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SAFETY
Spectrophotometer Health & Safety Document including General Operating Instructions are available as a booklet provided with each instrument. The booklet, translated into the European Union languages, is available on the delivered CD. The instructions provide the user with basic use, troubleshooting and how to use the instrument in a safe manner.

**CAUTION**
This instrument contains a UV source that generates a light beam which traverses the sample cell holder. Do not attempt to divert the beam or operate with casework removed as prolonged exposure to the beam may cause permanent eye damage.

**WARNING**
High voltages exist inside these units. Repair and maintenance should only be carried out by individuals trained specifically to work on these instruments.

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conditions not appropriate for safe operation, the protection provided may be impaired and the instrument warranty withdrawn.

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 40°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 (< 3.5 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 to 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.
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™ 100" offering the choice of:

- Life Science Methods: Standard Life Science methods such as nucleic acid assays, protein assays and cell counting
- Application: Absorbance & Concentration measurements
- Methods: Folder for storing user defined methods
- Utilities: Instrument set up: date, time, language, etc

A printer is available for the instrument; this may either be supplied pre-installed or is available as an optional accessory.

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**

- **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.

- **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.

#### Summary

<table>
<thead>
<tr>
<th>Function</th>
<th>Keypad number</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>DNA</td>
<td>1</td>
<td>DNA Mode</td>
</tr>
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<tr>
<td>Utilities</td>
<td>8</td>
<td>Utilities: Instrument set-up e.g. date, time, language</td>
</tr>
</tbody>
</table>
**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 \( \mu g/ml \) in the case of RNA. Oligonucleotides have a corresponding factor of 33 \( \mu g/ml \), although this does vary with base composition; this can be calculated if the base sequence is known.

  Concentration = \( \text{Abs260} \times \text{Factor} \)

- 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 \( \geq 1.8 \) and \( \geq 2.0 \), 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 = \( (\text{Abs 260} - \text{Abs 320}) \times \text{Factor} \)
  - Abs ratio = \( (\text{Abs 260} - \text{Abs 320}) / (\text{Abs 280} - \text{Abs 320}) \)
  - Abs ratio = \( (\text{Abs 260} - \text{Abs 320}) / (\text{Abs 230} - \text{Abs 320}) \)

- 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**

![Spectral scan graph]

**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:

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 Press to return to the Home page.

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 Home page.

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.
4. Sample number – add a prefix to the sample number and reset the incrementing number to the desired value.
5. Save method – use the alpha-numeric keys to enter a name for the method and press Save.

Exit options by pressing Esc or wait.
2: RNA
The procedure is as follows:

**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 Press to return to the Home page.

**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 Home page.

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.
4. Sample number – add a prefix to the sample number and reset the incrementing number to the desired value.
5. Save method – use the alpha-numeric keys to enter a name for the method and press Save.

Exit options by pressing Esc, 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 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 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 and pmol/µl. If pmol/µl 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 pmol/µl)**
Enter the factor using the keypad numbers. Default value is 33, range is 0.01 to 9999.

OR

**Step 6 (units pmol/µl)**
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 to enter the Results screen and start taking measurements OR to return to the Home page.
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 \[ \text{[button]} \]. 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 \[ \text{[button]} \] to return to the Home page.

Press \[ \text{[button]} \] 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 \[ \text{[button]} \].

Exit options by pressing \[ \text{[button]} \], or wait.
4. Absorbance/Concentration

The procedure is as follows:

**Step 1**
Press 4 to select Absorbance/Concentration mode.

**Step 2**
Select the wavelength using either arrow or alphanumeric keys.
Press the down arrow.

**Step 3**
Enter the measurement mode Absorbance, Concentration using factor or single standard. If Absorbance selected press OK to enter the Results screen. If Factor or Standard selected press the down arrow.

**Step 4 (if Factor Selected)**
Enter relevant Factor and units, press OK to enter the Results screen.

**Step 5 (if Standard selected)**
Enter the Concentration and units of the standard to be measured using the keypad numbers. Press OK to enter the Results screen.

**Step 6**
Insert the reference sample. Press 0A/100%T Key. This will be used for all subsequent samples until changed.

**Step 7**
Insert sample and press . This measures at the selected wavelength and displays the results. Repeat step 7 for all samples.

**Step 8 (if Standard selected)**
Insert standard, and press . Change the concentration value of the standard if necessary and press OK to measure the standard. Insert sample and press . This measures at the selected wavelength and displays the results. Repeat for all samples.

Press to display available Options which are described below.

Press Cancel to cancel selections and return to the Home page.
Options (select using key pad numbers)
1. Return to parameters screen (step 1 above).
2. Print result via selected method.
4. Run Standard
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.

Exit options by pressing Esc or wait.
5. 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 x 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 5 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 Home page.
6. Methods Folder

This folder is the storage locations for any user modified Applications (Methods) that are saved using the Options menu and is accessible from the Home page.

<table>
<thead>
<tr>
<th>Methods - Methods</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
</tr>
<tr>
<td>254nm Abs</td>
</tr>
</tbody>
</table>

Up to 9 Methods may be stored, 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 \( \leftarrow \) to delete the method OR cancel \( \text{Esc} \) 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 \( \leftarrow \) to lock the method OR cancel \( \text{Esc} \) to return to the 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 \( \leftarrow \) to unlock the method OR cancel \( \text{Esc} \) to return to the Methods folder.
7. Protein Determination
The GeneQuant™ 100 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 \(\lambda\)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 bichromonic 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 color obtained from the reaction of Folin-Ciocalteu phenol reagent with the tylsryl 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 \( \text{dilution factor} \) 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 \( \text{dilution factor} \) to calculate the dilution factor and return to the Parameters screen.
OR Press \( \text{Esc} \) 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**
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 \( \text{Results} \) to enter the Results screen
OR
Cancel \( \text{Esc} \) to return to the Protein folder.
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.

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.
4. Sample number – add a prefix to the sample number and reset the incrementing number to the desired value.
5. Save method – use the alpha-numeric keys to enter a name for the method and press Save .

Exit options by pressing , or wait.
2: BCA

The procedure is as follows:

**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, µg/l, µl, %, 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 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 the measurement button 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 the measurement button 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 Esc 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 Esc 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.
4. Sample number – add a prefix to the sample number and reset the incrementing number to the desired value.
5. Save method – use the alpha-numeric keys to enter a name for the method and press Save .

Exit options by pressing Esc , or wait.
3. Bradford

The procedure is as follows

**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 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.

Exit options by pressing , or wait.
4: Lowry

The procedure is as follows:

**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.

**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 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.

### 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.

#### 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.
4. Sample number – add a prefix to the sample number and reset the incrementing number to the desired value.
5. Save method – use the alpha-numeric keys to enter a name for the method and press Save.
6. Auto-Print – toggles auto-print on/off.

Exit options by pressing , or wait.
5: Biuret

The procedure is as follows:

**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.

**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.

**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 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.

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.

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.

Exit options by pressing , or wait.
UTILITIES FOLDER

Press 8 to enter the utilities folder.

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<tr>
<th>Utilities</th>
<th>Keypad number</th>
<th>Description</th>
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</thead>
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<td>Set correct time and date</td>
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<tr>
<td>Regional</td>
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<td>Select preferred language and number format</td>
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<tr>
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<tr>
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<td>Contrast</td>
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</tr>
<tr>
<td>About</td>
<td>6</td>
<td>Serial number and software version</td>
</tr>
</tbody>
</table>
1: **Date and Time**

The procedure is as follows:

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

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:

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 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:

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

Ambient temperature can affect the display. This function optimise the display for local conditions.

The procedure is as follows

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
6: About

Displays the instrument serial number and software version.

Press OK ← to close the window and return to the Utilities folder.
ACCESSORIES INSTALLATION

8.1 Printer installation

Step 1.
Remove the power cable and turn the instrument over onto a soft surface, taking care not to damage the sampling head.

Release the outermost screws using the Allen key provided.

Step 2.
Turn the instrument back over and remove the accessory covers.

Step 3.
Attach the printer cable.
Step 4.
Lower the printer onto the locating bosses.

Figure. 4

Step 5.
Replace the top cover plate, invert the instrument and replace the cap head screws.

Figure. 5

Step 6.
Switch the instrument on and go to utilities/instrument/preferences and select the Built-in printer.

Figure. 6
8.2 Loading / Changing the printer paper

Step 1
Lift off the paper cover.

Step 2
Lock the platen and turn the knob to feed the paper.

Step 3
Feed in the paper.

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

Step 5
Paper gripped.

Step 6
Replace cover.
ACCESSORIES

USB cable  source locally
Built-in printer accessory  80-3003-84
Print via Computer Software  80-2120-20

DATRYS SYSTEM CONTROL SOFTWARE

For many users, having an external PC to control their spectrophotometer and manipulate data, gives them the ultimate in flexibility and control. Whether looking for small differences in multiple spectral overlays, carrying out post-run manipulations on large numbers of samples, Datrys software has the flexibility to work in the way you want.

Datrys software is supplied in different modules to meet the application requirements of different customer groups and offers a simple upgrade path should your requirements change.

Choose:
• Datrys Lite for Quick Read and fast scanning only
• Datrys for all routine measurements
• Datrys Life Science for nucleic acids, proteins and cell density measurements
• Datrys CFR supports 21 CFR part 11 compatibility

Offering the familiar look and feel of Microsoft™ Office 2007, Datrys software is compatible with Windows™ XP, Windows Vista™, Windows 7, and Windows 8, 8.1 operating systems. Data export options include Microsoft Word™ and Excel plus Adobe™ PDF formats.

<table>
<thead>
<tr>
<th>Modules</th>
<th>Datrys Lite</th>
<th>Datrys</th>
<th>Datrys Life Science</th>
<th>Datrys CFR</th>
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<td>●</td>
<td>●</td>
<td>●</td>
<td>●</td>
</tr>
</tbody>
</table>

PRINT VIA COMPUTER

PVC can store data either in a common directory or can be configured to save to independent directories by both file format and connection. The data may be stored as an Excel spreadsheet, an EMF graphics file, a comma delimited (csv) data file, a tab delimited (txt) data file, rich text format (RTF) which is compatible with Word or in native PVC format.

Some users may find it convenient to use PVC to “print through” the PC directly to a local or networked printer.
1. PVC format that can only be opened by Print via Computer software Once a file has been opened in PVC it can be exported into ASCII (comma or tab separated), rich text format, Extensible meta format or Excel format (only if Excel is installed on the PC).
2. Tab Separated Variable (TSV) allowing the data to be opened directly into Excel.
Step 1.
Remove the power cable from the instrument. Turn the instrument over and place onto a soft surface, for example a folded up towel. Release the outermost cap head screws using the Allen key provided.

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

Step 3.
Plug the accessory cable into the SD memory card PCB module.

Step 4.
Note the slots in the base of the case. The two lugs on the SD memory card PCB module plug into these. Take care not to damage or snap off the lugs. Lower the PCB card module into place ensuring the lugs fit into these slots.

Step 5.
Fit the oval back cover ensuring it is fitted the correct way up – the continuous lip goes at the top.
Step 6.
Invert the instrument holding the SD Card accessory in position and replace the 2 cap head screws using the Allen key provided.

The accessory is now ready for use.

OPERATION
SD memory cards are inserted into the accessory with the contacts facing towards the user and the cut out corner on the right hand side (i.e. downwards). When a compatible SD card is inserted into the accessory, the red light flashes momentarily and the SD memory card icon appears on the instrument home page;

Saving methods to SD memory card
When an SD memory card is inserted into the accessory it is possible to save methods directly to the card.

Methods are stored on the card in a directory named Instrument Type\Methods (instrument type will be NanoVue Plus); this directory structure is evident when the SD card is inserted into a PC.

To save a method to the SD memory card, the instructions for the relevant application from the instrument user manual must be followed. Typically:
• Press the Options button (or relevant numerical short cut)
• Press Save Method
• Use the right and left arrows to select the folder on the SD memory card to which you wish to save the method
• Change the filename if required
• Press Save.

NOTE: A maximum of 9 methods can be stored in the SD memory card folder and in the Instrument Type\Methods directory.

These stored methods can also be opened on different instruments and then stored into other method folders if required.

When a method is being stored the LED next to the card will light up, the card MUST NOT be removed whilst the light is on otherwise the stored method will be corrupted.

Loading methods from SD memory card
Selecting the SD memory card by pressing the relevant number on the home page shows the methods stored on the card.

The required method can be loaded by pressing the relevant number on the keyboard and run in the same way as methods stored in any of the method folders on the instrument.
Saving data to SD memory card

Data from all applications on your instrument can be stored onto the SD memory card.

To enable data to be stored on the card, the SD memory card must be selected as the output device:
- **Select utilities\printer**
- Under printer select SD memory card
- Ensure Auto-Print is selected.

Start an application or load a method in the usual way. Note that when SD memory card and Auto-Print are both selected in utilities, an SD icon appears in the top right hand corner of the display.

For applications that print continuously, such as Single Wavelength or Nucleic Acids, the LED next to the SD memory card will stay on continuously until the complete set of results is finished. To close the results file the application should be exited using the ESC key in the usual way. Removing the card whilst the LED is on will corrupt the collected data set. All results are stored as an individual file in a directory called \Serial no\PVC on the SD memory card; this directory structure is evident when the SD card is connected to a PC.

Results are identified by application type followed by an incrementing number. For example:

DNA-A001.PVC for a DNA file
BCA001.PVC for a BCA Protein file

For applications that print whole documents in one go, such as Wavescan or Kinetics, the LED next to the SD memory card will go off after saving each measurement. In this case the card can be removed, when the light is off, without leaving the application. Each result is stored as an individual file in a directory called \Serial no\PVC on the SD memory Card; this directory structure is evident when the SD card is connected to a PC.

Results are identified by application type followed by an incrementing number. For example:

WAVE-001.PVC for a Wavelength scan
KINET001.PVC for a Kinetics file
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

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>Specification</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Wavelength range</strong></td>
<td>190 - 900 nm</td>
</tr>
<tr>
<td><strong>Monochromator</strong></td>
<td>Flat grating</td>
</tr>
<tr>
<td><strong>Wavelength calibration</strong></td>
<td>Automatic upon switch on</td>
</tr>
<tr>
<td><strong>Spectral bandwidth</strong></td>
<td>5 nm</td>
</tr>
<tr>
<td><strong>Wavelength accuracy</strong></td>
<td>± 2 nm</td>
</tr>
<tr>
<td><strong>Wavelength reproducibility</strong></td>
<td>± 1 nm</td>
</tr>
<tr>
<td><strong>Light sources</strong></td>
<td>Pulsed xenon lamp</td>
</tr>
<tr>
<td><strong>Detector</strong></td>
<td>1024 element CCD array</td>
</tr>
<tr>
<td><strong>Photometric range</strong></td>
<td>- 0.300 to 2.500A, 0 to 199%T</td>
</tr>
<tr>
<td><strong>Photometric linearity</strong></td>
<td>±0.005 Abs or 1% of the reading, whichever is the greater @ 546 nm</td>
</tr>
<tr>
<td><strong>Photometric reproducibility</strong></td>
<td>±0.003 Abs (0 to 0.5 Abs), ±0.007 Abs (0.5-1.0 Abs)</td>
</tr>
<tr>
<td><strong>Stray light</strong></td>
<td>&lt;0.5% at 220 nm and 340 nm using NaNO₂</td>
</tr>
<tr>
<td><strong>Zero stability</strong></td>
<td>±0.01 Abs/hour after 20 min warm up @ 340 nm</td>
</tr>
<tr>
<td><strong>Noise</strong></td>
<td>0.005 pk to pk 0.002 pms</td>
</tr>
<tr>
<td><strong>Digital output</strong></td>
<td>USB port standard</td>
</tr>
<tr>
<td><strong>Dimensions</strong></td>
<td>260 x 390 x 100 mm</td>
</tr>
<tr>
<td><strong>Weight</strong></td>
<td>&lt;3.5 kg</td>
</tr>
<tr>
<td><strong>Power input</strong></td>
<td>18Vdc from a 100 to 240 V~, 50/60 Hz, Max 30 VA mains power adapter</td>
</tr>
</tbody>
</table>

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**
- Biochrom 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. Biochrom can accept no liability for loss or damage, however caused, arising from the faulty or incorrect use of this product.