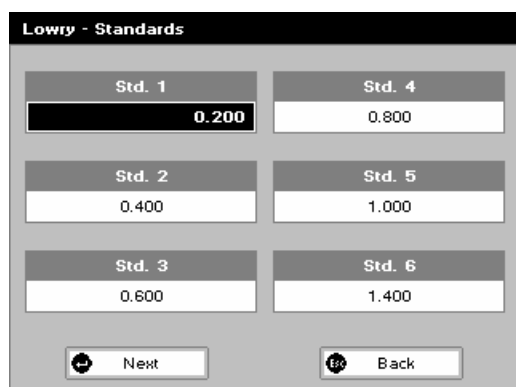
Step 7 (standards selected)

Select the number of replicates using the left and right arrows. This determines the number of standards to be measured and averaged at each standard concentration point. Can be OFF (1), 2 or 3.

Step 8 (standards selected)

Press Next  to enter the Standards screen

OR Press Cancel  to cancel selections and return to the Protein folder.



Lowry - Standards


| | |
|-----------------|-----------------|
| Std. 1 0.200 | Std. 4 0.800 |
| Std. 2 0.400 | Std. 5 1.000 |
| Std. 3 0.600 | Std. 6 1.400 |
| Next | Back |

Standards Screen

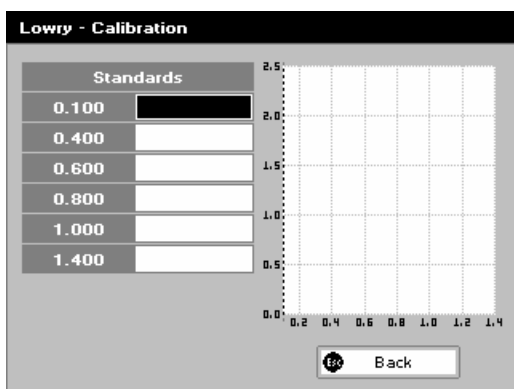
Step 9 (standards/manual selected)

Enter the concentration values by using the keypad numbers and the up and down arrows to move between the different standard boxes. Range 0.001 to 9999. C button backspaces and clears the last digit entered.

Step 10 (standards/manual selected)

Press Next  to enter the Calibration screen. If there are duplicate or non-monotonic (increasing) entries the unit will beep and highlight the incorrect entry.

OR Press Back  to return to the Parameters screen



Calibration Screen (replicates off)

This shows the calibration values and allows standards to be measured or entered using the keypad numbers (if calibration mode is manual).

Step 11 (standards selected)

Insert the reference sample. Press 0A/100% key.

This will be used for all subsequent samples until changed.

Step 12 (standards selected)

Insert the standard (use C to clear previously stored results before measuring)

Press to measure the standard and store the result.

Repeat step 12 for all standards. A graph will display the results and the fitted curve as the measurements are made.

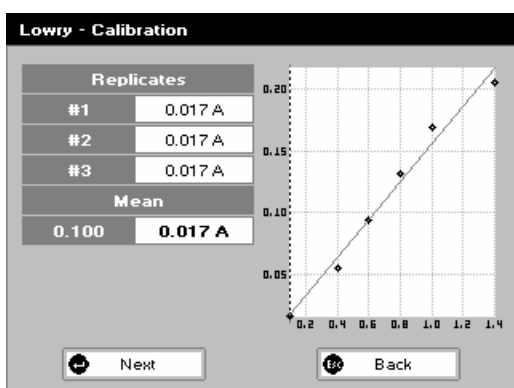
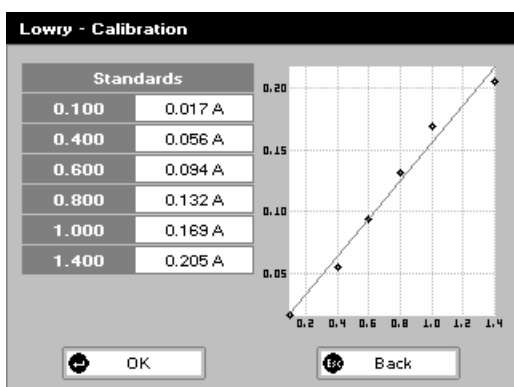
Use the up and down arrows to select a standard to be repeated if a poor reading has been obtained. Use C to clear the previous reading.

Step 13 (standards/manual selected)

When all standards are measured the OK box appears. Press

OK to accept the calibration and go to the Results screen (see below)

OR Press Back to cancel selections and return to the Standards screen.



Calibration Screen (replicates on)

This shows the calibration values and allows standards to be measured.

Step 11 (standards selected)

Insert the reference sample. Press 0A/100% key.

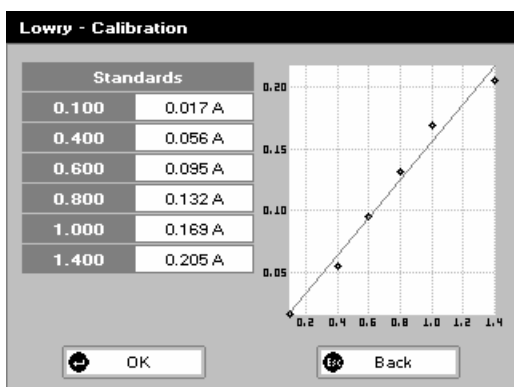
This will be used for all subsequent samples until changed.

Step 12 (standards selected)

Press replicates to display the replicate entry boxes. Use C to clear previously stored results before measuring.

Insert the standard and press to measure the standard and store the result. Repeat for all replicates and standards.

Press Next to move from replicates of one standard to replicates of the next standard.



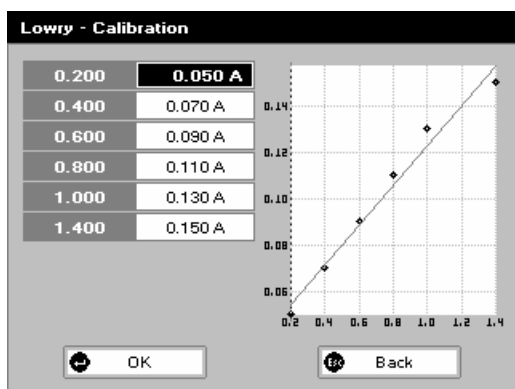
A graph will display the results and the fitted curve as the measurements are input.

Use the up and down arrows to select a standard to be repeated if a poor reading has been obtained. Use C to clear the previous reading.

Step 13 (standards/manual selected)

Press Next to accept the calibration and go to the Results screen (see below)


OR Press Back to return to the Standards screen.



Calibration (Manual entry)

Shows previously entered calibration values and allows values to be entered via the keypad.

The highlighted box can be edited in order to enter an absorbance value corresponding to a given concentration value using the keypad numbers. Range 0.001 to 9999. Use C to backspace and clear the last digit entered and the up and down arrows to move between boxes.

Press OK  to accept the calibration and go to the Results screen (see below)

OR Press Back  to return to the Standards screen.

Lowry


| | |
|-----------------------------------|-------------------------------------|
| Wavelength 750 nm | Sample 1 |
| Absorbance 0.095 A | Concentration 0,61 |
| Curve Fit Interpolation | Units µg/ml |

Results screen

Step 14


Insert the reference sample and press the 0A/100%T key. This will be used for all subsequent samples until changed.


Step 15


Insert the sample and press .

The concentration of the sample is taken and displayed.


Repeat step 15 for all samples.

Press  to return to the Protein Folder.

Press  to display available Options which are described below.

- 1 Parameters...
- 2 Print
- 3 Graph
- 7 Sample Number...
- 8 Save Method...
- 9 Auto-Print 

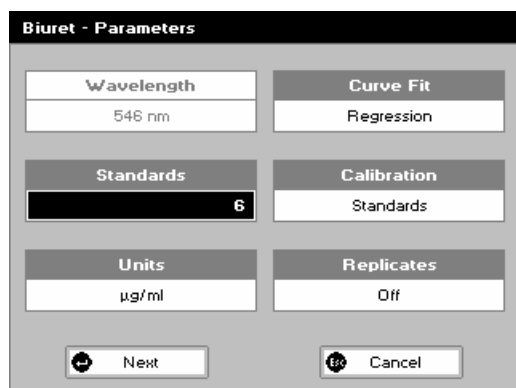
Options (select using key pad numbers)

1. Return to parameters screen (step 1 above).
2. Print result via selected method.
3. Toggle graph on/off. Displays the calibration graph, cursors give values for last measured sample.
7. Sample number – add a prefix to the sample number and reset the incrementing number to the desired value.
8. Save method – use the alpha-numeric keys to enter a name for the method and press Save .
9. Auto-print – toggles auto-print on/off.

Exit options by pressing , or wait.

5: Biuret

The procedure is as follows:



The 'Biuret - Parameters' screen displays several settings in a grid. The 'Wavelength' is set to 546 nm. 'Curve Fit' is set to Regression. 'Standards' is set to 6. 'Calibration' is set to Standards. 'Units' is set to µg/ml. 'Replicates' is set to Off. At the bottom are 'Next' and 'Cancel' buttons.

| | | | |
|------------|--------|-------------|------------|
| Wavelength | 546 nm | Curve Fit | Regression |
| Standards | 6 | Calibration | Standards |
| Units | µg/ml | Replicates | Off |

Step 1

Press 5 to select Biuret method.

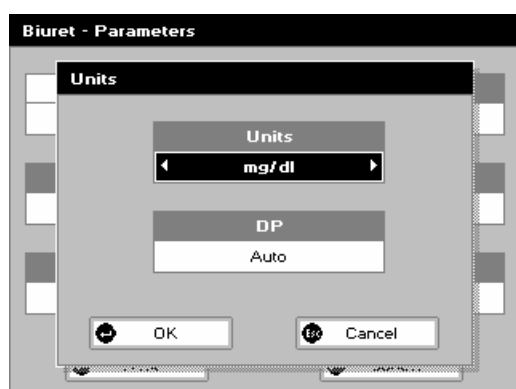
Step 2

The wavelength for this method is set at 546 nm.

Step 3

Enter the number of standard concentration points (1-9) to be used in the curve using the keypad numbers or left and right arrows.


Press the down arrow.



The 'Biuret - Parameters' screen is shown with a 'Units' dialog box open. The dialog has a 'Units' dropdown menu set to 'mg/dl' and a 'DP' (Decimal Points) dropdown menu set to 'Auto'. 'OK' and 'Cancel' buttons are at the bottom of the dialog.



Step 4

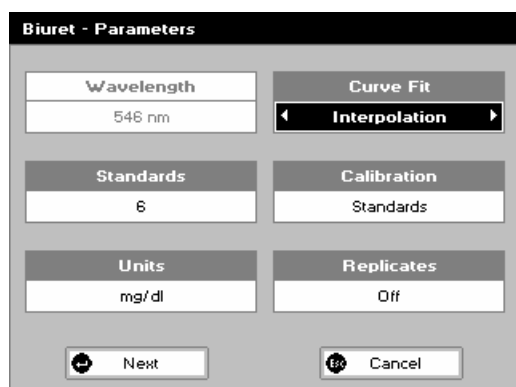
Units: The user can enter a text string up to 8 characters long.

To access a list of pre-defined units press the Options key  and then use the left/right arrows (µg/ml, µg/µl, pmol/µl, mg/dl, mmol/l, µmol/l, g/l, mg/l, µg/l, U/l, %, ppm, ppb, conc or none).

These units can also be edited once OK is pressed.

This screen also allows the number of displayed decimal points (DP) to be selected, from 0 to 2. Note that the result will always be fixed to 5 significant figures regardless of how many decimal points are selected (so 98768.2 will display as 98768 even with 1 decimal point selected).

Press OK  to store the chosen parameters or Cancel .



The 'Biuret - Parameters' screen is shown with 'Curve Fit' set to Interpolation. Other settings remain the same: Wavelength 546 nm, Standards 6, Units µg/ml, Replicates Off.

Step 5

Enter the type of curve fit. Options are straight line regression, zero regression (forces the straight line through the origin), interpolated or cubic spline.

Press the down arrow.


Step 6


Select the calibration mode, either standards (measure prepared standards) or manual (keypad data entry, go to step 9)

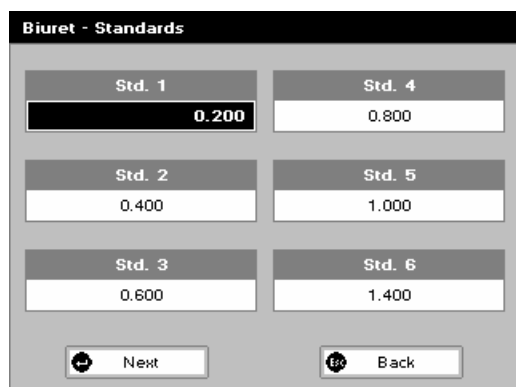
Step 7 (standards selected)

Select the number of replicates using the left and right arrows. This determines the number of standards to be measured and averaged at each standard concentration point. Can be OFF (1), 2 or 3.

Step 8 (standards selected)

Press Next  to enter the Standards screen
OR

Press Cancel  to cancel selections and return to the Protein folder.



The 'Biuret - Standards' screen displays six standard concentration boxes. Std. 1 is 0.200, Std. 2 is 0.400, Std. 3 is 0.600, Std. 4 is 0.800, Std. 5 is 1.000, and Std. 6 is 1.400. 'Next' and 'Back' buttons are at the bottom.

| | | | |
|--------|-------|--------|-------|
| Std. 1 | 0.200 | Std. 4 | 0.800 |
| Std. 2 | 0.400 | Std. 5 | 1.000 |
| Std. 3 | 0.600 | Std. 6 | 1.400 |

Standards Screen

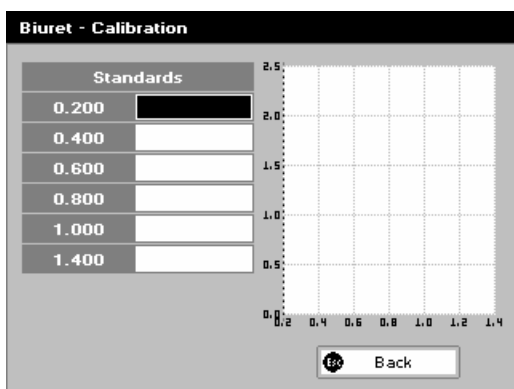
Step 9 (standards/manual selected)

Enter the concentration values by using the keypad numbers and the up and down arrows to move between the different standard boxes. Range 0.001 to 9999. C button backspaces and clears the last digit entered.

Step 10 (standards/manual selected)

Press Next  to enter the Calibration screen

OR Press Back  to return to the Parameters screen



Calibration Screen (replicates off)

This shows the calibration values and allows standards to be measured or entered using the keypad numbers (if calibration mode is manual).

Step 11 (standards selected)

Insert the reference sample. Press 0A/100% key.

This will be used for all subsequent samples until changed.

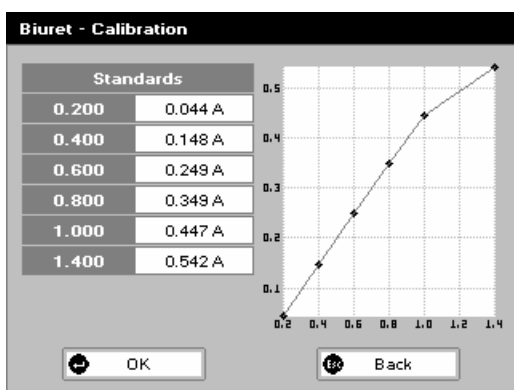
Step 12 (standards selected)

Insert the standard (use C to clear previously stored results before measuring)



Press to measure the standard and store the result.

Repeat step 12 for all standards. A graph will display the results and the fitted curve as the measurements are made.



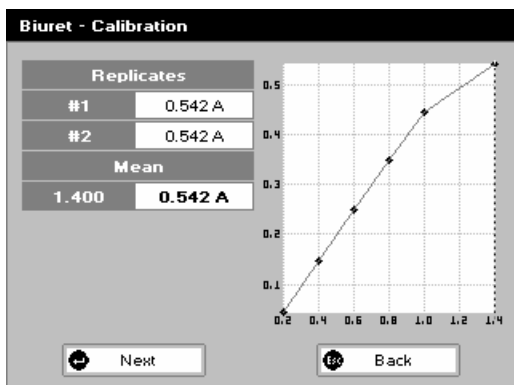
Use the up and down arrows to select a standard to be repeated if a poor reading has been obtained. Use C to clear the previous reading.

Step 13 (standards/manual selected)

When all standards are measured the OK box appears. Press

OK to accept the calibration and go to the Results screen (see below)

OR Press Back to cancel selections and return to the Standards screen.



Calibration Screen (replicates on)

This shows the calibration values and allows standards to be measured.

Step 11 (standards selected)

Insert the reference sample. Press 0A/100% key.

This will be used for all subsequent samples until changed.

Step 12 (standards selected)

Press replicates to display the replicate entry boxes. Use C to clear previously stored results before measuring.

Insert the standard and press to measure the standard and store the result.

Repeat for all replicates and standards. Press Next to move from replicates of one standard to replicates of the next standard.

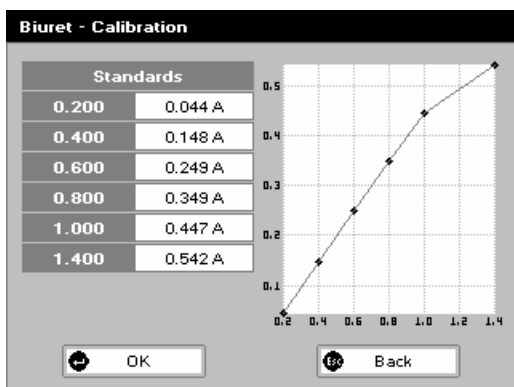
A graph will display the results and the fitted curve as the measurements are input.

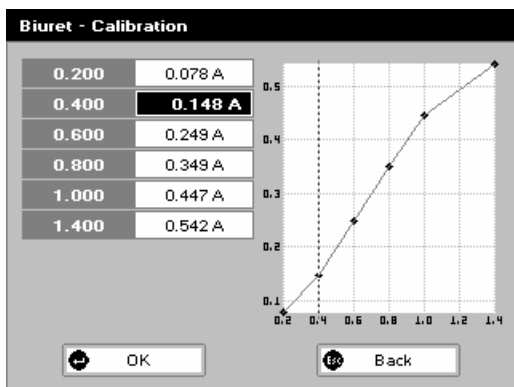
Use the up and down arrows to select a standard to be repeated if a poor reading has been obtained. Use C to clear the previous reading.

Step 13 (standards/manual selected)

Press OK to accept the calibration and go to the Results screen (see below)

OR Press Back to return to the Standards screen.






Calibration (Manual entry)

Shows previously entered calibration values and allows values to be entered via the keypad.

The highlighted box can be edited in order to enter an absorbance value corresponding to a given concentration value using the keypad numbers. Range 0.001 to 9999. Use C to backspace and clear the last digit entered and the up and down arrows to move between boxes.

Press OK  to accept the calibration and go to the Results screen (see below)

OR

Press Back  to return to the Standards screen.

Biuret

| | |
|--------------------------------|-------------------------------------|
| Wavelength 546 nm | Sample 1 |
| Absorbance 0,249 A | Concentration 0,62 |
| Curve Fit Regression | Units µg/ml |

Results screen

Step 14


Insert the reference sample and press the 0A/100%T key. This will be used for all subsequent samples until changed.




Step 15


Insert the sample and press .

The concentration of the sample is taken and displayed.


Repeat step 15 for all samples.


Press  to return to the Protein Folder.

Press  to display available Options which are described below.

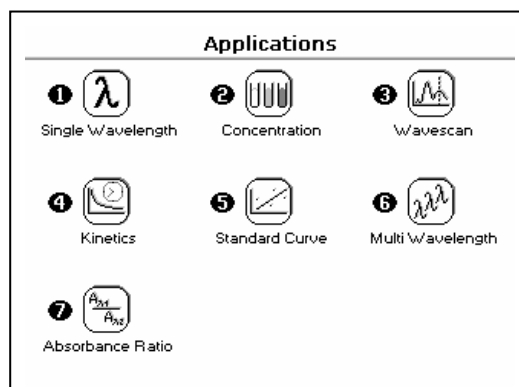
- 1 Parameters...
- 2 Print
- 3 Graph
- 7 Sample Number...
- 8 Save Method...
- 9 Auto-Print 

Options (select using key pad numbers)






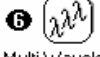
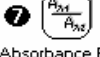
1. Return to parameters screen (step 1 above).
2. Print result via selected method.
3. Toggle graph on/off. Displays the calibration graph, cursors give values for last measured sample.
7. Sample number – add a prefix to the sample number and reset the incrementing number to the desired value.
8. Save method – use the alpha-numeric keys to enter a name for the method and press Save .
9. Auto-print – toggles auto-print on/off.

Exit options by pressing , or wait.

THE APPLICATIONS FOLDER



SUMMARY:

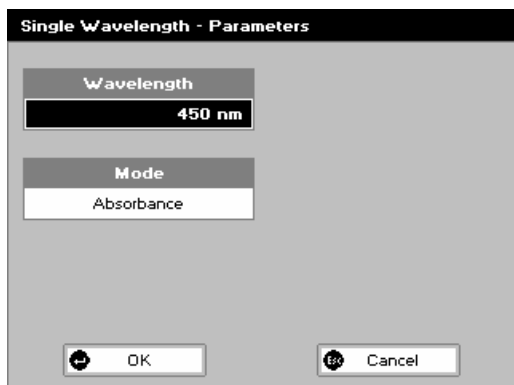
| Function | Key pad number | Description |
|---|----------------|---|
|  Single Wavelength | 1 | Absorbance or %T (transmission) at a single user defined wavelength. |
|  Concentration | 2 | Concentration measurement at a single wavelength based on a simple Factor entered or calculated from a single standard. |
|  Wavelengthscan | 3 | Wavelength scan between two user defined wavelengths. Range 200-900 nm, with user configurable peak finding function. |
|  Kinetics | 4 | Absorbance versus time measurements either rate or end value based. |
|  Standard Curve | 5 | Generation of calibration curve by measuring standards at a single wavelength. |
|  Multi Wavelength | 6 | Absorbance or %T (transmission) at up to 5 user defined wavelengths. |
|  Absorbance Ratio | 7 | Ratio of absorbance values at two user specified wavelengths. |

OPTIONS

Within each application the user has the possibility to select various options that define the way results are treated. If not using a stored method, it is advisable to check that these Options have been appropriately set for your experiment when coming to the instrument. Note that setting the "History" parameter to on (see Preferences later) will cause the instrument to store its last settings. If the "History" parameter is turned off, all parameters and options will return to their default settings when you leave that application. (Unless it has been saved as a method).

1: Single Wavelength – Abs and %T

This makes simple absorbance (A) and % transmission (%T) measurements on samples, measuring the amount of light that has passed through a sample relative to a reference (this can be air).
The procedure is as follows:



Step 1

Set wavelength by using keypad numbers or left and right arrows. Range 190 – 1100 nm.

Press the down arrow key.

Step 2

Select the mode, *Absorbance* or *%T*, using the left and right arrows.

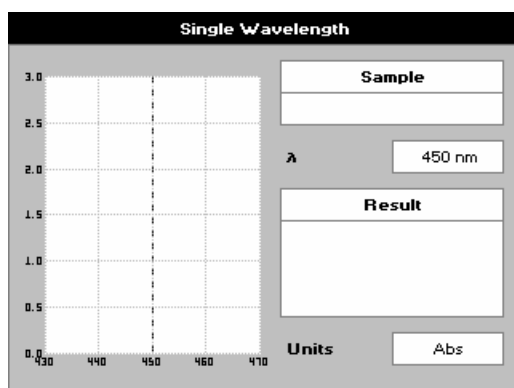
Step 3

To enter the results screen with the selected parameters press

OK

OR

Cancel the selections and return to the Applications Folder by pressing Cancel .



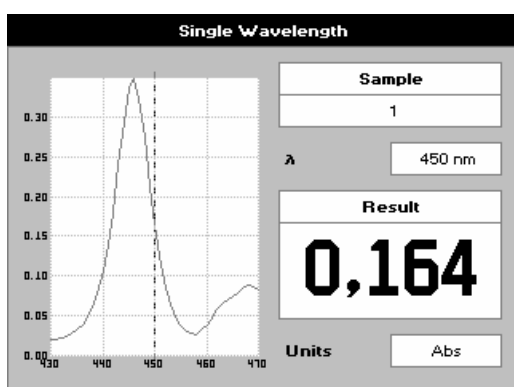
Step 4

Insert the reference. Press 0A/100% key. This will be used for all subsequent samples until changed.

Step 5

Insert sample and press .

Repeat step 5 for all samples.

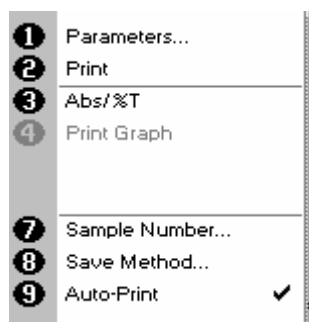


Results

The result at the selected wavelength is displayed on screen. Use the left and right arrows to move the cursor and display the value at the cursor position (+/- 15nm from set wavelength).

Press Cancel to return to the Applications Folder.

Press to display available Options which are described below.



Options (select using key pad numbers)

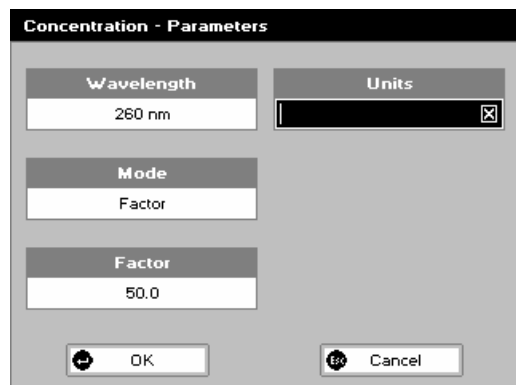
1. Return to parameters screen (step 1 above).
2. Print result via selected method.
3. Toggle between Absorbance and %T mode.
4. Print graph – greyed out if no data are available.
7. Sample number – add a prefix to the sample number and reset the incrementing number to the desired value.
8. Save method – use the left and right arrows to select a folder to store in (Favourites/Methods 1-9), press the down arrow and enter name.
9. Auto-print – toggles auto-print on/off.

Exit options by pressing **Esc**, or wait.

2: Concentration

This makes simple concentration measurements on samples, by measuring the amount of light that has passed through a sample relative to a reference (this can be air). Concentration is obtained by multiplying the measured absorbance at a specific wavelength by a factor. The factor may be known in advance, or may be calculated by the instrument by measuring a standard of known concentration.

The procedure is as follows:



The 'Concentration - Parameters' screen displays four input fields: 'Wavelength' (260 nm), 'Units' (a dropdown menu with a checkmark icon), 'Mode' (Factor), and 'Factor' (50.0). At the bottom are 'OK' and 'Cancel' buttons.

Step 1

Set wavelength by using keypad numbers or left and right arrows. Range 190-1100 nm.

Press the down arrow key.

Step 2

Select the mode, Factor (user entered) or Standard (factor is calculated from a calibration sample), using the left and right arrows.

Press the down arrow key.

Step 3 (if Factor is selected)

Enter the Factor using the keypad numbers. Range 0.001 to 9999. Use the C button to delete the last digit entered.

Press the down arrow key.


Step 3 (if Standard is selected)


Enter the concentration using keypad numbers. Range 0.01-9999. Use the C button to delete the last digit entered.


Press the down arrow key.

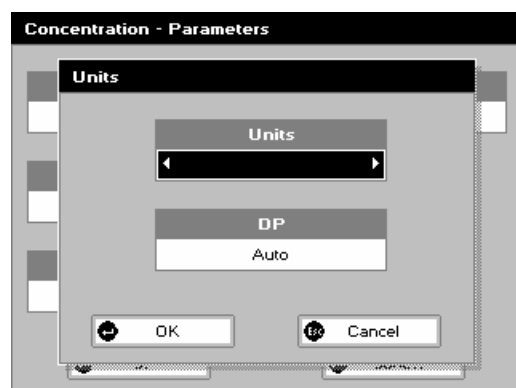
Step 4

Units: The user can enter a text string up to 8 characters long.

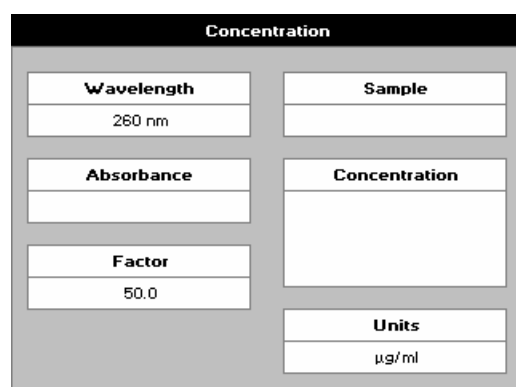
To access a list of pre-defined units press the Options key  and then use the left/right arrows ($\mu\text{g/ml}$, $\mu\text{g}/\mu\text{l}$, $\text{pmol}/\mu\text{l}$, mg/dl , mmol/l , $\mu\text{mol/l}$, g/l , mg/l , $\mu\text{g/l}$, U/l , $\%$, ppm , ppb , conc or none). These units can also be edited once OK is pressed.

This screen also allows the number of displayed decimal points (DP) to be selected, from 0 to 2. Note that the result will always be fixed to 5 significant figures regardless of how many decimal points are selected (so 98768.2 will display as 98768 even with 1 decimal point selected). Press OK  to store the chosen

parameters or Cancel .



The 'Units' sub-screen shows a 'Units' dropdown menu and a 'DP' (Decimal Points) field set to 'Auto'. It includes 'OK' and 'Cancel' buttons at the bottom.



The 'Concentration' screen displays 'Wavelength' (260 nm), 'Absorbance' (blank), 'Factor' (50.0), 'Sample' (blank), 'Concentration' (blank), and 'Units' ($\mu\text{g/ml}$). It includes 'OK' and 'Cancel' buttons at the bottom.


Step 5

To enter the results screen with the selected parameters press

OK .

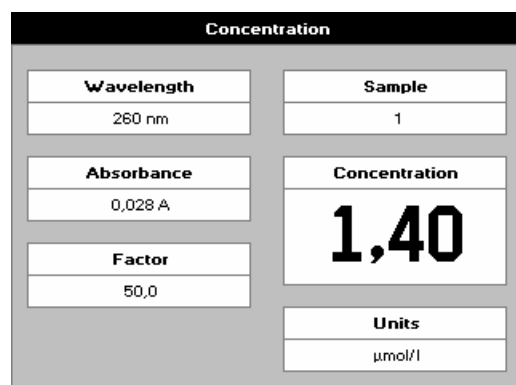
OR

Cancel the selections and return to the Applications Folder by

pressing Cancel .


Step 6 (if using a Factor)

Insert the reference. Press 0A/100% key. This will be used for all subsequent samples until changed.




The 'Concentration' screen displays 'Wavelength' (260 nm), 'Absorbance' (0.028 A), 'Factor' (50.0), 'Sample' (1), 'Concentration' (1.40), and 'Units' ($\mu\text{mol/l}$). It includes 'OK' and 'Cancel' buttons at the bottom.


Step 7

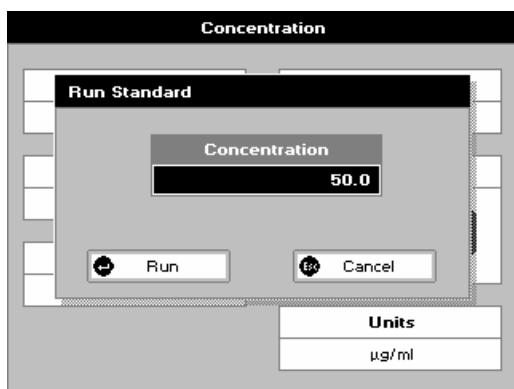
Insert sample and press .

The concentration of the sample is displayed. Results shown as ---- indicate the concentration is out of range.

Repeat step 7 for all samples.


Press  to return to the Applications folder.


Press  to display available Options which are described below.



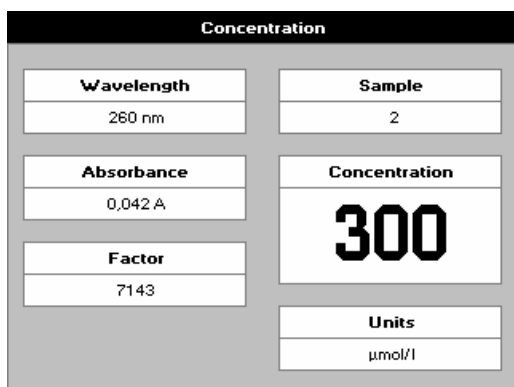
Step 6 (if using standard mode)

Insert the reference. Press 0A/100% key. This will be used for all subsequent samples until changed.


Press  to display the Run Standard screen.

Run the standard by pressing 
OR


Press cancel  to return to the measure screen.






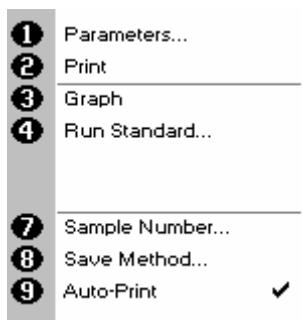
Step 7

Insert the sample and press .
The concentration of the sample is displayed. Results shown as ---- indicate the concentration is out of range.

Repeat step 7 for all samples.


Press  to return to the Applications Folder.

Press    to display available Options which are described below.



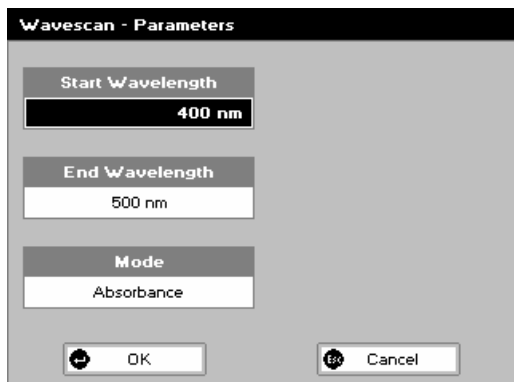
Options (select using key pad numbers)

1. Return to parameters screen (step 1 above).
2. Print result via selected method.
3. Toggles on/off, displaying a graph of wavescan +/- 20 nm from selected wavelength.
4. Return to Run Standard screen.
7. Sample number – add a prefix to the sample number and reset the incrementing number to the desired value.
8. Save method – use the left and right arrows to select a folder to store in (Favourites/Methods 1-9), press the down arrow and enter name.
9. Auto-print – toggles auto-print on/off.

Exit options by pressing , or wait.

3: Wavescan

An absorption spectrum can be obtained from your instrument, enabling simple identification of peak height and position. The procedure is as follows:



Wavescan - Parameters

Start Wavelength
400 nm

End Wavelength
500 nm

Mode
Absorbance

OK Cancel

Step 1

Set start wavelength by using keypad numbers or left and right arrows. Range 200 – 890 nm.

Press the down arrow key.

Step 2


Set end wavelength by using keypad numbers or left and right arrows. Range 210 – 900 nm.

Press the down arrow key.


Step 3

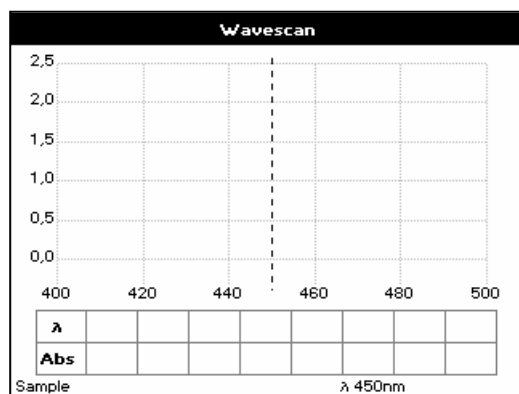
Select the mode, *Absorbance* or *%T*, using the left and right arrows.

Step 4

To enter the measurements screen with the selected parameters press OK .

OR


Cancel the selections and return to the Applications Folder by pressing Cancel .



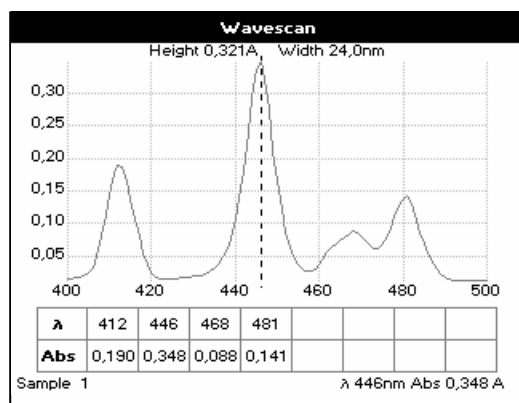
Step 5

Insert the reference. Press 0A/100% key. This will be used for all subsequent samples until changed.

Step 6

Insert sample and press .

Repeat step 6 for all samples.





Results

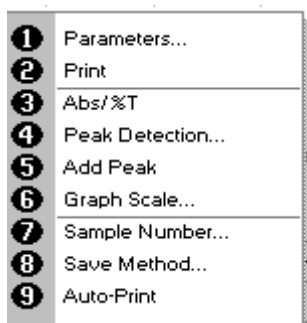
A graph of the wavescan is displayed, along with a table of Absorbance/%T at each peak. Use the left and right arrows to move the cursor along the graph. When it reaches a peak the peak height and width of the peak is displayed at the top of the screen.

To zoom in on the wavelength scale, use the up arrow. This auto-scales on the Absorbance/%T scale (dependent on the Graph Scale option) and this is retained for subsequent measurements.

To zoom out again, use the down arrow.

Press  to return to the Applications Folder.

Press  to display available Options which are described next.



Options (select using key pad numbers)

1. Return to parameters screen (step 1 above).
2. Print result via selected method.
3. Toggle between Absorbance and %T mode.
4. Displays Peak Detection Parameter Screen. See description below.
5. Manually adds a peak position to the peak table in the results screen at the position set by the cursor. If the cursor is returned to this position the legend "User Defined Peak" is displayed at the top of the scan and this option changes to Delete Peak.
6. Displays Graph Scale Parameter Screen. See description below.
7. Sample number – add a prefix to the sample number and reset the incrementing number to the desired value.
8. Save method – use the left and right arrows to select a folder to store in (Favourites/Methods 1-9), press the down arrow and enter name.
9. Auto-print – toggles auto-print on/off.

Exit options by pressing **Esc**, or wait.

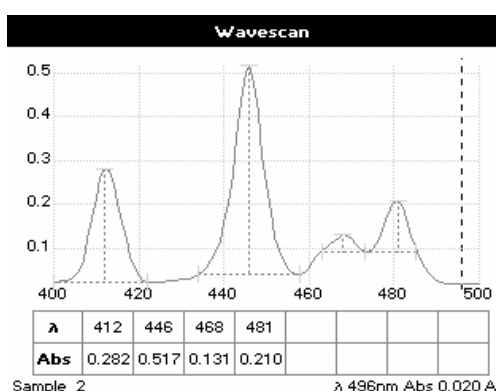
| Peak Detection | |
|--------------------------|--------------------------------|
| Auto-detect Peaks Yes | Peak Detect on Zoom Yes |
| Min Pk Height 0.01 | Sort Peaks By... Wavelength |
| Min Pk Width 5 nm | Draw Peaks No |
| OK | Cancel |

Peak Detection (Shortcut button 4)

AutoDetect Peaks: Turns on and off the automatic peak detection. The following options determine how peaks are detected:

Minimum peak height: Minimum height the peak has to be above the higher of the two adjacent minima for the peak to be detected


Minimum peak width: Minimum width of the peak as determined by the difference in wavelength between the higher of the two adjacent minima and the opposing intersection of that higher minimum level and the peak profile. (See the screen displayed below).

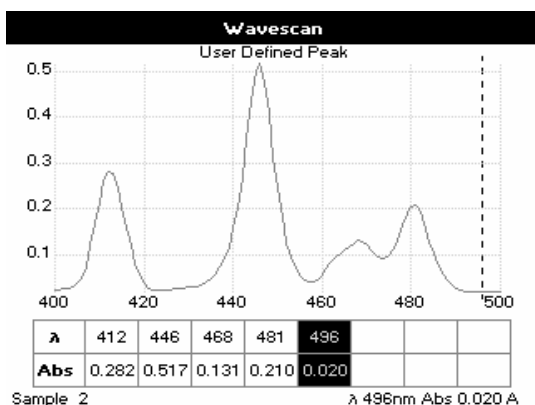


Peak Detect on Zoom: Determines whether peaks are re-assessed and tabulated when the user zooms into a region of the wavescan. If off leaves the peak detection as determined on the un-zoomed display

Sort peaks by...: Determines the sequence that peaks are reported by. Can be wavelength, peak height or peak width.

Draw Peaks: Switches display of peak cursors on and off. These show vertical dashed lines displaying the measured peak height and horizontal dashed lines showing the peak width

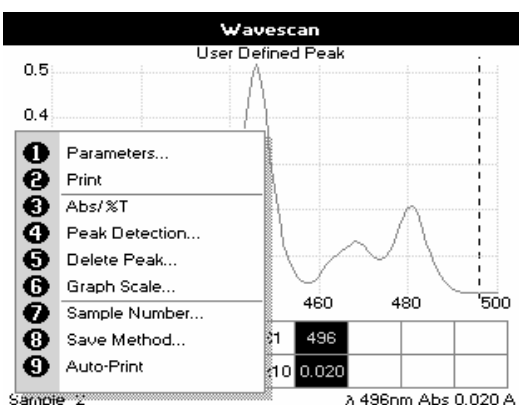
Pressing Cancel **Esc** ignores the selection, pressing OK  accepts them.



Add Peak... (Shortcut button 5)

Adds a user defined peak at the current cursor position. The entry is then displayed in inverse colouring to discriminate between user defined peaks and auto-detect peaks. When the cursor is positioned over the user defined peak a legend "User Defined Peak" appears at the top of the graph. The option then changes to Delete Peak to enable the user to remove the peak.

Note Storing a method at this stage will save these user defined wavelengths, each time method is run Absorbance value at these wavelengths is reported



Graph Scale

Zoom Mode
 ◀ x axis ▶

x axis limits
 Off

y axis limits
 Off

x1: 400 nm y1: 0.00
 x2: 500 nm y2: 2.50

OK Cancel

Graph Scale... (Shortcut button 6)



This enables the user to set up a defined graph by defining the limits in either or both of the x and y axes.

Zoom mode:

This sets up the operation of the Zoom keys (up and down arrows). "x & y axes" expands the display around the cursor measurement point, whilst the other options select the absorbance or wavelength axes respectively. With x or y axis limits set to on, zooming out will only be permitted to the set limits.

x/y axis limits:

Setting "x (or y) axis limits" to "On" activates the start and finish points of the desired graph to user defined specific wavelengths and/or absorbance values.

Pressing Cancel  ignores the selection; pressing OK  accepts them and displays the required graph.

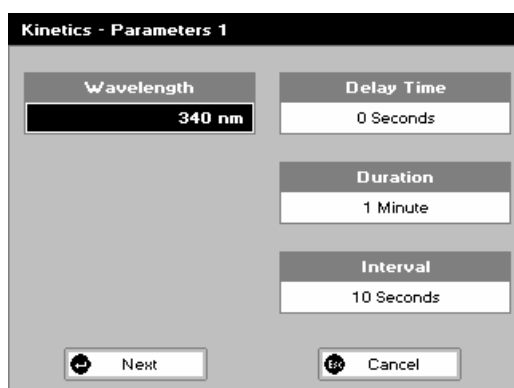
4: Simple Kinetics

Kinetics studies, where the change in absorbance needs to be followed as a function of time at a fixed wavelength, can be readily performed.

Reagent test kits are routinely used for the enzymatic determination of compounds in food, beverage and clinical laboratories by measuring NAD / NADH conversion at 340 nm. The change in absorbance over a specified time period can be used to provide useful information when an appropriate factor, defined in the reagent kit protocol, is applied. Reaction rate and enzyme activity can be calculated if the factor used takes account of the absorbance difference per unit time, as opposed to the absorbance difference *per se*.

For this reason, the change in absorbance per minute ($\Delta A/\text{min}$), concentration ($\Delta A/\text{min} \times \text{factor}$) and **correlation coefficient** (calculated from a best fit of the data points) are displayed. They may not be relevant for simple kinetics experiments.

The procedure to define a new method is as follows:



The screenshot shows the 'Kinetics - Parameters 1' screen. It has a dark header with the title. Below the header, there are four input fields arranged in two columns. The left column has 'Wavelength' with '340 nm' entered. The right column has 'Delay Time' with '0 Seconds' entered. Below these, there are two more input fields: 'Duration' with '1 Minute' and 'Interval' with '10 Seconds'. At the bottom, there are two buttons: 'Next' and 'Cancel', each with a small circular icon to its left.

Kinetics Parameter 1 Screen

Step 1 (Wavelength)

Enter the wavelength using the keypad numbers or the left and right arrows. Range 190-1100 nm.

Press the down arrow

Step 2 (Delay time)

Enter the delay time in seconds before measurements are taken. This can be a maximum of 600 seconds (10 minutes).

Press the down arrow.

Step 3 (Duration)

Enter the time in minutes over which measurements are taken. This can be a maximum of 60 minutes.


Press the down arrow.


Step 4 (Interval)

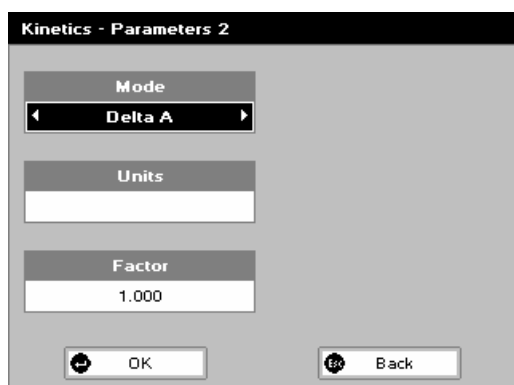
Enter the interval time in seconds between measurements using the left and right arrows. Options are: 1, 5, 10, 20, 30 or 60 seconds.

Press the down arrow.

Step 5

Press Next  to go to the next parameters screen
OR

Press Cancel  to return to the Applications Folder.



The screenshot shows the 'Kinetics - Parameters 2' screen. It has a dark header with the title. Below the header, there are three input fields. The first is 'Mode' with a dropdown menu showing 'Delta A'. The second is 'Units' with an empty text box. The third is 'Factor' with '1.000' entered. At the bottom, there are two buttons: 'OK' and 'Back', each with a small circular icon to its left.

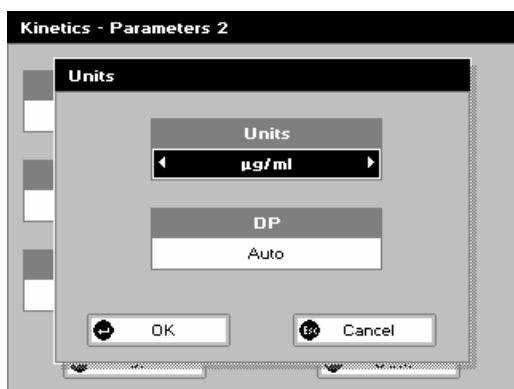
Kinetics Parameters 2 Screen

Step 6




Select the measurement mode using the left and right arrows. Delta A: change in absorbance over the measurement duration (or selected period).

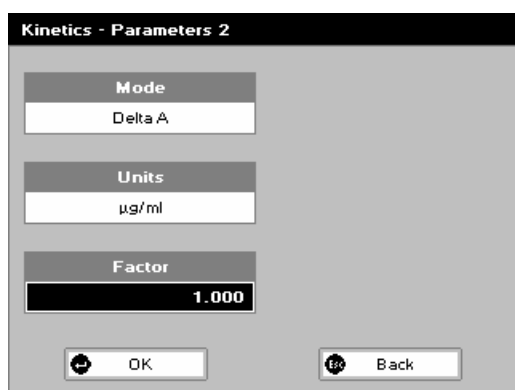
Final A: absorbance at the end of the measurement duration (or selected time).

Slope: rate of change of absorbance over the measurement duration or selected period.



Step 7


Units: The user can enter a text string up to 8 characters long. To access a list of pre-defined units press the Options key  and then use the left/right arrows (µg/ml, µg/µl, pmol/µl, mg/dl, mmol/l, µmol/l, g/l, mg/l, µg/l, U/l, %, ppm, ppb, conc or none). These units can also be edited once OK is pressed. This screen also allows the number of displayed decimal points (DP) to be selected, from 0 to 2. Note that the result will always be fixed to 5 significant figures regardless of how many decimal points are selected (so 98768.2 will display as 98768 even with 1 decimal point selected). Press OK  to store the chosen parameters or Cancel .




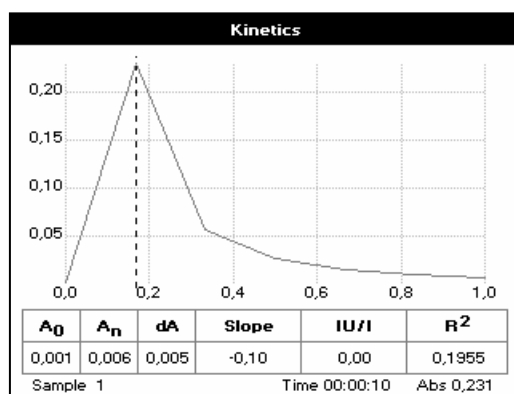
Step 8

Set the Factor by which the result is multiplied to give the amount in the chosen range using the left and right arrows. Range of 0.01 to 9999.

Step 9

Press OK  to enter the Results screen
OR

Press Back  to return to the Parameters 1 screen.



Results

Insert the reference and press the 0A/100%T key.


Insert the sample and press  to start the run.

Time (min) is displayed at the bottom of the screen, and absorbance data are plotted on the graph as testing proceeds. The table below the graph gives: absorbance values at T₀ (start of calculation), T_n (finish of calculation, change in absorbance, slope, regression parameter (R²) of the calculated slope and the result calculated from the selected parameter (dA, final A or slope).

Use the left and right arrows to move the cursor and display the time and absorbance value at measured data points.

Use the up and down arrows to zoom in or out.

Press Cancel  to return to the Applications Folder.

Press  to display available Options which are described below.



Options (select using key pad numbers)

1. Return to parameter 1 screen (step 1 above).
2. Print data on the results screen via selected method.
3. Print all the data.
4. Set the t_0 position (starting point for the slope and dA calculation) at the current cursor position. Value is retained for subsequent samples.
5. Set the t_n position (finishing point for the slope and dA calculation) at the current cursor position. Value is retained for subsequent samples.
6. Toggle the calculated slope line on and off.
Note: if any data points enclosed by t_0 and t_n are beyond the range of the instrument ($>2.5A$ or $<-0.3A$) then this option is greyed out.
7. Sample number – add a prefix to the sample number and reset the incrementing number to the desired value.
8. Save method – use the left and right arrows to select a folder to store in (Favourites/Methods 1-9), press the down arrow and enter name.
9. Auto-print – toggles auto-print on/off.

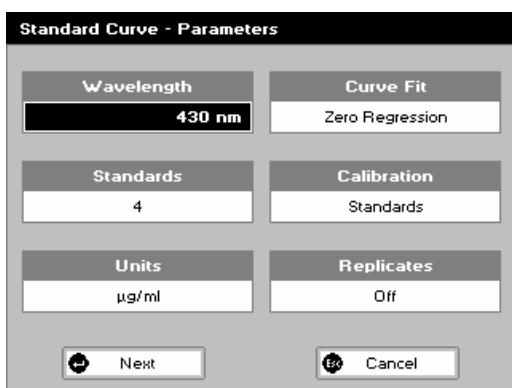
Exit options by pressing **Esc**, or wait.

5: Standard Curve

The construction of a multi-point calibration curve from standards of known concentration to quantify unknown samples is a fundamental use of a spectrophotometer; this instrument has the advantage of being able to store this curve as a method, using up to 9 standards.

To include a zero concentration standard, include this in the number of standards to be entered and enter 0.00 for concentration; use a reagent blank when required to enter the zero standard.

The procedure is as follows:



The 'Standard Curve - Parameters' screen displays several settings in a grid. The 'Wavelength' field is set to '430 nm'. The 'Curve Fit' field is set to 'Zero Regression'. The 'Standards' field is set to '4'. The 'Calibration' field is set to 'Standards'. The 'Units' field is set to 'µg/ml'. The 'Replicates' field is set to 'Off'. At the bottom, there are 'Next' and 'Cancel' buttons.

Step 1

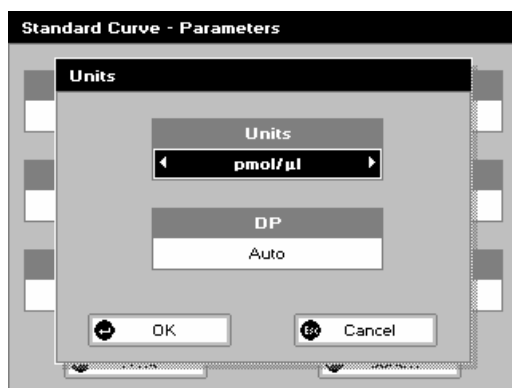
Select the wavelength using the keypad numbers or left and right arrows. Range 190-1100 nm.

Press the down arrow.

Step 2

Enter the number of standard concentration points to be used in the curve (1-9).


Press the down arrow.



The 'Units' selection screen is shown as a modal window. It has a 'Units' field with a dropdown menu currently showing 'pmol/µl'. Below it is a 'DP' (Decimal Points) field set to 'Auto'. At the bottom are 'OK' and 'Cancel' buttons.

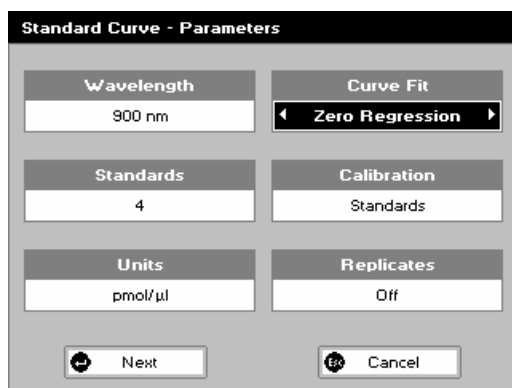
Step 3

Units: The user can enter a text string up to 8 characters long.

To access a list of pre-defined units press the Options key  and then use the left/right arrows (µg/ml, µg/µl, pmol/µl, mg/dl, mmol/l, µmol/l, g/l, mg/l, µg/l, U/l, %, ppm, ppb, conc or none). These units can also be edited once OK is pressed.

This screen also allows the number of displayed decimal points (DP) to be selected, from 0 to 2. Note that the result will always be fixed to 5 significant figures regardless of how many decimal points are selected (so 98768.2 will display as 98768 even with 1 decimal point selected).

Press OK  to store the chosen parameters or Cancel .



The 'Standard Curve - Parameters' screen is shown again. The 'Wavelength' field is now set to '900 nm'. The 'Curve Fit' field is set to 'Zero Regression'. The 'Standards' field is set to '4'. The 'Calibration' field is set to 'Standards'. The 'Units' field is set to 'pmol/µl'. The 'Replicates' field is set to 'Off'. At the bottom, there are 'Next' and 'Cancel' buttons.

Step 4

Select the type of curve fit using the left and right arrows.

Options: straight line regression, a zero regression (this forces the straight line through the origin), interpolated or cubic spline.

Step 5


Select the calibration mode: either Standards (measure prepared standards) or Manual (keypad data entry).


Press the down arrow.

Step 6 (if standards has been selected in step 5)

Select the number of standards to be measured and averaged at each standard concentration point. Can be OFF (1), 2 or 3.

Step 7

Press Next  to enter the Standards screen
OR

Press Cancel  to cancel selections and return to the Applications Folder.

Standard Curve - Standards

| | |
|--------|--------|
| Std. 1 | Std. 4 |
| 10.0 | 62.0 |
| Std. 2 | |
| 20.0 | |
| Std. 3 | |
| 31.0 | |


Next Back

Standards screen

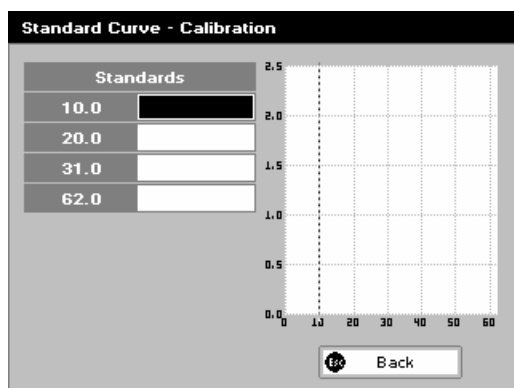
Step 8

Enter the concentration values by using the keypad numbers and the up and down arrows to move between the different standard boxes. Range 0.001 to 9999.

Step 9

Press Next  to enter the Calibration screen. If any duplicate or non-monotonic (increasing entries) are present the unit will beep and highlight the incorrect entry
OR

Press Back  to return to the Parameter screen.



Calibration Screen (replicates off)

This shows the calibration values and allows standards to be measured.


Step 10

Insert the reference. Press 0A/100% key.

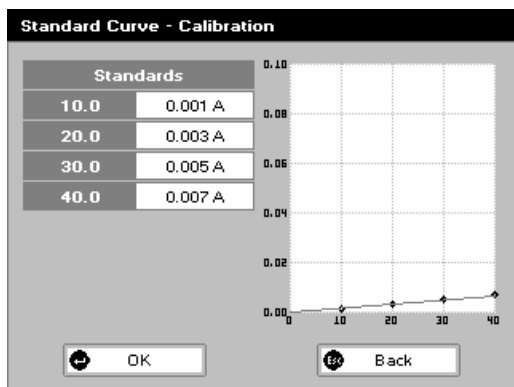
This will be used for all subsequent samples until changed.

Step 11

Insert the standard (use C to clear previously stored results before measuring).

Press  to measure the standard and store the result.


Repeat for all standards.



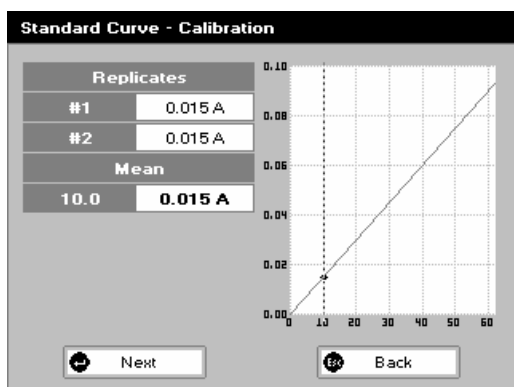
A graph will display the results and the fitted curve as the measurements are input.

Use the up and down arrows to select a standard to be repeated if a poor reading has been obtained. Use C to clear the previous reading.

Step 12

Press OK  to accept the calibration and go to the Results screen (see below)
OR

Press Back  to return to the Standards screen.



Calibration Screen (replicates on)

This shows the calibration values and allows standards to be measured.

Step 10

Insert the reference. Press 0A/100% key.

This will be used for all subsequent samples until changed.

Step 11

Press replicates to display the replicate entry boxes. Use C to clear previously stored results before measuring.

Insert the standard and press to measure the standard and store the result.

Repeat for all replicates. Press Next to measure the next standard and repeat the process for all standards.

A graph will display the results and the fitted curve as the measurements are input.

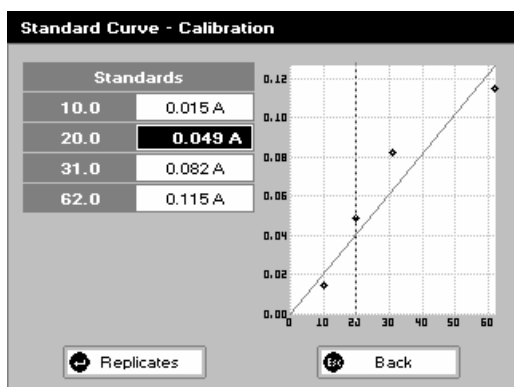
Use the up and down arrows to select a standard to be repeated if a poor reading has been obtained. Use C to clear the previous reading.

Step 12

Press Next to accept the calibration and go to the Results screen (see below)

OR

Press Back to return to the Standards screen.



Calibration (Manual entry)

Shows previously entered calibration values and allows values to be entered via the keypad.

The highlighted box can be edited in order to enter an absorbance value corresponding to a given concentration value using the keypad numbers. Range 0.001 to 9999. Use C to backspace and clear the last digit entered and the up and down arrows to move between boxes.

Press OK to accept the calibration and go to the Results screen (see below)

OR

Press Back to return to the Standards screen.

Standard Curve

| | |
|-------------------------------------|-------------------------------------|
| Wavelength 430 nm | Sample 1 |
| Absorbance 0.083 A | Concentration 40.8 |
| Curve Fit Zero Regression | Units mg/l |

Results screen

Step 13

Insert the reference and press the 0A/100%T key. This will be used for all subsequent samples until changed.

Step 14

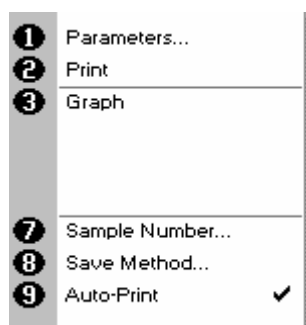
Insert the sample and press .

The concentration of the sample is taken and displayed.

Repeat step 14 for all samples.

Press to return to the Applications Folder.

Press to display available Options which are described



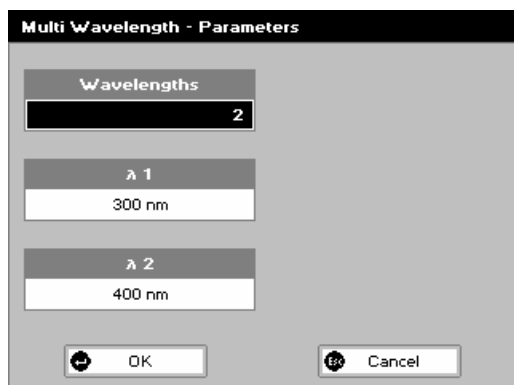
Options (select using key pad numbers)

1. Return to parameters screen (step 1 above).
2. Print result via selected method.
3. Toggle graph on/off. Displays calibration graph, cursors give values for last measured sample.
7. Sample number – add a prefix to the sample number and reset the incrementing number to the desired value.
8. Save method – use the left and right arrows to select a folder to store in (Favourites/Methods 1-9), press the down arrow and enter name.
9. Auto-print – toggles auto-print on/off.

Exit options by pressing **Esc**, or wait.

6: Multiple Wavelength

This makes up to 5 absorbance measurements on the same sample. The procedure is as follows:



The 'Multi Wavelength - Parameters' screen shows a 'Wavelengths' field with the value '2'. Below it are two wavelength input fields: 'λ 1' with '300 nm' and 'λ 2' with '400 nm'. At the bottom are 'OK' and 'Cancel' buttons.


Step 1

Select the number of wavelengths. Range 2-5.
Press the down arrow.

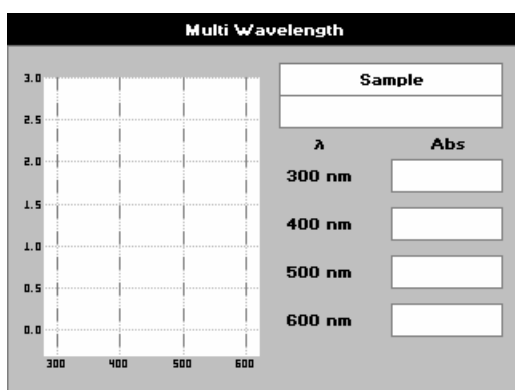
Step 2

Enter the first wavelength using either the number keys or the left and right arrows.
Press the down arrow.
Enter the second wavelength as above and repeat for the number of wavelengths selected (up to 5).

Step 3

Press OK  to enter the results screen
OR


Press Cancel  to return to the Applications Folder.



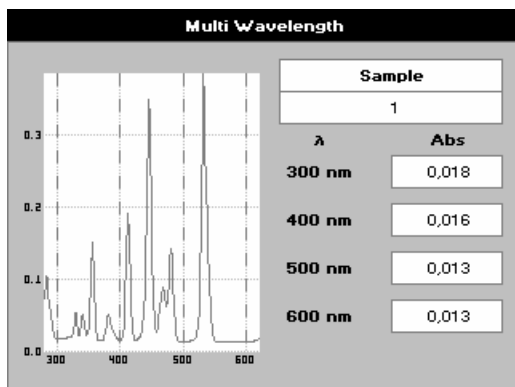
Step 4

Insert the reference. Press 0A/100% key. This will be used for all subsequent samples until changed.

Step 5


Insert sample and press .


Repeat step 5 for all samples.

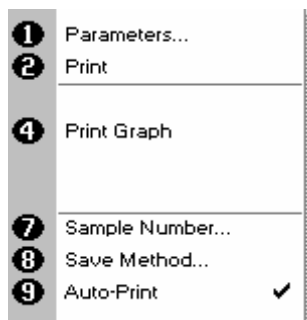


Results

A scan plot covering the range of wavelengths selected (with cursors at the relevant wavelengths) and a table of values is displayed.

Press  to return to the Applications Folder.

Press  to display available Options which are described below.



The 'Options' menu is a vertical list with the following items: 1 Parameters..., 2 Print, 4 Print Graph, 7 Sample Number..., 8 Save Method..., and 9 Auto-Print. The 'Auto-Print' option is checked with a small checkmark.

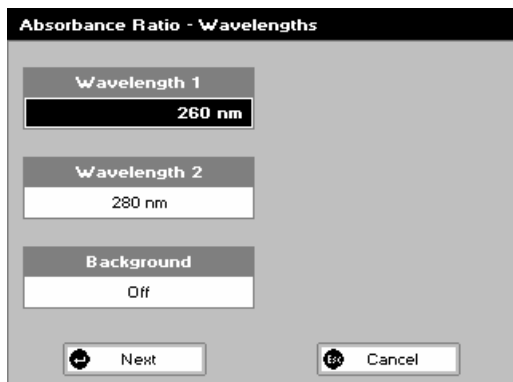
Options (select using key pad numbers)

1. Return to parameters screen (step 1 above).
2. Print result via selected method.
4. Print graph using selected method. Grayed out if no data are available.
7. Sample number – add a prefix to the sample number and reset the incrementing number to the desired value.
8. Save method – use the left and right arrows to select a folder to store in (Favourites/Methods 1-9), press the down arrow and enter name.
9. Auto-print – toggles auto-print on/off.

Exit options by pressing , or wait.

7: Absorbance Ratio

This makes simple absorbance ratio measurements on samples, measuring the amount of light that has passed through a sample relative to a blank (this can be air) at two wavelengths. The procedure is as follows:



The 'Absorbance Ratio - Wavelengths' screen has a black header. Below it, there are three input fields: 'Wavelength 1' with '260 nm', 'Wavelength 2' with '280 nm', and 'Background' with 'Off'. At the bottom, there are two buttons: 'Next' and 'Cancel', each with a small circular icon to its left.

Step 1

Enter the first wavelength by using the keypad numbers or the left and right arrows.

Press the down arrow.

Step 2

Enter the second wavelength as above.

Press the down arrow.


Step 3

Select whether a background correction is applied to both wavelengths 1 and 2 using the left and right arrows.

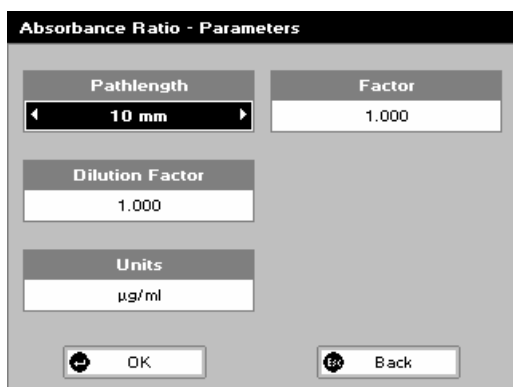
Step 4 (If background correction is On)

Enter the third wavelength, from which the background correction will be obtained).

Step 5

Press Next  to enter the Parameters screen
OR

Press Cancel  to return to the Applications Folder.



The 'Absorbance Ratio - Parameters' screen has a black header. It contains four input fields: 'Pathlength' with '10 mm', 'Factor' with '1.000', 'Dilution Factor' with '1.000', and 'Units' with 'µg/ml'. At the bottom, there are two buttons: 'OK' and 'Back', each with a small circular icon to its left.

Absorbance Ratio – Parameters Screen

Step 6

Select the pathlength (5 or 10 mm) using the left and right arrows.


Press the down arrow.

Step 7 (Dilution Factor known)

Enter a dilution factor by using the keypad numbers within the range 1.00 – 9999.

OR


Step 7 (Calculate Dilution Factor)

Press the options key: .

Enter the volume of the sample (range 0.01 – 9999), using the keypad numbers.

Press the down arrow.

Enter the volume of diluent (range 0.01-9999) by using the keypad numbers.

Press OK  to calculate the dilution factor and return to the

Parameters screen (or press Cancel,  to cancel selections).



Step 8

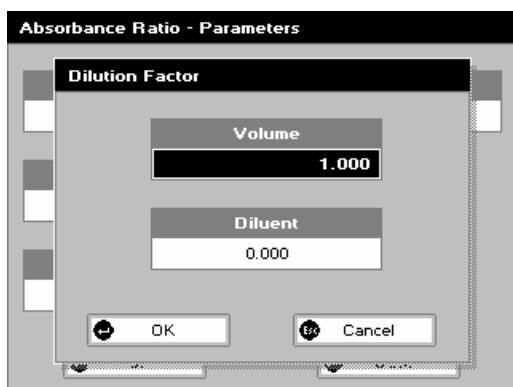
Select units of measurement, using left and right arrows. Options are: µg/ml, ng/µl, µg/µl.

Press the down arrow.

Step 9

Enter the factor using the keypad numbers (Range 0.001 to 9999).

Press OK  to enter the results screen or Cancel  to return to the Applications Folder.



The 'Absorbance Ratio - Parameters' screen is shown with a sub-screen titled 'Dilution Factor' overlaid. The sub-screen has two input fields: 'Volume' with '1.000' and 'Diluent' with '0.000'. At the bottom of the sub-screen are 'OK' and 'Cancel' buttons, each with a small circular icon to its left.


| Absorbance Ratio | |
|------------------|-------------|
| 260 nm | Sample |
| 0,258 A | 1 |
| 280 nm | Ratio |
| 0,166 A | 1,55 |
| Concentration | |
| 0,26 µg/ml | |

Results Screen

Step 10


Insert the reference. Press 0A/100% key. This will be used for all subsequent samples until changed.


Step 11


Insert sample and press .

Repeat step 11 for all samples.

The absorbance at selected wavelengths is measured and the ratio between wavelengths 1 and 2 is calculated (both corrected by the background wavelength value if this was selected).

Press  to return to the Applications Folder.

Press  to display available Options which are described below.

| | |
|---|--|
| 1 | Parameters... |
| 2 | Print |
| 3 | Graph |
| | |
| 7 | Sample Number... |
| 8 | Save Method... |
| 9 | Auto-Print  |

Options (select using key pad numbers)

1. Return to parameters screen (step 1 above).
2. Print result via selected method.
3. Toggle graph on/off. Graph shows a wavescan plot across the selected wavelengths in place of the individual wavelength.
7. Sample number – add a prefix to the sample number and reset the incrementing number to the desired value.
8. Save method – use the left and right arrows to select a folder to store in (Favourites/Methods 1-9), press the down arrow and enter name.
9. Auto-print – toggles auto-print on/off.

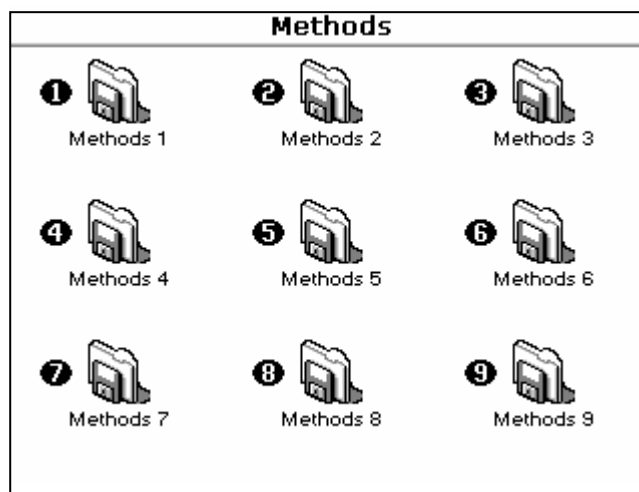
Exit options by pressing , or wait.

FAVOURITES AND METHODS FOLDERS

These folders are the storage locations for any user modified Applications (Methods) that are saved in the Options menu. Both are accessible from the home folders page.

Favourites:

This folder enables the user to quickly select any frequently used Methods. Up to 9 Methods may be stored in the folder.

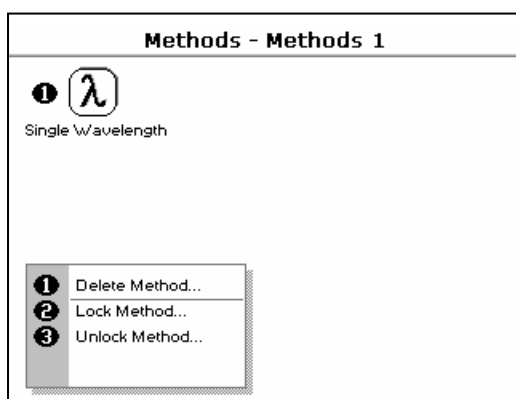


Methods:

These are further storage folders enclosed in the top level Methods folder. Up to 9 Methods may be stored in each folder.

Operation is identical to the Favourites Folder.

Saved methods can be locked, unlocked and deleted using the Options menu. Select the method by pressing the relevant key pad number and then press the **☒☒☑** key.



Delete Method

Press 1 to select delete method.

Select the method to be deleted using the left and right arrows.

Press **←** to delete the method OR cancel **Esc** to return to Favourites/Methods folder.

Lock Method

Press 2 to select lock method.

Select the method to be locked using the left and right arrows.

Press the down arrow.

Select a pass code using the keypad numbers or left and right arrows.

Press **←** to lock the method OR cancel **Esc** to return to the Favourites/Methods folder.

Unlock Method

Press 3 to select unlock method.

Select the method to be unlocked using the left and right arrows.

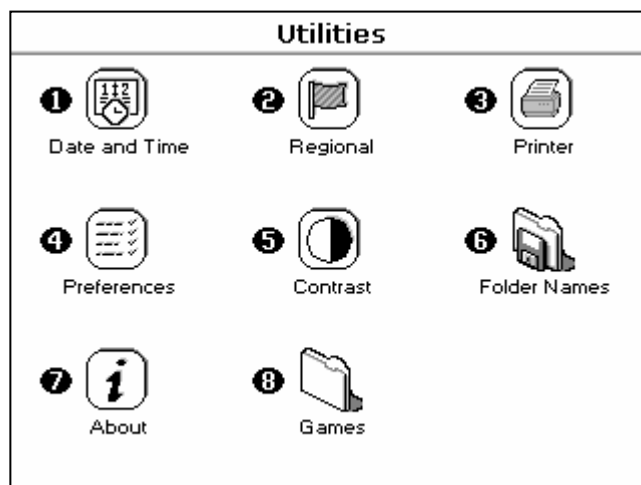
Press the down arrow.

Enter the pass code using the keypad numbers or left and right arrows.

Press **←** to unlock the method OR cancel **Esc** to return to the Favourites/Methods folder.

UTILITIES FOLDER

Press 5 to enter the utilities folder.



Summary Function

Keypad number

Description



Date and Time

1

Set correct time and date



Regional

2

Select preferred language and number format



Printer

3

Printer/output options



Preferences

4

Select screen layout (themes) and history



Contrast

5

Adjust screen contrast & brightness



Folder Names

6

Re-name Method folders



About

7

Serial number and software version



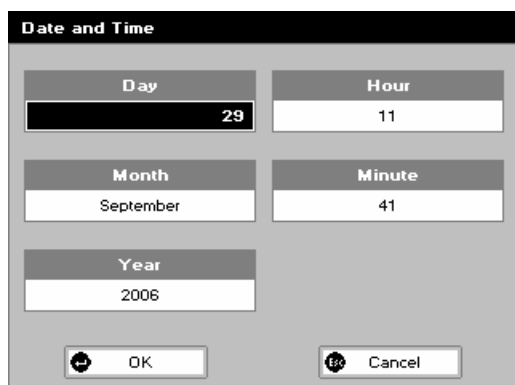
Games

8

Spectro Blocks/Sudoku


1: Date and Time


The procedure is as follows:



The 'Date and Time' screen has a black header with the title in white. Below the header, there are four input fields arranged in a 2x2 grid. The top-left field is labeled 'Day' and contains the number '29'. The top-right field is labeled 'Hour' and contains the number '11'. The bottom-left field is labeled 'Month' and contains the text 'September'. The bottom-right field is labeled 'Minute' and contains the number '41'. Below these fields is a 'Year' field containing '2006'. At the bottom of the screen are two buttons: 'OK' on the left and 'Cancel' on the right, both with a small circular icon to their left.

Enter the day using the keypad numbers or left and right arrows.
Press the down arrow.
Enter the month as above.
Press the down arrow.
Enter the year.
Press the down arrow.
Enter the hour.
Press the down arrow.
Enter the minute. Seconds are zeroed when OK is pressed.

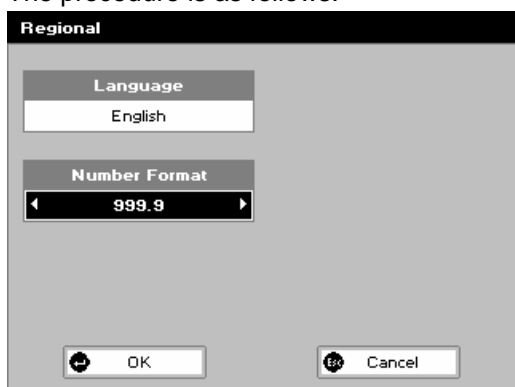
Press OK  to store the settings and return to the Utilities folder
OR

Press Cancel  to return to the Utilities folder without storing the time.

2: Regional

Sets Language and Number Format

The procedure is as follows:




The 'Regional' screen has a black header with the title in white. Below the header, there are two input fields. The top field is labeled 'Language' and contains the text 'English'. The bottom field is labeled 'Number Format' and contains the text '999.9'. At the bottom of the screen are two buttons: 'OK' on the left and 'Cancel' on the right, both with a small circular icon to their left.


Select a language. Options are English, French, Spanish, Italian or Japanese.

Press the down arrow.

Set the decimal point style. Options are “,” or “.”.

Press OK  to store the settings and return to the Utilities folder

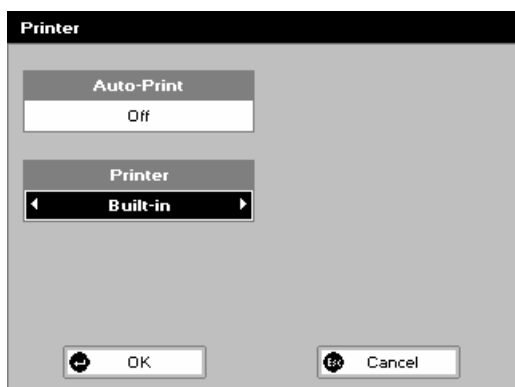
OR

Press Cancel  to return to the Utilities folder without storing the settings.


3: Printer

Sets up printing options

The procedure is as follows:




The 'Printer' screen has a black header with the title in white. Below the header, there are two input fields. The top field is labeled 'Auto-Print' and contains the text 'Off'. The bottom field is labeled 'Printer' and contains the text 'Built-in'. At the bottom of the screen are two buttons: 'OK' on the left and 'Cancel' on the right, both with a small circular icon to their left.


Select whether auto-print is on or off using the left and right arrows. When auto-print is on, the results are automatically printed after a measurement is taken. When it is off, printing has to be initiated manually. This can also be set using the Options key () in each application or method. The default is OFF.

Press the down arrow.

Select how the data are sent. Options are Built in (internal printer), or to a computer via USB port or Bluetooth.

Press OK  to store the settings and return to the Utilities folder

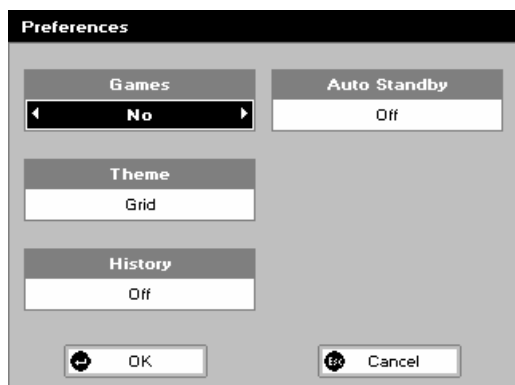
OR

Press Cancel  to return to the Utilities folder without storing the settings.

4: Preferences

Sets user preferences

The procedure is as follows:



Select games function. This determines whether the games folder is displayed or not. Options are yes or no.

Press the down arrow.


Define the screen layout of folders. Options are either a grid format (default) or a list.

Press the down arrow.


Select whether to use previously entered parameters when the instrument is switched on or to use defaults.

Press the down arrow.

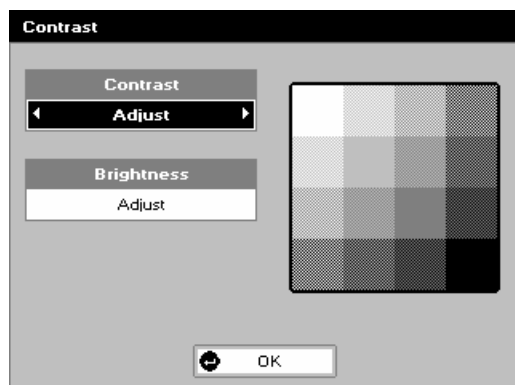
Select whether to use a standby mode after defined periods. Options are 1 hour, 2 hours, at night or off.

Press OK  to store the settings and return to the Utilities folder

OR

Press Cancel  to return to the Utilities folder without storing the settings.

5: Contrast




Adjust the contrast using the left and right arrows.

Press the down arrow.

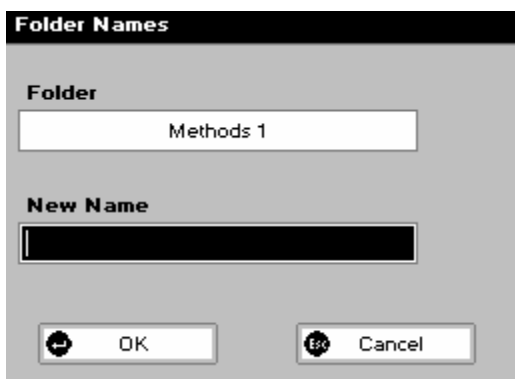
Adjust the brightness using the left and right arrows.

Press the down arrow.

Press OK  to store the settings and return to the Utilities folder

Ambient temperature can affect the display. This function can optimise the display for local conditions
The procedure is as follows:


6: Folder Names




Select the folder you wish to rename using the left and right arrows.

Press the down arrow.

Input the new name for the folder.

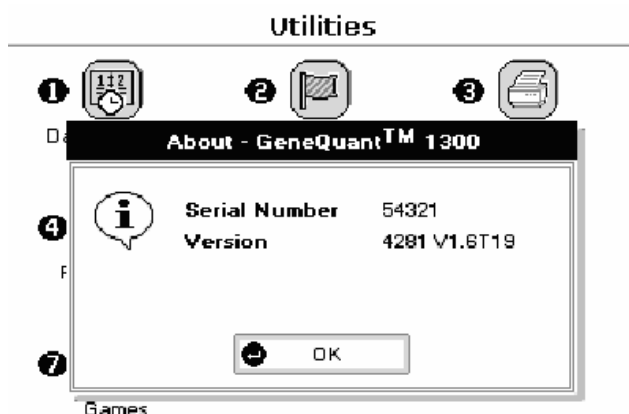
Press OK  to store the settings and return to the Utilities folder

OR


Press Cancel  to return to the Utilities folder without storing the settings.

This folder allows you to rename the method or favourite folders

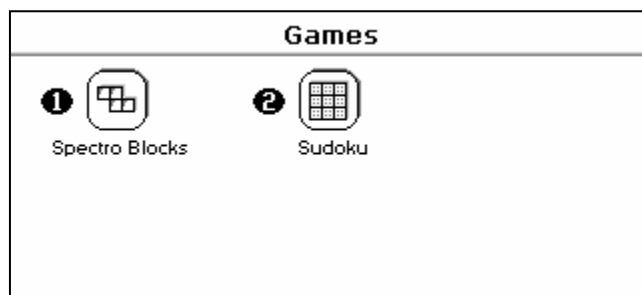
7: About



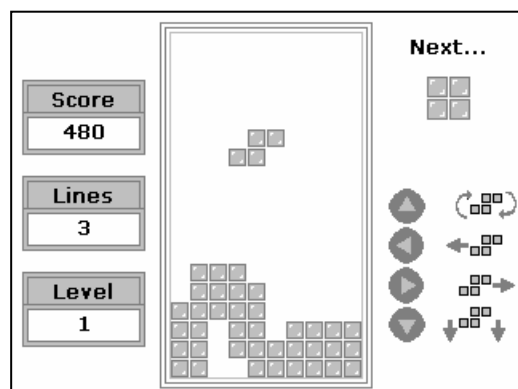
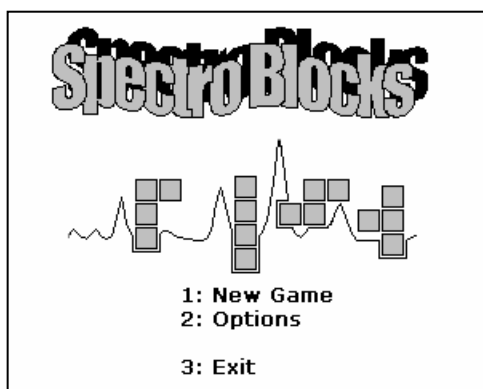
Displays the instrument serial number and software version.

Press OK  to close the window and return to the Utilities folder

8: Games



1: Spectroblocks



Classic block dropping game. Follow the instructions!

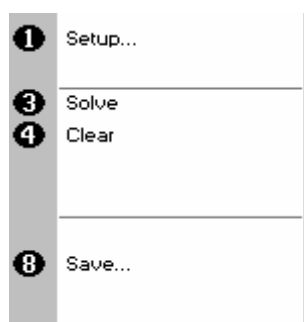
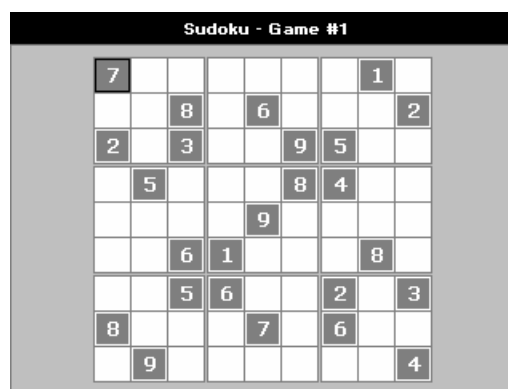
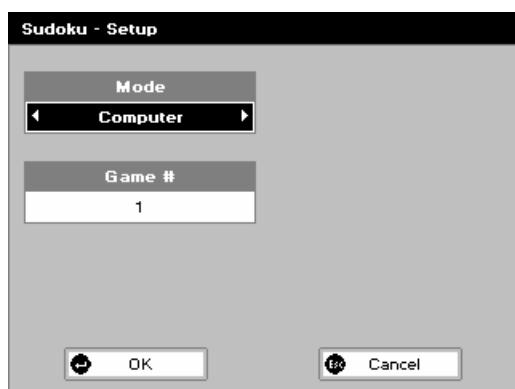
Press Cancel  to return to the Utilities folder without storing the settings.

2: Su Doku

Can be set up as Computer mode (50 preset games) or User mode (enter your own pattern)

Use the cursors to select the square and the key pad to enter a number. Invalid numbers cannot be entered. Cells can be locked (or unlocked) by using the decimal point. Unlocked cells can be cleared using the C key (see also option key below)

The user mode starts with a blank grid.



Options

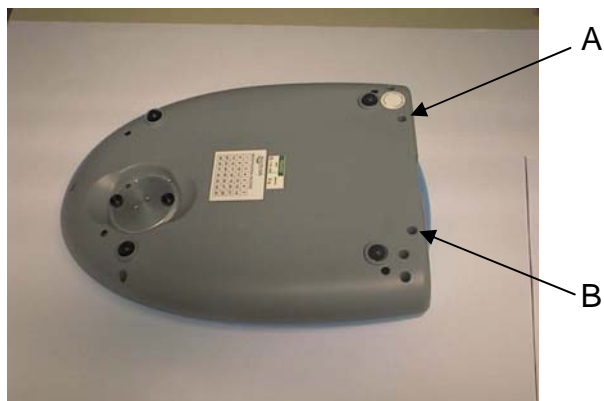
Press **ⓧⓧⓧ** to display the options menu

1. Return to the set-up screen.
3. The instrument solves the game for you!
4. Clear all entries.
8. Save the game. Use the left and right arrows to select a folder to store the game in (Favourites, Methods 1-9), press the down arrow and enter name.

Press Cancel **Esc** to return to the Utilities folder.

ACCESSORIES INSTALLATION

Printer installation



1. REMOVE THE POWER CABLE FROM THE INSTRUMENT. Turn the instrument over and remove cap head screws from positions A and B using the Allen key provided.



2. Turn the instrument back over and lift the accessory cover vertically upwards to remove. Remove the tie-wrap from the cable.



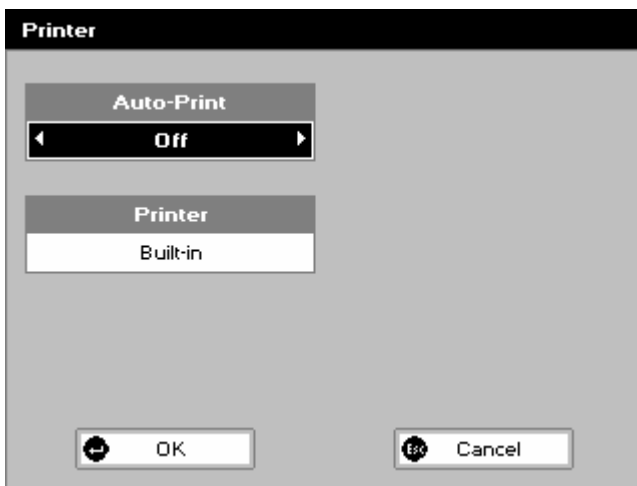
3. Plug the accessory cable into the printer.



4. Lower the printer onto the locating bosses and push down firmly.
5. Invert the instrument and replace the cap head screws at A and B.

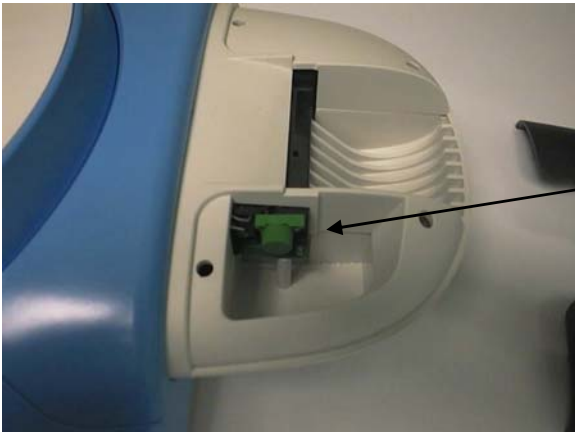


6. Replace the top cover plate, invert the instrument and replace the cap head screws at locations A and B shown in step 1.

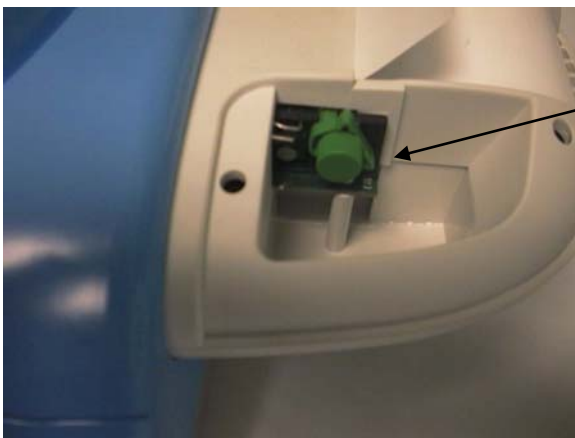


7. Switch the instrument on and go to utilities/instrument/preferences and select the Built-in printer

Loading / changing the printer paper



1. Lift off the paper cover.
2. Lock the platen and turn the knob to feed the paper
3. Feed in the paper.



4. Sometimes it helps if the platen lock is released.



5. Paper gripped.

6. Cover replaced.



Bluetooth accessory installation



1. REMOVE THE POWER CABLE FROM THE INSTRUMENT. Turn the instrument over and remove the cap head screws from positions A and B using the Allen key provided.



2. Turn the instrument back over and lift the accessory cover vertically upwards to remove. Remove the tie-wrap from the cable



3. Plug the accessory cable into the Bluetooth module.



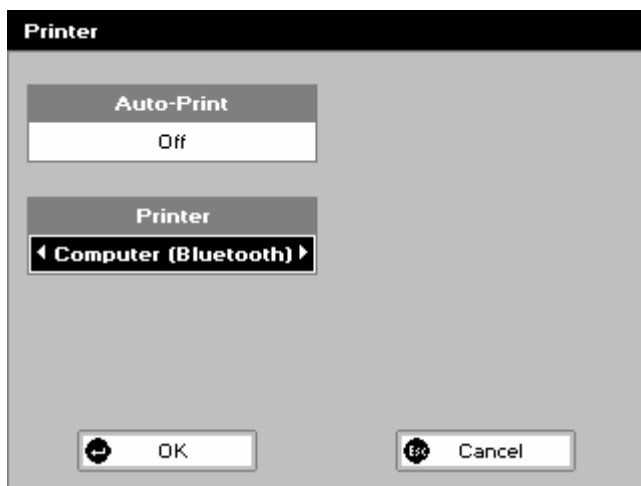
5. Note the slots in the base of the case. The two lugs on the Bluetooth module plug into these



5. Load the rear cover into the two slots provided, note the large flange is to face upwards. Re-fit the top plate.
6. Invert the instrument and replace the cap head screws at A and B as shown in section 1 earlier.



6. Attach the license label as shown.



6. Switch the instrument on and go to the preferences page under utilities/instrument, and select the Bluetooth option.

PRINT VIA COMPUTER

- PVC (Print Via Computer) is a small application running under Windows 2000™, Windows XP™ or Windows Vista™ to enable a GeneQuant™ 1300 to transfer data into a PC environment. From there the user has a selection of choices, the data can be both printed or saved (in a variety of formats). PVC is capable of supporting several instruments simultaneously, limited only by hardware and the speed of the host system.
- PVC can operate via USB and Bluetooth simultaneously
- PVC can store data either to a common directory or be configured to save to independent directories by both file format and connection.
- PVC can save data in graphics format, text format or as an Excel™ file

Installation

See the manual included on the PVC CDROM for installation and operating instructions.

ACCESSORIES

| | |
|----------------------------|----------------|
| USB cable | source locally |
| Built-in printer accessory | 80-3003-84 |
| Bluetooth accessory | 80-3003-96 |

MAINTENANCE

After Sales Support

Support agreements that help you to fulfil the demands of regulatory guidelines concerning GLP/GMP are available.

- Calibration, certification using filters traceable to international standards
- Certificated engineers and calibrated test equipment
- Approved to ISO 9001 standard

Choice of agreement apart from break down coverage can include

- Preventative maintenance
- Certification

When using calibration standard filters, insert such that the flat surface is facing away from the spring end of the cell holder.

Observe all necessary precautions if dealing with hazardous samples or solvents.

Lamp Replacement

The xenon lamp should not need replacement until after several years of use. In the unlikely event that it does need replacing, this should be undertaken by a service engineer from your supplier.

Cleaning and general care of the instrument

External cleaning

Switch off the instrument and disconnect the power cord.

Use a soft damp cloth.

Clean all external surfaces.

A mild liquid detergent may be used to remove stubborn marks.

Changing cell holder or removal for cleaning

This can be removed by undoing the appropriate screws on the bottom of the instrument.

SPECIFICATION AND WARRANTY

| | |
|------------------------------------|--|
| <i>Wavelength range</i> | 190 - 1100 nm |
| <i>Monochromator</i> | Flat grating |
| <i>Wavelength calibration</i> | Automatic upon switch on |
| <i>Spectral bandwidth</i> | 5 nm |
| <i>Wavelength accuracy</i> | ±2 nm |
| <i>Wavelength reproducibility</i> | ±1 nm |
| <i>Light sources</i> | Pulsed xenon lamp |
| <i>Detector</i> | 1024 element CCD array |
| <i>Photometric range</i> | - 0.300 to 2.500A, 0 to 199%T |
| <i>Photometric linearity</i> | ±0.005 Abs or 1% of the reading, whichever is the greater @ 546 nm |
| <i>Photometric reproducibility</i> | ±0.003 Abs (0 to 0.5 Abs), ±0.007 Abs (0.5-1.0 Abs) |
| <i>Stray light</i> | <0.5% at 220 nm and 340 nm using NaNO ₂ |
| <i>Zero stability</i> | ±0.01 Abs/hour after 20 min warm up @ 340 nm |
| <i>Noise</i> | 0.005 pk to pk 0.002 pms |
| <i>Digital output</i> | USB port standard, Bluetooth option |
| <i>Dimensions</i> | 260 x 390 x 100 mm |
| <i>Weight</i> | <4.5 kg |
| <i>Power input</i> | 18Vdc from a 90-250 V, 50/60 Hz, Max 30 VA mains power pack |

Specifications are measured after the instrument has warmed up at a constant ambient temperature and are typical of a production unit. As part of our policy of continuous development, we reserve the right to alter specifications without notice.

Warranty

- General Electric Healthcare guarantees that the product supplied has been thoroughly tested to ensure that it meets its published specification. The warranty included in the conditions of supply is valid for 12 months only if the product has been used according to the instructions supplied. General Electric Healthcare can accept no liability for loss or damage, however caused, arising from the faulty or incorrect use of this product.
- This product has been designed and manufactured for General Electric Healthcare by Biochrom Ltd, 22 Cambridge Science Park, Milton Road, Cambridge CB4 0FJ, UK. However, please contact General Electric Healthcare in the first instance if you experience technical or sample handling difficulties.