LAMBDA Bio/Bio+

User’s Guide
Release History

<table>
<thead>
<tr>
<th>Part Number</th>
<th>Release</th>
<th>Publication Date</th>
</tr>
</thead>
<tbody>
<tr>
<td>L6050016</td>
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<td>January 2014</td>
</tr>
</tbody>
</table>

Any comments about the documentation for this product should be addressed to:

User Assistance
PerkinElmer Ltd
Chalfont Road
Seer Green
Beaconsfield
BUCKS
HP9 2FX
United Kingdom

Or emailed to: info@perkinelmer.com

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Introduction
About this Manual

This user’s guide describes the installation and operating procedures for your Lambda Bio/Bio+ UV/Vis spectrometer.

The manual contains the following sections:

• Introduction;
• Safety Information;
• Installing your Instrument;
• Using your Instrument;
• Instrument Methods;
• Accessories;
• Maintenance;
• Appendices.
Conventions Used in this Manual

Normal text is used to provide information and instructions.

**Bold** text refers to text that is displayed on the screen.

UPPERCASE text, for example ENTER or ALT, refers to keys on the PC keyboard. The symbol “+” is used to show that you have to press two keys at the same time, for example, ALT+F.

All eight digit numbers are PerkinElmer part numbers unless stated otherwise.

Unless stated otherwise, in this manual “instrument” refers to the Lambda Bio or Lambda Bio+ instrument.

**Notes, cautions and warnings**

Three terms, in the following standard formats, are also used to highlight special circumstances and warnings.

**NOTE:** A note indicates additional, significant information that is provided with some procedures.

![WARNING]

We use the term **WARNING** to inform you about situations that could result in **personal injury** to yourself or other persons. Details about these circumstances are in a box like this one.

![CAUTION]

We use the term **CAUTION** to inform you about situations that could result in **serious damage to the instrument** or other equipment. Details about these circumstances are in a box like this one.
Safety Information
**General Safety**


Standards to which conformity is declared:

- EN 61010-1 Safety requirements for electrical equipment for measurement, control and laboratory use.
- EN 61010-2-101 Particular requirements for IVD medical equipment.
- BS EN 591 Instruction for use for in vitro diagnostic instruments for professional use.
- BS EN 13612 Performance evaluation of in vitro diagnostic medical devices.
- EN 61326-2.3 Electromagnetic compatibility – generic emission standard Electrical equipment for measurement, control and laboratory use.
- EN 61326 Electromagnetic compatibility – generic emission standard Electrical equipment for measurement, control and laboratory use. Classified as Class B for conducted and radiated emissions.

The Lambda Bio/XLS complies with the following environmental legislation regarding the restriction of the use of certain hazardous substances:

- China: Administration on the Control of Pollution Caused by Electronic Information Products No 39.

This appliance is marked according to the European directive 2002/96/EC on Waste Electrical and Electronic Equipment (WEEE). See the *Lambda Bio/XLS Safety Manual* (L6050014) for more information.

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 familiarize yourself with these symbols and their meaning.

This instrument is subject to the following hazards:

---

*The UV source contained within the unit generates a light beam that passes through the sample chamber during sample measurements. Under normal use, this beam is contained within the unit and no UV radiation is emitted from the system. However, care should be taken that no reflective items are placed in the beam during sample measurements so that the beam is reflected out of the system. Also, the sample holder should be removed for cleaning only when the power is disconnected from the instrument. Prolonged exposure to the beam may cause permanent eye damage.*
- High voltages exist inside the unit. Repair and maintenance should only be carried out by individuals trained specifically to work on these instruments.

There are no bio-hazardous materials within the unit; however, this unit could be used with bio-hazardous samples. Given the general-purpose nature of the instruments it is not possible to define exact decontamination procedures for the many types of samples being tested. These should be established by the user, or their Health and Safety representative, before use of the instrument. Guidance can be found in document M29-A3 Protection of Laboratory Workers from Occupationally Acquired Infections: Approved Guidelines published by the US Clinical and Laboratory Standards Institute. The sample compartment may be removed and cleaned by soaking in a disinfectant appropriate for the bio-hazard for at least 30 minutes. The compartment should then be rinsed in distilled water and allowed to dry. Similarly, the outer cover can be wiped over with an appropriate disinfectant with a wipe or soft cloth. Any internal spills should be wiped up using absorbent material through the sample compartment aperture, and then similarly decontaminated using disinfectant soaked wipes.

**Decontamination Certificates**

If the instrument needs to be returned, a decontamination certificate is required. Decontamination certificates can be found at the following web address or be provided by Customer Care.

http://www.perkinelmer.com/LambdaBioXLSSupport

It is the responsibility of the user to ensure a safe working environment is provided to the engineer or staff by appropriate risk assessments and, if appropriate, decontamination procedures before work commences.

**Chemicals**

Use, store, and dispose of chemicals that you require for your analyses in accordance with the manufacturer’s recommendations and local safety regulations.

**Toxic Fumes**

If you are working with volatile solvents or toxic substances, then you must provide an efficient laboratory ventilation system to remove vapors that may be produced when you are performing analyses.
Waste Disposal

Waste containers may contain corrosive or organic solutions and small amounts of the substances that were analyzed. If these materials are toxic, you may have to treat the collected effluent as hazardous waste. Refer to your local safety regulations for proper disposal procedures.

Personal Protective Equipment

No Personal Protective Equipment (PPE) is required for operation of the equipment, although the samples under test may require the use of such PPE and should be covered by a risk assessment made by the user or the appropriative Health and Safety representative.

Intended User

This instrument is intended for use by individuals trained in and familiar with the use of spectrophotometers and their associated hazards as detailed above. In the event of a malfunction or hazard occurring, the user responsible shall disconnect the unit from power, and isolate the instrument for decontamination by an appropriate means if biohazardous material is spilled on, in or around the instrument.
Unpacking and Installation

- This equipment is designed to be installed in accordance with the Canadian Electrical Code (CEC) Part 1, CSA C22.1 and CSA C22.2 No. 0.

- Inspect the instrument for any signs of damage caused in transit. If any damage is discovered, access the Troubleshooting Guide on the PerkinElmer website http://www.perkinelmer.com/LambdaBioXLSSupport and follow the process there. If you do not have access to the website, contact Customer Care (see Appendix 2: Customer Care Contacts on page 121).

- Ensure your proposed installation site conforms to the environmental conditions for safe operation:
  - Indoor use only.
  - Temperature range 5 °C to 35 °C.
  - Maximum relative humidity of 80% up to 31 °C, decreasing linearly to 50% at 40 °C.

  **NOTE:** 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).

- 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 turning the instrument on. This will prevent calibration failure as a result of internal condensation.

- The instrument must be placed on a stable, level bench or table that can take its weight (approximately 4.5 kg) with enough space around the instrument so that air can circulate freely.

- This equipment must be connected to the supply outlet with the power cord and power supply provided. It can be used on 100–240 V, 50–60 Hz supplies. The power cord or power supply outlet should be is fused at 3 A, 250 V.

- The instrument should be positioned so that the power cable can be readily disconnected from the unit in the event of a hazard or malfunction occurring.

- Site the instrument in an atmosphere free from dust and corrosive fumes.

- Please read through the instrument User’s Guide supplied on the Lambda Bio/XLS Documentation CD (L6050018) prior to use.

- Switch on the instrument via the ON/OFF button on the keypad after it has been plugged in. The instrument will perform a series of self-diagnostic checks.

If the equipment is used in a manner not specified herein, then the protection provided by the equipment may be impaired and instrument warranty withdrawn.
Installing your Instrument
Unpacking

Take great care when installing your instrument, and follow the procedures described in this manual.

1. Check that you have the items listed in the following table.

<table>
<thead>
<tr>
<th>Part Number</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>L7110184/L7110186</td>
<td>Lambda Bio/Bio+ (as applicable)</td>
</tr>
<tr>
<td>L7110185/L7110187</td>
<td>Lambda Bio/Bio+ with printer (as applicable)</td>
</tr>
<tr>
<td>L7110188</td>
<td>Lambda Bio+ with SD (as applicable)</td>
</tr>
<tr>
<td>L6050014</td>
<td>Lambda Bio/XLS Safety Manual</td>
</tr>
<tr>
<td>L6050018</td>
<td>Lambda Bio/XLS Documentation CD</td>
</tr>
<tr>
<td>L7111023</td>
<td>Cuvette dust cover</td>
</tr>
<tr>
<td>L7110231</td>
<td>Lambda Bio/XLS Print Utility and Cable (as applicable)</td>
</tr>
<tr>
<td>L7110263</td>
<td>UV micro cuvettes (8 pack)</td>
</tr>
<tr>
<td>N/A</td>
<td>Power cable</td>
</tr>
</tbody>
</table>

2. Examine the components for any signs of damage in shipment:
   - Check the enclosure of the instrument for damage, and make sure that the terminals are not damaged.
   - Make sure that the compartment is free of dust or other foreign matter.

NOTE: In the event of damage, or missing parts, access the Troubleshooting Guide on the PerkinElmer website at http://www.perkinelmer.com/LambdaBioXLSSupport and follow the process there. If you do not have access to the website, contact Customer Care (see Appendix 2: Customer Care Contacts on page 121).
Connecting to the Line Power Supply

Electrical Hazard

WARNING

To prevent potential injury to yourself and damage to the instrument, make any electrical connections in the system before connecting to the line power supply.

The instrument automatically adjusts to the correct operating voltage.

➢ Connect to the supply outlet with power supply provided and the power cord that is appropriate for your region.

You must use the power cord and power supply supplied with the instrument.

NOTE: If the instrument has just been unpacked or has been stored in a cold environment, it should be allowed to come to thermal equilibrium in the laboratory for 2–3 hours before turning the instrument on. This will prevent calibration failure as a result of internal condensation.

Figure 1 Rear connections on the Lambda Bio/ XLS instrument

The ON/OFF switch is located at the top left-hand of the keypad panel.
Using your Instrument
Overview of the Instrument

The Lambda Bio/Bio+ instrument is a simple-to-use UV/Visible spectrometer with a CCD array detector (1024 pixels).

To access the folders and functions on your Lambda Bio/Bio+ instrument, navigate around the display using the alphanumeric keys and the navigation arrows on the keypad.

<table>
<thead>
<tr>
<th>Key</th>
<th>Action</th>
</tr>
</thead>
<tbody>
<tr>
<td>Display panel</td>
<td>Displays folders and menu options that guide you through taking measurements and viewing your results.</td>
</tr>
<tr>
<td>ON/OFF</td>
<td>Turns the instrument on or off.</td>
</tr>
<tr>
<td>View Options</td>
<td>Use the four arrows to navigate around the display and select the required setting from the active (highlighted) option.</td>
</tr>
<tr>
<td>Options</td>
<td>The Options key displays the options for that method or folder. See Options on page 25 for more information. Options unique to a specific method are described in the relevant section.</td>
</tr>
<tr>
<td>0A/100%T (scan reference)</td>
<td>The 0A/100%T key sets a reference solution measurement to 0.000 A or 100%T at the current wavelength. When in scan mode, it performs a reference scan.</td>
</tr>
<tr>
<td>Button</td>
<td>Description</td>
</tr>
<tr>
<td>--------</td>
<td>-------------</td>
</tr>
<tr>
<td>❌</td>
<td>The Cancel/Back/Stop key Cancels a selection and returns to the previous folder, goes Back to previous screen in a method or Stops a measurement.</td>
</tr>
<tr>
<td>✅</td>
<td>The <strong>OK/Next/Run/Scan</strong> key, enters or confirms a selection, moves to the Next screen or takes a measurement.</td>
</tr>
<tr>
<td>Alphanumeric keys</td>
<td>Use these to enter Method Settings, make Options menu selections and to write text descriptions, where appropriate. Use repeated presses to cycle through lower case, number and upper case. Leave for 1 second before entering the next character. Use the ⎪ key to backspace. Press 1 to enter a space.</td>
</tr>
</tbody>
</table>
Switching on the Instrument

NOTE: 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 being switched on. This will prevent calibration failure as a result of internal condensation.

CAUTION

Do not turn power to the instrument on and off quickly as this may damage the power supply.

Wait at least 30 seconds before restarting the instrument.

Switch on the instrument via the ON/OFF on the keypad, as shown in Figure 2. The instrument will perform a series of diagnostic checks.

NOTE: If during the calibration the instrument displays an error message it will prompt you to press OK to restart the calibration procedure. However, after three attempts you will still be able to view the default home page. You should NOT use the instrument under these circumstances. Instead, make a note of the error message and refer to the Troubleshooting Guide on the PerkinElmer website to address the problem.

After switch on and calibration, the default home page is displayed. To open a method or folder, press the appropriate number on the keypad.

Figure 3 Lambda Bio home page

NOTE: If you have an SD Memory Card installed in your instrument that contains methods, the SD Memory Card folder will be added to the home page. You can view and open the first 9 methods saved to this folder. Further methods can be saved to the SD Memory Card folder; see SD Memory Card on page 29 for information on how to view these methods on your PC. If the SD Memory Card is empty it will not be displayed on the home page.
**Using the Software**

The home page contains a list of folders and functions or methods. Each item in the list is numbered and is opened by using the associated number on the keypad. Opening a folder takes you to another screen of further options. Opening a method takes you to a Method Settings screen where you can set the required parameters before using the method to take measurements.

![Concentration - Method Settings](image)

**Figure 4 Features of a typical Method Settings screen**

**Navigation**

- Move between settings using the up and down arrows.

**Entering Method Settings**

- Enter Method Settings by using the keypad numbers.

  OR

  If the box contains the symbol ``, either type in a value or press options ``, and choose an option from the next screen.

  OR

  If the box contains arrow symbols, use the left and right arrows to select the required setting.
**Taking measurements**

After the method settings have been entered, press **OK** to start measurements. The results screen for the method is displayed.

![Single Wavelength](image)

**Figure 5 A typical results screen**

1. Insert the Reference sample in the sample holder, and press OA/100%T to take the reference measurement.

2. Insert your first sample and press.

3. Repeat Step 2 for each sample.

**Results**

The results are displayed on screen.

**NOTE:** Results shown as ---- indicate that the concentration is out of range, for example, if a negative absorbance value is obtained.

![Single Wavelength](image)

**Figure 6 The Single Wavelength method results screen**
**Options**

Within each method you are able to select various options that define the way results are treated. These options may be specific to the method, allow you to print the results or view method settings.

- Press Options to view the Options menu.

<table>
<thead>
<tr>
<th>Option</th>
<th>Text</th>
<th>Function</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Method Settings</td>
<td>Returns to the Method Settings screen for the method.</td>
</tr>
<tr>
<td>2</td>
<td>Print</td>
<td>Prints the results.</td>
</tr>
<tr>
<td>3–6</td>
<td>N/A</td>
<td>Specific to the method.</td>
</tr>
<tr>
<td>7</td>
<td>Sample Number</td>
<td>Defines the sample number you wish to start taking measurements from.</td>
</tr>
</tbody>
</table>
| 8      | Save Method      | Allows you to save the Method Settings as a new method to the Methods or Favorites folders or, if installed, to an SD Memory Card. You can save up to 9 methods in each folder.  
**NOTE:** There is no Favorites folder on the Lambda Bio.  
**NOTE:** Methods from more than one type of instrument can be saved to the same SD Memory Card. The Methods are saved to the card in a default directory that depends on the instrument type: \<Instrument type>\Methods. For example, \Lambda XLS\Methods  |
| 9      | Auto-Print       | Toggles Auto-Print on and off. The default is off.                      |
Press \[ \rightarrow \text{ or } \leftarrow \text{, or wait 20 seconds to exit the method options.}

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

If you are not using a previously stored method, it is advisable to check that these options have been appropriately set for your experiment before running your samples.

**NOTE:** Setting the History method setting to On (see Preferences on page 37) will cause the instrument to store its last settings. If the History method setting is Off, all method settings and options will return to their defaults when you leave that method.
Methods and Favorites

The Methods folder allows you to store user-modified methods, based on the default instrument methods, which can be saved using the Options menu. You can save up to 9 methods in each folder. To retrieve previously stored methods, press the appropriate keypad number to enter the Methods folder. You can also export (backup) methods to an SD card or import (restore) methods from an SD Memory Card.

<table>
<thead>
<tr>
<th>Methods</th>
<th>Text</th>
<th>Function</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Folder Names</td>
<td>Allows you to rename the Methods folders.</td>
</tr>
<tr>
<td>2</td>
<td>Lock Folder</td>
<td>Allows you to lock the folder.</td>
</tr>
<tr>
<td>3</td>
<td>Unlock Folder</td>
<td>Allows you to unlock the folder.</td>
</tr>
<tr>
<td>4</td>
<td>SD Memory Card</td>
<td>Allows you to access options for the SD card. (This option is only available if you have an SD installed in the instrument.)</td>
</tr>
</tbody>
</table>

Folder Options

Press to display the available Options in the Methods folder, which you can select using the keypad numbers:

- Press to display the available Options in the Methods folder, which you can select using the keypad numbers:
Folder Names

1. Open the Methods folder.
2. Press \( \text{Menu} \) to display the available Options.
3. Press 1 to select Folder Names.
4. Select the Folder you wish to rename using the left and right arrows, and then press the down arrow.
5. Enter a New Name for the folder using the alphanumeric keypad.
6. Press OK \( \text{Enter} \) to rename the folder.

Lock Folder

1. Open the Methods folder.
2. Press \( \text{Menu} \) to display the available Options.
3. Press 2 to select Lock Folder.
4. Select the Folder you wish to lock using the left and right arrows, and then press the down arrow.
5. Enter a Pass Code for the folder using the keypad numbers or left and right arrows.
6. Press Lock \( \text{Lock} \) to lock the folder.

Unlock Folder

1. Open the Methods folder.
2. Press \( \text{Menu} \) to display the available Options.
3. Press 3 to select Unlock Folder.
4. Select the Folder you wish to unlock using the left and right arrows, and then press the down arrow.
5. Enter the Pass Code for the folder using the keypad numbers or left and right arrows.
6. Press Unlock \( \text{Unlock} \) to unlock the folder.
**SD Memory Card**

If an SD Memory Card is installed in your instrument, then you can access the SD Memory Card folder option. The options **Backup Folder** or **Backup All Folders** allow you to copy a methods folder or all of the methods folders on your instrument, respectively, to the SD Memory Card. Methods from more than one instrument can be saved to the same card. The methods are saved to a default directory `\<Serial Number>\BACKUP`.

For example, `\1000\BACKUP\METHODS\Methods 1`

The SD Memory Card can be plugged into a card reader attached to your PC. Methods can be renamed (up to a maximum of 24 characters) and moved between folders.

The options **Restore Folder** or **Restore All Folders** restore the contents of the folder or folders, respectively, to the content of the SD Memory Card BACKUP directory. All methods in the folder(s) will be overwritten if you select **Restore Folder** or **Restore All Folders**. If you have renamed an instrument folder, the folder name will be overwritten by those in the BACKUP directory of the SD Memory Card.

**NOTE:** If you rename a folder on the SD Memory Card and then try to restore the contents, your instrument will not recognize the folder and it will not be restored.

The **Restore All Folders** function can also be used if you wish to set multiple instruments of the same type to have the same methods and folder structure. Navigate in Windows Explorer to the `\<Serial Number>\BACKUP` folder that contains the methods you would like to use and then rename the folder `\<Instrument Type>\BACKUP`. You can then restore each instrument in the normal way.

To Backup or Restore your folders:

1. Open the Methods folder.

2. Press `Johnny` to display the available Options.

3. Press 4 to select **SD Memory Card**.
   The SD Memory Card screen is displayed.

4. Select the mode of **Operation** using the left and right arrows, and then press the down arrow.
   The options are **Backup Folder**, **Backup All Folders**, **Restore Folder** or **Restore All Folders**.
5. Select the **Folder** using the left and right arrows.

6. Press **OK**.

**NOTE:** The LED next to the card will be lit while methods are saved to the card. The card should not be removed from the instrument while the LED is lit as this could corrupt your data.

**Method Options**

- Press **** to display the available Options in the Methods folder, which you can select using the keypad numbers:

<table>
<thead>
<tr>
<th>Option</th>
<th>Text</th>
<th>Function</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Delete Method</td>
<td>Allows you to delete the Method.</td>
</tr>
<tr>
<td>2</td>
<td>Lock Method</td>
<td>Allows you to lock the method.</td>
</tr>
<tr>
<td>3</td>
<td>Unlock Method</td>
<td>Allows you to unlock the method.</td>
</tr>
</tbody>
</table>

**Delete Method**

1. Open the appropriate methods folder.

2. Press **** to display the available Options.

3. Press 1 to select **Delete Method**.

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

5. Press **Delete** to delete the method.

**Lock Method**

1. Open the appropriate methods folder.

2. Press **** to display the available Options.

3. Press 2 to select **Lock Method**.

4. Select the method to be locked using the left and right arrows, and then press the down arrow.

5. Select a **Pass Code** using the keypad numbers or left and right arrows.

6. Press **Lock** to lock the method.
Unlock Method

1. Open the appropriate methods folder.

2. Press [ ] to display the available Options.

3. Press 3 to select Unlock Method.

4. Select the method to be unlocked using the left and right arrows, and then press the down arrow.

5. Enter a Pass Code using the keypad numbers or left and right arrows.

6. Press Unlock [ ] to unlock the method.
Lambda Bio/Bio+ Instrument Methods

The pre-defined methods available on your Lambda Bio/Bio+ instrument are:

**Standard Methods (Lambda Bio+ only)**
- Single Wavelength
- Multi Wavelength
- Spectrum
- Concentration
- Standard Curve
- Kinetics
- Absorbance Ratio

**Nucleic Acids**
- DNA
- RNA
- Oligo

**Protein**
- Protein UV
- BCA
- Bradford
- Lowry
- Biuret

- OD 600

- Absorbance and concentration (Lambda Bio only).
NOTE: If you have an SD Memory Card installed in your instrument that contains methods, the SD Memory Card folder will be added to the home page.
Utilities

You can use the Utilities folder to modify the instrument setup.

- From the home page, press the appropriate keypad number to enter the Utilities folder. The Utilities screen is displayed.

<table>
<thead>
<tr>
<th>Utilities</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>1 Date and Time</td>
<td>Set correct time and date.</td>
</tr>
<tr>
<td>2 Regional</td>
<td>Select preferred language and number format.</td>
</tr>
<tr>
<td>3 Printer</td>
<td>Printer/output options.</td>
</tr>
<tr>
<td>4 Preferences</td>
<td>Select screen layout (themes) and history.</td>
</tr>
<tr>
<td>5 Contrast</td>
<td>Adjust screen contrast and brightness.</td>
</tr>
<tr>
<td>6 About</td>
<td>Serial number and software version.</td>
</tr>
<tr>
<td>7 Games</td>
<td>Spectro Blocks/Sudoku.</td>
</tr>
</tbody>
</table>

Figure 10 The Utilities screen
**Date and Time**

1. Press 1 to select **Date and Time**.  
The Date and Time screen is displayed.

<table>
<thead>
<tr>
<th>Date and Time</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Day</strong></td>
</tr>
<tr>
<td><strong>Hour</strong></td>
</tr>
<tr>
<td><strong>Month</strong></td>
</tr>
<tr>
<td><strong>Minute</strong></td>
</tr>
<tr>
<td><strong>Year</strong></td>
</tr>
</tbody>
</table>

2. Using the keypad numbers or left and right arrows, enter the **Day**, **Month**, **Year**, **Hour** and **Minute**.

3. Press **OK** to store the settings and return to the Utilities folder.  
   Seconds are zeroed when you press **OK**.

**Regional**

1. Press 2 to select **Regional**.  
The Regional screen is displayed.

<table>
<thead>
<tr>
<th>Regional</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Language</strong></td>
</tr>
<tr>
<td></td>
</tr>
<tr>
<td><strong>Number Format</strong></td>
</tr>
</tbody>
</table>

2. Using the left and right arrows, select a **Language** and then press the down arrow.  
The options are Chinese, English, French, German, Italian, Japanese or Spanish.
3. Select the **Number Format** (the type of decimal separator) using the left and right arrows.  
The options are “,” or “.”.

4. Press **OK** to store the settings and return to the Utilities folder.

**Printer**

1. Press 3 to select **Printer**.  
The Printer screen is displayed.

2. Select whether **Auto-Print** is **On** or **Off** using the left and right arrows, and then press the down arrow.  
When **Auto-Print** is **On**, the results are automatically printed after a measurement is taken or when you exit the application, depending on the method. The appropriate icon for your Printer option will be displayed in the top right corner of the method results screen.  
When **Auto-Print** is **Off**, printing has to be initiated manually.

3. Select how the data are sent.  
The options are **Built-in** (the internal printer), **Computer (USB)** (to a computer via USB port), **SD Memory Card** or **Computer (Bluetooth)** (to a computer via Bluetooth).  
The options available depend on what is installed in your instrument.

**NOTE:** If **SD Memory Card** is selected, data is saved as .pvc files in a folder that depends upon the instrument serial number: \<Serial number>\PVC. The method type is saved in the file name. For information on viewing your results and saving your data into other formats, see “Lambda Bio XLS Report Utility Viewer” in the *Lambda Bio/XLS Print Utility User’s Guide* (L6050015).

**NOTE:** If an SD Memory Card is installed in your instrument, the LED next to the card will be lit while data is being printed to the card. The card should not be removed from the instrument while the LED is lit as this could corrupt your data. For some methods you have to exit the method to end printing. See the “Receiving Print Data” in the *Lambda Bio/XLS Print Utility User’s Guide* (L6050015) for more information.

4. Press **OK** to store the settings and return to the Utilities folder.
Preferences

1. Press 4 to select Preferences.
The Preferences screen is displayed.

<table>
<thead>
<tr>
<th>Preferences</th>
<th></th>
<th>Auto Standby</th>
</tr>
</thead>
<tbody>
<tr>
<td>Games</td>
<td>No</td>
<td>Off</td>
</tr>
<tr>
<td>Theme</td>
<td>List</td>
<td></td>
</tr>
<tr>
<td>History</td>
<td>On</td>
<td></td>
</tr>
</tbody>
</table>

2. Select whether Games are turned available using the left and right arrow keys.
The options are Yes or No.

3. Define the Theme (the on-screen layout of folders).
The options are either a Grid format or a List.

4. Select the History mode using the left and right arrow keys.
If Off is selected the instrument will not remember your method settings unless you restore them as a new method. The default is Off.

5. Select whether to use an Auto Standby mode after defined periods.
The options are 1 hour, 2 hours, At Night or Off.

6. Press OK to store the settings and return to the Utilities folder.
**Contrast**

Ambient temperature can affect the display. The contrast function can optimize the display for local conditions.

The procedure is as follows:

1. Press 5 to select **Contrast**.
   The Contrast screen is displayed.

   ![Contrast Screen](image)

   2. Adjust the **Brightness** using the left and right arrows, and then press the down arrow.

   3. Adjust the **Contrast** using the left and right arrows.

   4. Press **OK** to store the settings and return to the Utilities folder.

**About**

The About screen displays the instrument serial number and the software version.

1. Press 6 to select **About**.
   The About screen for your instrument is displayed.

   ![About Screen](image)

   2. Press **OK** to close the window and return to the Utilities folder.
Sample Handling

- The light beam is directed from RIGHT to LEFT through the cell chamber, as indicated by the white arrows on the instrument enclosure. Make sure that 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 approximately 10 µl in an ultra-micro cell.

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

**NOTE:** A cover is provided to keep the sample compartment free from dust and debris. When the instrument is in use, the dust cover should be kept in a safe place, nearby.
Instrument Methods
The Single Wavelength method makes absorbance (A) and percentage transmission (%T) measurements on samples by measuring the amount of light that has passed through a sample relative to a reference (this can be air).

The procedure is as follows:

1. From the home page, press 1 to open the Standard Methods folder. The Standard Methods screen is displayed.

<table>
<thead>
<tr>
<th>Standard Methods</th>
</tr>
</thead>
<tbody>
<tr>
<td>1 Single Wavelength</td>
</tr>
<tr>
<td>2 Multi Wavelength</td>
</tr>
<tr>
<td>3 Spectrum</td>
</tr>
<tr>
<td>4 Concentration</td>
</tr>
<tr>
<td>5 Standard Curve</td>
</tr>
<tr>
<td>6 Kinetics</td>
</tr>
<tr>
<td>7 Absorbance Ratio</td>
</tr>
</tbody>
</table>


<table>
<thead>
<tr>
<th>Single Wavelength - Method Settings</th>
</tr>
</thead>
<tbody>
<tr>
<td>Wavelength</td>
</tr>
<tr>
<td>620 nm</td>
</tr>
<tr>
<td>Mode</td>
</tr>
<tr>
<td>Absorbance</td>
</tr>
</tbody>
</table>

3. Set the Wavelength by using the keypad numbers or the left and right arrows, and then press the down arrow.

4. Select the Mode, using the left and right arrows. The options are Absorbance or % Transmission.
5. Press **OK** to start measurements. The Single Wavelength results screen is displayed.

<table>
<thead>
<tr>
<th>Single Wavelength</th>
</tr>
</thead>
<tbody>
<tr>
<td><img src="image1.png" alt="Graph" /></td>
</tr>
<tr>
<td><img src="image2.png" alt="Graph" /></td>
</tr>
<tr>
<td><img src="image3.png" alt="Graph" /></td>
</tr>
</tbody>
</table>

6. Insert the reference sample and press **OK**. This reference measurement will be used for all subsequent samples until repeated.

7. Insert your first sample and press **OK**. 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 (±20 nm from the set wavelength).

8. Repeat Step 7 for each sample.
Press \( \square \) to display the available Options, which you can select using the keypad numbers:

<table>
<thead>
<tr>
<th></th>
<th>Method Settings</th>
<th>Returns to the Method Settings screen.</th>
</tr>
</thead>
<tbody>
<tr>
<td>2</td>
<td>Print</td>
<td>Prints the result using the printer selected in the Utilities folder.</td>
</tr>
<tr>
<td>3</td>
<td>A/%T</td>
<td>Toggles between Absorbance and %Transmission mode.</td>
</tr>
<tr>
<td>4</td>
<td>Print Graph</td>
<td>Prints the graph (this option is grayed out if no data are available).</td>
</tr>
<tr>
<td>7</td>
<td>Sample Number</td>
<td>Adds a prefix to the sample number and resets the incrementing number to the desired value.</td>
</tr>
<tr>
<td>8</td>
<td>Save Method</td>
<td>Use the left and right arrows to select the folder you want to store the method in (Favorites/Methods 1–9/SD Memory Card), then press the down arrow and enter a name for the method. Press Save ( \square ) to save the method.</td>
</tr>
<tr>
<td>9</td>
<td>Auto-Print</td>
<td>Toggles Auto-Print on and off.</td>
</tr>
</tbody>
</table>

Press \( \square \) or \( \square \), or wait 20 seconds to exit the method options.

Press \( \square \) to return to the Standard Methods folder after all your samples have been measured.
NOTE: This method is available on the Lambda Bio+ only.

The Multi Wavelength method can provide absorbance readings at up to 5 wavelengths.

The procedure is as follows:

1. From the home page, press 1 to open the Standard Methods folder. The Standard Methods screen is displayed.

<table>
<thead>
<tr>
<th>Standard Methods</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
</tr>
<tr>
<td>2</td>
</tr>
<tr>
<td>3</td>
</tr>
<tr>
<td>4</td>
</tr>
<tr>
<td>5</td>
</tr>
<tr>
<td>6</td>
</tr>
<tr>
<td>7</td>
</tr>
</tbody>
</table>

   1. Single Wavelength
   2. Multi Wavelength
   3. Spectrum
   4. Concentration
   5. Standard Curve
   6. Kinetics
   7. Absorbance Ratio

2. Press 2 to open the Multi Wavelength method. The Multi Wavelength – Method Settings screen is displayed.

<table>
<thead>
<tr>
<th>Multi Wavelength - Method Settings</th>
</tr>
</thead>
<tbody>
<tr>
<td>Wavelengths</td>
</tr>
<tr>
<td>2</td>
</tr>
<tr>
<td></td>
</tr>
<tr>
<td>λ1</td>
</tr>
<tr>
<td>303 nm</td>
</tr>
<tr>
<td></td>
</tr>
<tr>
<td>λ2</td>
</tr>
<tr>
<td>400 nm</td>
</tr>
</tbody>
</table>

3. Select the number of Wavelengths and then press the down arrow. The options are between 2 and 5.

4. Enter the first wavelength (λ1) using either the number keys or the left and right arrows, and then press the down arrow.

5. Repeat Step 4 for each of the wavelengths.
6. Press **OK** to start measurements. The Multi Wavelength results screen is displayed.

7. Insert the Reference sample and press **OK**. This reference measurement will be used for all subsequent samples until repeated.

8. Insert your first sample and press **OK**. A spectrum covering the range of wavelengths is displayed, with cursors marking the chosen wavelengths. A table of the absorbance values at those wavelengths is also displayed.

9. Repeat Step 8 for each sample.
Press press to display the available Options, which you can select using the keypad numbers:

<table>
<thead>
<tr>
<th></th>
<th>Method Settings</th>
<th>Returns to the Method Settings screen.</th>
</tr>
</thead>
<tbody>
<tr>
<td>2</td>
<td>Print</td>
<td>Prints the data on the results screen (the absorbance table) using the printer selected in the Utilities folder.</td>
</tr>
<tr>
<td>4</td>
<td>Print Graph</td>
<td>Prints the graph (this option is grayed out if no data are available).</td>
</tr>
<tr>
<td>7</td>
<td>Sample Number</td>
<td>Adds a prefix to the sample number and resets the incrementing number to the desired value.</td>
</tr>
<tr>
<td>8</td>
<td>Save Method</td>
<td>Use the left and right arrows to select the folder you want to store the method in (Favorites/Methods 1-9/SD Memory Card), then press the down arrow and enter a name for the method. Press Save to save the method.</td>
</tr>
<tr>
<td>9</td>
<td>Auto-Print</td>
<td>Toggles Auto-Print on and off.</td>
</tr>
</tbody>
</table>

Press press or press, or wait 20 seconds to exit the method options.

Press press to return to the Standard Methods folder after all your samples have been measured.
Spectrum

NOTE: This method is available on the Lambda Bio+ only.

The Spectrum method enables you to collect an absorption spectrum, and determine peak heights and positions.

The procedure is as follows:

1. From the home page, press 1 to open the Standard Methods folder.
   The Standard Methods screen is displayed.

   ![Standard Methods](image)

   - **1** Single Wavelength
   - **2** Multi Wavelength
   - **3** Spectrum
   - **4** Concentration
   - **5** Standard Curve
   - **6** Kinetics
   - **7** Absorbance Ratio

2. Press 3 to open the Spectrum method.
   The Spectrum - Method Settings screen is displayed.

   ![Spectrum - Method Settings](image)

   - **Start Wavelength**: 400 nm
   - **End Wavelength**: 500 nm
   - **Mode**: Absorbance

3. Set the **Start Wavelength** by using the keypad numbers or the left and right arrows, and then press the down arrow.

4. Set the **End Wavelength** by using the keypad numbers or the left and right arrows, and then press the down arrow.
5. Select the **Mode** using the left and right arrows, and then press the down arrow. The options are **Absorbance** or **%Transmission**.

6. Press **OK** to start measurements. The Spectrum results screen is displayed.

7. Insert the Reference sample and press **OK**. This reference measurement will be used for all subsequent samples until repeated.

8. Insert your first sample and press **OK**. A spectrum and a table of the Absorbance/%Transmission values at each peak are displayed. Use the left and right arrows to move the cursor along the graph. When it reaches a peak, the peak height and width are displayed at the top of the screen. To zoom in on the wavelength scale, use the up arrow key. (This automatically scales the Absorbance/%Transmission axis, depending upon the Graph Scale option, and this is retained for subsequent measurements.) To zoom out again, use the down arrow key.

9. Repeat Step 8 for each sample.
Press \( \) to display the available Options, which you can select using the keypad numbers:

<table>
<thead>
<tr>
<th></th>
<th>Method Settings</th>
<th>Returns to the Method Settings screen.</th>
</tr>
</thead>
<tbody>
<tr>
<td>2</td>
<td>Print</td>
<td>Prints the result using the printer selected in the Utilities folder.</td>
</tr>
<tr>
<td>3</td>
<td>( A/%T )</td>
<td>Toggles between Absorbance and ( % )Transmission mode</td>
</tr>
</tbody>
</table>

4 Peak Detection

Displays the Peak Detection settings screen.

<table>
<thead>
<tr>
<th></th>
<th>Auto-detect Peaks</th>
<th>Peak Detect on Zoom</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Yes</td>
<td>Yes</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th></th>
<th>Min Peak Height</th>
<th>Sort Peaks By…</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>0.00</td>
<td>( )Wavelength</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th></th>
<th>Min Peak Width</th>
<th>Indicate Peaks</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>5 nm</td>
<td>No</td>
</tr>
</tbody>
</table>

Press \( \) to cancel the selections; press \( \) to accept them.
Add Peak manually adds a peak position to the peak table in the results screen at the position set by the cursor. The entry in the peak table is then displayed in inverse shading to discriminate between User Defined Peaks and Auto-Detect peaks. If the cursor is positioned over a user-defined peak, the legend **User Defined Peak** is displayed at the top of the scan. The option then changes to **Delete Peak** to enable you to remove the peak.

**NOTE:** Saving a method at this stage will save these user-defined wavelengths, so that each time the method is run the Absorbance values at these wavelengths are reported.
6  Graph Scale | Displays the Graph Scale settings screen. This enables you to set up a defined graph by defining the limits in either or both of the x and y axes.

**Graph Scale**

<table>
<thead>
<tr>
<th>Zoom Mode</th>
</tr>
</thead>
<tbody>
<tr>
<td>x axis</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>x axis limits</th>
<th>y axis limits</th>
</tr>
</thead>
<tbody>
<tr>
<td>Off</td>
<td>Off</td>
</tr>
<tr>
<td>x1 200 nm</td>
<td>y1 0.00</td>
</tr>
<tr>
<td>x2 950 nm</td>
<td>y2 2.50</td>
</tr>
</tbody>
</table>

- **Zoom Mode**: This sets up the operation of the Zoom keys (up and down arrows). The mode x axis zooms the display around the cursor point x axis, the mode y axis zooms the display around the cursor point y axis, and x & y axes expands both axes about the cursor point. With x or y axis limits set to On, zooming out will only be permitted within the set limits.

- **x axis limits/y axis limits**: Setting to On activates the start and finish points of the desired graph to user-defined, specific wavelengths and/or absorbance values.

  - Press 🚯 to cancel the selections; press ✅ to accept them and display the required graph.

7  Sample Number | Adds a prefix to the sample number and resets the incrementing number to the desired value.

8  Save Method   | Use the left and right arrows to select the folder you want to store the method in (Favorites/Methods 1–9/SD Memory Card), then press the down arrow and enter a name for the method. Press 🟢 Save to save the method.

9  Auto-print    | Toggles Auto-Print on and off.

  - Press 🟢 or 🟥, or wait 20 seconds to exit the method options.

  - Press 🟥 to return to the Standard Methods folder after all your samples have been measured.
**Concentration**

**NOTE:** This method is available on the Lambda Bio+ only.

The Concentration method 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). The concentration is determined by measuring the absorbance at a specific wavelength and then multiplying by a factor. If the factor is known in advance it can be entered into the method. If the factor is not known, a standard of known concentration can be measured and the factor then calculated by the instrument.

The procedure is as follows:

1. From the home page, press 1 to open the Standard Methods folder. The Standard Methods screen is displayed.

   - **Standard Methods**
     - 1. Single Wavelength
     - 2. Multi Wavelength
     - 3. Spectrum
     - 4. Concentration
     - 5. Standard Curve
     - 6. Kinetics
     - 7. Absorbance Ratio

2. Press 4 to open the Concentration method. The Concentration - Method Settings screen is displayed.

   - **Concentration - Method Settings**
     - **Wavelength**: 260 nm
     - **Units**: 
     - **Mode**: Enter Factor
     - **Factor**: 50.0

3. Enter the **Wavelength** by using the keypad numbers or the left and right arrows, and then press the down arrow.
4. Select the **Mode** using the left and right arrows, and then press the down arrow.
   The options are **Enter Factor** (where a known factor is entered), **Measure Standard** (where the factor is calculated from a calibration sample) or **Enter Neg. Factor** (where a known negative factor is entered).

5. If you selected **Enter Factor** or **Enter Neg. Factor**, enter the **Factor** (or **Negative Factor**) using the keypad numbers, and then press the down arrow.
   The available range is from 0.01 to 9999.

   OR

   If you selected **Measure Standard**, enter the **Concentration** using the keypad numbers and then press the down arrow.
   The available range is from 0.001 to 9999.

6. Enter the **Units** and then press the down arrow.

   You can enter text up to 8 characters long using the keypad, or press **Options** to display the Units screen and access a list of pre-defined units.

   ![Units](image)

   In the Units screen, use the left and right arrows to select from the available options.
   The options are 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.
   The Units screen also enables you to select the number of displayed decimal points (DP). The options are Auto, 0, 1 and 2.

   **NOTE:** The result will always be fixed to 5 significant figures, regardless of how many decimal points are selected (so 98768.2 is displayed as 98768, even with 1 decimal point selected).

   Press **OK** to save your options and return to the Method Settings screen.
   You can still edit the units.
7. Press **OK** to start measurements. The Concentration results screen is displayed.

8. Insert the Reference sample and press **OK**. This reference measurement will be used for all subsequent samples until repeated.

9. If you selected Measure Standard, insert your standard and press **OK**. The Run Standard screen is displayed.

OR

If you selected Factor or Negative Factor, go to Step 11.
10. Press Run to run the standard. The Factor is calculated and displayed.

<table>
<thead>
<tr>
<th>Wavelength</th>
<th>Sample</th>
</tr>
</thead>
<tbody>
<tr>
<td>260 nm</td>
<td>Standard</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Absorbance</th>
<th>Concentration</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.006 A</td>
<td>50.0</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Factor</th>
<th>Units</th>
</tr>
</thead>
<tbody>
<tr>
<td>8333</td>
<td>μg/ml</td>
</tr>
</tbody>
</table>

11. Insert your first sample and press . The Concentration of the sample is displayed.

<table>
<thead>
<tr>
<th>Wavelength</th>
<th>Sample</th>
</tr>
</thead>
<tbody>
<tr>
<td>261 nm</td>
<td>7</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Absorbance</th>
<th>Concentration</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.016 A</td>
<td>0.800</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Factor</th>
<th>Units</th>
</tr>
</thead>
<tbody>
<tr>
<td>50.0</td>
<td>μg/ml</td>
</tr>
</tbody>
</table>

12. Repeat Step 11 for each sample.
Press \( \square \) to display the available Options, which you can select using the keypad numbers:

<table>
<thead>
<tr>
<th></th>
<th>Method Settings</th>
<th>Returns to the Method Settings screen.</th>
</tr>
</thead>
<tbody>
<tr>
<td>2</td>
<td>Print</td>
<td>Prints the result using the printer selected in the Utilities folder.</td>
</tr>
<tr>
<td>3</td>
<td>Show Graph</td>
<td>Toggles the graph on and off. The wavelength range of the graph displayed is ±20 nm from the selected wavelength, which is marked by the cursor.</td>
</tr>
<tr>
<td>4</td>
<td>Run Standard</td>
<td>Returns to the Run Standard screen.</td>
</tr>
<tr>
<td>7</td>
<td>Sample Number</td>
<td>Adds a prefix to the sample number and resets the incrementing number to the desired value.</td>
</tr>
<tr>
<td>8</td>
<td>Save Method</td>
<td>Use the left and right arrows to select the folder you want to store the method in (Favorites/Methods 1-9/SD Memory Card), then press the down arrow and enter a name for the method. Press Save ( \square ) to save the method.</td>
</tr>
<tr>
<td>9</td>
<td>Auto-Print</td>
<td>Toggles Auto-Print on and off.</td>
</tr>
</tbody>
</table>

Press \( \square \) or \( \square \), or wait 20 seconds to exit the method options.

Press \( \square \) to return to the Standard Methods folder after all your samples have been measured.
**Standard Curve**

**NOTE:** This method is available on the Lambda Bio+ only.

This method enables the construction of a multi-point calibration curve from standards of known concentration that can then be used to quantify unknown samples. This instrument has the advantage of being able to store this curve as a method, using up to nine standards.

If you wish to have a zero concentration standard, include this in the number of standards to be entered and enter 0.00 for the Concentration, then use a reagent blank when required to enter the zero standard.

The procedure is as follows:

1. From the home page, press 1 to open the Standard Methods folder.
   
   The Standard Methods screen is displayed.

   ![Standard Methods Table]

   - **Single Wavelength**
   - **Kinetics**
   - **Multi Wavelength**
   - **Absorbance Ratio**
   - **Spectrum**
   - **Concentration**
   - **Standard Curve**

2. Press 5 to open the Standard Curve method.
   
   The Standard Curve – Method Settings screen is displayed.

   ![Standard Curve - Method Settings Table]

   - **Wavelength:** 430 nm
   - **Curve Fit:** Zero Regression
   - **Standards:** 4
   - **Calibration:** Standards
   - **Units:** µg/ml
   - **Replicates:** Off

3. Enter the required **Wavelength** using the keypad numbers or left and right arrows, and then press the down arrow.
4. Enter the number of **Standards** to be used in the standards curve using the keypad numbers or left and right arrows, and then press the down arrow.
   The options are 1–9.

5. Enter the **Units** and then press the down arrow.
   You can enter text up to 8 characters long using the keypad, or press Options to display the Units screen and access a list of pre-defined units.

   In the Units screen, use the left and right arrows to select from the available options.
   The options are \( \mu g/ml, \mu g/\mu l, pmol/\mu l, mg/dl, mmol/l, \mu mol/l, g/l, mg/l, \mu g/l, U/l, \% \\), ppm, ppb, conc or none.
   The Units screen also enables you to select the number of displayed decimal points (DP). The options are Auto, 0, 1 and 2.

   **NOTE:** The result will always be fixed to 5 significant figures, regardless of how many decimal points are selected (so 98768.2 is displayed as 98768, even with 1 decimal point selected).

   Press **OK** to save your options and return to the Method Settings screen.
   You can still edit the units.

6. Select the type of **Curve Fit** using the left and right arrows, and then press the down arrow.
   The options are **Zero Regression** (this forces the straight line through the origin), **Regression** (straight-line regression), **Interpolation** (linear interpolation) or **Cubic Spline**.

7. Select the **Calibration** mode using the left and right arrows.
   The options are **Standards** (to measure prepared standards) or **Manual** (entering absorbance values by keypad) or **New Standards** (to replace any standards that have already been collected).

8. If you selected **Standards**, press the down arrow and enter the number of **Replicates**.
   This determines the number of standards to be measured and averaged at each standard concentration point.
   The options are **Off** (1), 2 or 3.

   **NOTE:** If you selected **Manual** in Step 7, the option **Replicates** is not available.
9. Press **Next**.

The Standard Curve – Standards screen is displayed.

```
<table>
<thead>
<tr>
<th>Conc. Std. 1</th>
<th>Conc. Std. 4</th>
</tr>
</thead>
<tbody>
<tr>
<td>10.0</td>
<td>62.0</td>
</tr>
<tr>
<td>20.0</td>
<td></td>
</tr>
<tr>
<td>31.0</td>
<td></td>
</tr>
</tbody>
</table>
```

10. Enter the concentration values for each standard using the keypad numbers and the up and down arrows to move between the different standard boxes. The available range is from 0.001 to 9999.

11. Press **Next**.

The Standard Curve – Calibration screen is displayed.

```
<table>
<thead>
<tr>
<th>Standards</th>
</tr>
</thead>
<tbody>
<tr>
<td>10.0</td>
</tr>
<tr>
<td>20.0</td>
</tr>
<tr>
<td>31.0</td>
</tr>
<tr>
<td>62.0</td>
</tr>
</tbody>
</table>
```

**NOTE:** If any duplicate or non-monotonic entries are entered on the Standards screen, when **Next** is pressed the instrument will beep and highlight the incorrect entry.
12. If you selected **Standards**, insert the reference sample and then press \[ \text{OAB} \].
   This reference measurement will be used for all subsequent samples until repeated.

   OR

   If you selected **Manual**, enter the known absorbance value for each concentration using the keypad. Go to Step 15.
   The available range is from 0.001 to 9999.

13. Insert your first standard and press \[ \text{Up} \].
   If there are any replicates, press **Replicates** \[ \text{Up} \] to view them and then press \[ \text{Up} \] to measure each replicate.

14. Repeat Step 13 for all your standards.
   A graph will display the results and the curve fit (for example, zero regression) as the measurements are made.

**NOTE:** You can use the up and down arrows to select a standard to be repeated. Press \[ \text{C} \] to clear the previous reading before measuring.
If you selected Replicates, then when all replicates have been measured press Next to return to the Standards screen.

15. Press OK to accept the calibration. The Standard Curve results screen is displayed.

16. If you selected Manual, insert the reference sample and then press.

This reference measurement will be used for all subsequent samples until repeated.

OR

If you selected Standards, go to Step 17.
17. Insert your first sample and then press \( \rightarrow \).
The absorbance of the sample is measured, and its concentration is calculated and displayed.

<table>
<thead>
<tr>
<th>Wavelength</th>
<th>Sample</th>
</tr>
</thead>
<tbody>
<tr>
<td>430 nm</td>
<td>1</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Absorbance</th>
<th>Concentration</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.121 A</td>
<td>19.4 μg/ml</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Curve Fit</th>
<th>Units</th>
</tr>
</thead>
<tbody>
<tr>
<td>Zero Regression</td>
<td>μg/ml</td>
</tr>
</tbody>
</table>

18. Repeat Step 17 for each sample.

- Press \( \rightarrow \) to display the available method options, which you can select using the keypad numbers:

<table>
<thead>
<tr>
<th>Method</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Method Settings Returns to the Method Settings screen.</td>
</tr>
<tr>
<td>2</td>
<td>Print Prints the data on the results screen using the printer selected in the Utilities folder.</td>
</tr>
<tr>
<td>3</td>
<td>Show Graph Toggles the calibration graph on and off. The cursors display the absorbance and corresponding concentration values of the last measured sample.</td>
</tr>
<tr>
<td>7</td>
<td>Sample Number Adds a prefix to the sample number and resets the incrementing number to the desired value.</td>
</tr>
<tr>
<td>8</td>
<td>Save Method Use the left and right arrows to select the folder you want to store the method in (Favorites/Methods 1–9/SD Memory Card), then press the down arrow and enter a name for the method. Press ( \rightarrow ) to save the method.</td>
</tr>
<tr>
<td>9</td>
<td>Auto-print Toggles Auto-Print on and off.</td>
</tr>
</tbody>
</table>

- Press \( \rightarrow \) or \( \square \), or wait 20 seconds to exit the method options.

- Press \( \square \) to return to the Standard Methods folder after all your samples have been measured.
Kinetics

**NOTE:** This method is available on the Lambda Bio+ only.

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

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 only the absorbance difference.

For this reason, the change in absorbance per minute ($\Delta A/min$), concentration ($\Delta A/min \times$ 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:

1. From the home page, press 1 to open the Standard Methods folder.
   The Standard Methods screen is displayed.

<table>
<thead>
<tr>
<th>Standard Methods</th>
</tr>
</thead>
<tbody>
<tr>
<td>3. Spectrum</td>
</tr>
<tr>
<td>4. Concentration</td>
</tr>
<tr>
<td>5. Standard Curve</td>
</tr>
</tbody>
</table>
2. Press 6 to open the Kinetics method.
   The Kinetics – Method Settings 1 screen is displayed.

   ![Kinetics - Method Settings 1](image)

   Enter all numerical values using the keypad numbers or the left and right arrows.

3. Set the **Wavelength** by using the keypad numbers or left and right arrows, and then press the down arrow.
   The default value is 340 nm.

4. Enter the **Delay Time** in seconds before measurements are taken and then press the down arrow.
   This can be a maximum of 600 seconds (10 minutes).

5. Enter the time in minutes over which measurements are taken (**Duration**) and then press the down arrow.
   This can be a maximum of 60 minutes.

6. Enter the **Interval** time in seconds between measurements using the left and right arrows, and then press the down arrow.
   The options are 1, 2, 5, 10, 15, 20, 30 or 60 seconds.
7. Press Next.

The Kinetics – Method Settings 2 screen is displayed.

8. Select the measurement **Mode** using the left and right arrows, and then press the down arrow.

The options are **Delta A** (the change in absorbance over the measurement duration, or selected period), **Final A** (the absorbance at the end of the measurement duration, or selected time) and **Slope** (the rate of change of absorbance over the measurement duration or selected period).

9. Enter the **Units** and then press the down arrow.

You can enter a text string up to 8 characters long. To access a list of pre-defined units on the Units screen, press Options 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.

The Units screen also enables you to select the number of displayed decimal points (DP). The options are **Auto**, **0**, **1** and **2**.

**NOTE:** The result will always be fixed to 5 significant figures, regardless of how many decimal points are selected (so 98768.2 is displayed as 98768, even with 1 decimal point selected).

Press OK to save your options and return to the Method Settings screen.

You can still edit the units.
10. Set the **Factor** by which the absorbance is multiplied to give the concentration using the left and right arrows. The available range is from 0.01 to 9999.

11. Press **OK** to start measurements. The Kinetics results screen is displayed.

12. Insert the reference sample and press **DA**. This reference measurement will be used for all subsequent samples until repeated.

13. Insert your first sample and then press **to start the run.** The running **Time** is displayed at the bottom of the screen, and absorbance data are plotted on the graph as the measurement proceed. The table below the graph displays $A_0$, the absorbance value at $t_0$ (start of calculation); $A_n$, the absorbance value at $t_n$ (finish of calculation); $dA$, the change in absorbance; the **Slope** and the regression parameter ($R^2$) of the calculated slope. The concentration is a calculated using the parameters selected in Method Settings 2 ($dA$, **Final A** or **Slope**) – the name of the **Result** table column depends on the units chosen in Step 9.

<table>
<thead>
<tr>
<th>$A_0$</th>
<th>$A_n$</th>
<th>$dA$</th>
<th>Slope</th>
<th>Result</th>
<th>$R^2$</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.644</td>
<td>0.006</td>
<td>0.638</td>
<td>-0.402</td>
<td>0.638</td>
<td>0.2290</td>
</tr>
</tbody>
</table>

- 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 \( \text{\textbullet} \) to display the available method options, which you can select using the keypad numbers:

<table>
<thead>
<tr>
<th></th>
<th>Method Settings</th>
<th>Returns to the Method Settings screen.</th>
</tr>
</thead>
<tbody>
<tr>
<td>2</td>
<td>Print</td>
<td>Prints the data on the results screen using the printer selected in the Utilities folder.</td>
</tr>
<tr>
<td>3</td>
<td>Print Data</td>
<td>Prints all the data.</td>
</tr>
<tr>
<td>4</td>
<td>Set ( t_0 ) at cursor</td>
<td>Sets the ( t_0 ) position (the starting point for the slope and dA calculations) at the current cursor position. The value is retained for subsequent samples.</td>
</tr>
<tr>
<td>5</td>
<td>Set ( t_n ) At Cursor</td>
<td>Sets the ( t_n ) position (the finishing point for the slope and dA calculations) at the current cursor position. The value is retained for subsequent samples.</td>
</tr>
<tr>
<td>6</td>
<td>Show Slope</td>
<td>Toggles the calculated slope line on and off.</td>
</tr>
</tbody>
</table>

**NOTE:** If any data points enclosed by \( t_0 \) and \( t_n \) are beyond the range of the instrument (that is, \( >2.5 \text{ A} \) or \( < -0.3 \text{ A} \)) then this option is grayed out.

<table>
<thead>
<tr>
<th></th>
<th>Sample Number</th>
<th>Adds a prefix to the sample number and resets the incrementing number to the desired value.</th>
</tr>
</thead>
<tbody>
<tr>
<td>8</td>
<td>Save Method</td>
<td>Use the left and right arrows to select the folder you want to store the method in (Favorites/Methods 1–9/SD Memory Card), then press the down arrow and enter a name for the method. Press ( \text{Save} ) to save the method.</td>
</tr>
<tr>
<td>9</td>
<td>Auto-print</td>
<td>Toggles Auto-Print on and off.</td>
</tr>
</tbody>
</table>

Press \( \text{\textbullet} \) or \( \text{\textminus} \), or wait 20 seconds to exit the method options.

Press \( \text{\textup{Next}} \) to return to the Standard Methods folder after all your samples have been measured.
**Absorbance Ratio**

**NOTE:** This method is available on the Lambda Bio+ only.

The Absorbance Ratio method makes simple absorbance ratio measurements on samples, by 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:

1. From the home page, press 1 to open the Standard Methods folder. The Standard Methods screen is displayed.

2. Press 7 to select the Absorbance Ratio method. The Absorbance Ratio – Wavelengths screen is displayed.

3. Enter **Wavelength 1** by using the keypad numbers or the left and right arrows, and then press the down arrow.

4. Enter **Wavelength 2** as above and then press the down arrow.
5. Select whether a **Background** correction is applied to both wavelengths 1 and 2 using the left and right arrows.

6. If background correction is **On**, enter **Wavelength 3**, from which the background correction will be obtained.

7. Press **Next**. The Absorbance Ratio – Method Settings screen is displayed.

8. Select the **Pathlength** using the left and right arrows, and then press the down arrow. The options are **5 mm** or **10 mm**.

9. If the **Dilution Factor** is known, enter a dilution factor by using the keypad numbers, press the down arrow and then go to Step 13. The available range is from 1.00 to 9999.

OR

If the dilution factor is unknown, press **Options** to display the Dilution Factor screen.

10. Enter the **Volume** of the sample using the keypad numbers and then press the down arrow. The available range is from 0.01 to 9999.
11. Enter the volume of **Diluent** by using the keypad numbers. The available range is from 0.01 to 9999.

12. Press **OK** to calculate the dilution factor and return to the Method Settings screen.

13. Select the **Units** of measurement using the left and right arrows, and then press the down arrow. The options are **µg/ml**, **ng/µl**, **µg/µl**.

14. Enter the **Factor** using the keypad numbers and then press the down arrow. The available range is from 0.001 to 9999.

15. Press **OK** to start measurements. The Absorbance Ratio results screen is displayed.

16. Insert the reference sample and then press **OK**. This reference measurement will be used for all subsequent samples until repeated.

17. Insert your first sample and press **OK**. The absorbance at each wavelength is measured. If Background was selected, the background absorbance is then subtracted from the absorbance at Wavelength 1 and Wavelength 2. The ratio between Wavelength 1 and Wavelength 2 is calculated.
18. Repeat Step 17 for each sample.

- Press [method options] to display the available method options, which you can select using the keypad numbers:

<table>
<thead>
<tr>
<th></th>
<th>Method Settings</th>
<th>Returns to the Method Settings screen.</th>
</tr>
</thead>
<tbody>
<tr>
<td>2</td>
<td>Print</td>
<td>Prints using the printer selected in the Utilities folder.</td>
</tr>
<tr>
<td>3</td>
<td>Show Graph</td>
<td>Toggles the graph on and off. The graph shows a spectrum across the range of the measured wavelengths, which are marked by cursors.</td>
</tr>
<tr>
<td>7</td>
<td>Sample Number</td>
<td>Adds a prefix to the sample number and resets the incrementing number to the desired value.</td>
</tr>
<tr>
<td>8</td>
<td>Save Method</td>
<td>Use the left and right arrows to select the folder you want to store the method in (Favorites/Methods 1-9/SD Memory Card), then press the down arrow and enter a name for the method. Press [Save] to save the method.</td>
</tr>
<tr>
<td>9</td>
<td>Auto-Print</td>
<td>Toggles Auto-Print on and off.</td>
</tr>
</tbody>
</table>

- Press [method options] or [method options] or wait 20 seconds to exit the method options.

- Press [method options] to return to the Standard Methods folder after all your samples have been measured.
DNA, RNA and Oligonucleotide Characterization

Introduction

The Lambda Bio/Bio+ includes three methods for nucleic acid quantification.

| DNA | RNA | Oligo |
| DNA | RNA | Oligo |

Figure 11 Lambda Bio+ Nucleic Acids screen

Nucleic acid quantifications (NAQ)

Nucleic acids can be quantified at 260 nm because it is well established that a solution of DNA or RNA in a 10 mm pathlength cell with an optical density of 1.0 has a concentration of 50 µg/ml or 40 µg/ml, respectively. 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:

\[
\text{Concentration} = A_{260} \times \text{Factor}
\]

The instrument uses factors 50, 40 and 33 as defaults for DNA, RNA and oligonucleotides, respectively, and compensates for dilution and the use of cells that do not have 10 mm pathlength; dilution factor and cell pathlength can be entered. In the Oligo method it is possible to calculate the factor from the composite bases by entering the proportions of the 4 bases.

Nucleic acid purity checks

Extensive purification is required to separate protein impurities from nucleic acids extracted from cells. The A260/A280 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 the interpretation of results.
The 260 nm reading is taken near the top of a broad peak in the absorbance spectrum for nucleic acids (Figure 12). The 280 nm reading is taken on a steep slope, where small changes in wavelength cause large changes in absorbance, and consequently, have a greater effect on the A260/A280 ratio than variations will at 260 nm. Thus different instruments, of the same or different types, may give slightly different ratios due to variations in wavelength accuracy. But each instrument can be expected to give consistent results within itself.

![Figure 12 Spectral scan of nucleic acid](image)

The important features of the spectrum are:

- Absorbance maximum near 260 nm and absorbance minimum near 230 nm;
- Flat peak near 260 nm and steep slope at 280 nm;
- Very low absorbance at 320 nm.

Solution concentration also affects the accuracy of A260/A280 readings. If a solution is too dilute, then the readings will be at the instrument’s detection limit, and results may vary as the 260 nm peak and the 280 nm slope will be less distinct from the background absorbance. This is one reason why the A260 value should be greater than 0.1 A for accurate measurements.

An elevated absorbance at 230 nm can also indicate the presence of impurities. The 230 nm wavelength is near the absorbance maximum of peptide bonds. EDTA and other buffer salts absorb at this wavelength. When measuring RNA samples, the A260/A230 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 that absorbs over the 230–260 nm range. A wavelength scan of the nucleic acid is particularly useful for RNA samples.

The nucleic acid methods display the A260/A280 and A260/A230 ratios, and compensate for dilution and the use of cells that do not have 10 mm pathlength – dilution factor and cell pathlength can be entered.
Use of Background correction

To compensate for the effects of background absorbance, background correction is sometimes used. The wavelength used is 320 nm, a wavelength totally separate from the nucleic acid and protein peaks at 260 and 280 nm, respectively. Background correction can allow for the effects of turbidity, high absorbance buffer solution and the use of reduced aperture cells. The use of background correction can also remove variability due to handling effects of low volume disposable cells.

Setting Background correction to On will give different results from those where the correction is Off, because the absorbance at 320 nm is subtracted from the absorbance at 280 and 230 nm, before the concentration or the absorbance rations are calculated:

Concentration = \((A_{260} - A_{320}) \times \text{Factor}\)

Absorbance ratio = \((A_{260} - A_{320}) / (A_{280} - A_{320})\)

Absorbance ratio = \((A_{260} - A_{320}) / (A_{230} - A_{320})\)

If your laboratory has not used background correction before, set this option to Off.

DNA

The procedure is as follows:

1. From the home page, press 2 to open the Life Science folder (Lambda Bio+ only).
2. Press 1 to open the Nucleic Acids folder (Lambda Bio+ only).
3. Press 1 to open the DNA method.
   The DNA – Method Settings screen is displayed.

<table>
<thead>
<tr>
<th>DNA - Method Settings</th>
</tr>
</thead>
<tbody>
<tr>
<td>Pathlength</td>
</tr>
<tr>
<td>10 mm</td>
</tr>
<tr>
<td>Dilution Factor</td>
</tr>
<tr>
<td>1.000</td>
</tr>
<tr>
<td>Background</td>
</tr>
<tr>
<td>On</td>
</tr>
</tbody>
</table>

4. Select the Pathlength using the left and right arrows, and then press the down arrow. The options are 0.5 mm, 5 mm or 10 mm (Lambda Bio) or 5 mm or 10 mm (Lambda Bio+).
5. If the **Dilution Factor** is known, enter it using the keypad numbers and go to Step 9. The available range is from 1.00 to 9999.

OR

If the **Dilution Factor** is unknown, then press \( \square \). The Dilution Factor screen is displayed.

6. Enter the **Volume** of the sample using the keypad numbers, and then press the down arrow. The available range is from 0.01 to 9999.

7. Enter the volume of the **Diluent** using the keypad numbers. The available range is from 0.01 to 9999.

8. Press **OK** to calculate the dilution factor and return to the Method Settings screen.

9. Select whether the **Background** correction at 320 nm is **On** or **Off** with the left and right arrows, and then press the down arrow.

10. Select the **Units** of measurement using the left and right arrows, and then press the down arrow. The options are \( \mu g/ml \), \( ng/\mu l \) and \( \mu g/\mu l \).

11. Enter the **Factor** using the keypad numbers. The available range is from 0.01 to 9999.
12. Press **OK** to start measurements. The DNA results screen is displayed.

<table>
<thead>
<tr>
<th>DNA</th>
<th>Sample</th>
</tr>
</thead>
<tbody>
<tr>
<td>A230</td>
<td></td>
</tr>
<tr>
<td>A260</td>
<td></td>
</tr>
<tr>
<td>A280</td>
<td></td>
</tr>
<tr>
<td>A320</td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>A260/A280</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>A260/A230</td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Units</th>
<th>µg/ml</th>
</tr>
</thead>
</table>

13. Insert the reference sample and press **OK**. This reference measurement will be used for all subsequent samples until repeated.

14. Insert your first sample and press **OK**. The absorbances at 260 nm and 280 nm are measured, corrected by the background wavelength value (320 nm) if selected, and the ratio of the two absorbances is calculated. The concentration is calculated based on the absorbance at 260 nm.

<table>
<thead>
<tr>
<th>DNA</th>
<th>Sample</th>
</tr>
</thead>
<tbody>
<tr>
<td>A230</td>
<td>0.189 A</td>
</tr>
<tr>
<td>A260</td>
<td>0.390 A</td>
</tr>
<tr>
<td>A280</td>
<td>0.093 A</td>
</tr>
<tr>
<td>A320</td>
<td>0.000 A</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>A260/A280</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>A260/A230</td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Concentration</th>
<th>Units</th>
</tr>
</thead>
<tbody>
<tr>
<td>19.50</td>
<td>µg/ml</td>
</tr>
</tbody>
</table>

15. Repeat Step 14 for each sample.
Press \( \text{Menu} \) to display the available Options, which you can select using the keypad numbers:

<table>
<thead>
<tr>
<th></th>
<th>Method Settings</th>
<th>Returns to the Method Settings screen.</th>
</tr>
</thead>
<tbody>
<tr>
<td>2</td>
<td>Print</td>
<td>Prints using the printer selected in the Utilities folder.</td>
</tr>
<tr>
<td>3</td>
<td>Show Graph</td>
<td>Toggles the graph on and off. The graph shows a spectrum across the range 220 nm to 320 nm with cursors denoting 230 nm, 260 nm, 280 nm and (if background correction selected) 320 nm.</td>
</tr>
<tr>
<td>7</td>
<td>Sample Number</td>
<td>Adds a prefix to the sample number and resets the incrementing number to the desired value.</td>
</tr>
<tr>
<td>8</td>
<td>Save Method</td>
<td>Use the left and right arrows to select the folder you want to store the method in (Favorites/Methods 1–9/SD Memory Card), then press the down arrow and enter a name for the method. Press ( \text{Save} ) to save the method.</td>
</tr>
<tr>
<td>9</td>
<td>Auto-Print</td>
<td>Toggles Auto-Print on and off.</td>
</tr>
</tbody>
</table>

Press \( \text{Menu} \) or \( \text{ESC} \), or wait 20 seconds to exit the method options.

Press \( \text{ESC} \) to return to the Nucleic Acids folder (Lambda Bio+) or the home page (Lambda Bio).

**RNA**

The procedure is as follows:

1. From the home page, press 5 to open the Life Science folder (Lambda Bio+ only).
2. Press 1 to open the Nucleic Acids folder (Lambda Bio+ only).
3. Press 2 to open the RNA method.
   The RNA – Method Settings screen is displayed.

4. Select the Pathlength using the left and right arrows, and then press the down arrow.
   The options are 0.5 mm, 5 mm or 10 mm (Lambda Bio) or 5 mm or 10 mm (Lambda Bio+).

5. If the Dilution Factor is known, enter it using the keypad numbers and go to Step 9.
   The available range is from 1.00 to 9999.
   OR
   If the Dilution Factor is unknown, press .
   The Dilution Factor screen is displayed.

6. Enter the Volume of the sample using the keypad numbers, and then press the down arrow.
   The available range is from 0.01 to 9999.

7. Enter the volume of the Diluent using the keypad numbers.
   The available range is from 0.01 to 9999.

8. Press OK to calculate the dilution factor and return to the Method Settings screen.
9. Select whether the background correction at 320 nm is used or not with the left and right arrows, and then press the down arrow.

10. Select the **Units** of measurement using the left and right arrows, and then press the down arrow.
    The options are **µg/ml**, **ng/µl** and **µg/µl**.

11. Enter the **Factor** using the keypad numbers.
    The available range is from 0.01 to 9999.

12. Press **OK** to start measurements.
    The RNA results screen is displayed.

13. Insert the reference sample and press **OA**.
    This reference measurement will be used for all subsequent samples until repeated.

14. Insert your first sample and press **OA**.
    The absorbances at 260 nm and 280 nm are measured, corrected by the background wavelength value (320 nm) if selected, and the ratio of the two absorbances is calculated. The concentration is calculated based on the absorbance at 260 nm.

15. Repeat Step 14 for each sample.
Press \( \textbullet \) to display the available options, which you can select using the keypad numbers:

<table>
<thead>
<tr>
<th></th>
<th>Method Settings</th>
<th>Returns to the Method Settings screen.</th>
</tr>
</thead>
<tbody>
<tr>
<td>2</td>
<td>Print</td>
<td>Prints using the printer selected in the Utilities folder.</td>
</tr>
<tr>
<td>3</td>
<td>Show Graph</td>
<td>Toggles the graph on and off. The graph shows a spectrum across the range 220 nm to 320 nm with cursors denoting 230 nm, 260 nm, 280 nm and (if background correction selected) 320 nm.</td>
</tr>
<tr>
<td>7</td>
<td>Sample Number</td>
<td>Adds a prefix to the sample number and resets the incrementing number to the desired value.</td>
</tr>
<tr>
<td>8</td>
<td>Save Method</td>
<td>Use the left and right arrows to select the folder you want to store the method in (Favorites/Methods 1-9/SD Memory Card), then press the down arrow and enter a name for the method. Press ( \textbullet ) to save the method.</td>
</tr>
<tr>
<td>9</td>
<td>Auto-Print</td>
<td>Toggles Auto-Print on and off.</td>
</tr>
</tbody>
</table>

Press \( \textbullet \) or \( \square \), or wait 20 seconds to exit the method options.

Press \( \square \) to return to the Nucleic Acids folder (Lambda Bio+) or the home page (Lambda Bio).

**Oligonucleotide**

The procedure is as follows:

1. From the home page, press 5 to open the Life Science folder (Lambda Bio+ only).
2. Press 1 to open the Nucleic Acids folder (Lambda Bio+ only).
3. Press 3 to open the Oligo method.
   The Oligo – Method Settings screen is displayed.

4. Select the **Pathlength** using the left and right arrows, and then press the down arrow.
   The options are **0.5 mm**, **5 mm** or **10 mm** (Lambda Bio) or **5 mm** or **10 mm** (Lambda Bio+).

5. If the **Dilution Factor** is known, enter it using the keypad numbers and go to Step 9.
   The available range is from 1.00 to 9999.
   OR

   If the **Dilution Factor** is unknown, press **OK**.
   The Dilution Factor screen is displayed.

6. Enter the **Volume** of the sample using the keypad numbers, and then press the down arrow.
   The available range is from 0.01 to 9999.

7. Enter the volume of the **Diluent** using the keypad numbers.
   The available range is from 0.01 to 9999.

8. Press **OK** to calculate the dilution factor and return to the Method Settings screen.
9. Select whether the **Background** correction at 320 nm is **On** or **Off** with the left and right arrows, and then press the down arrow.

10. Select the **Units** of measurement using the left and right arrows, and then press the down arrow.
    The options are **µg/ml**, **ng/µl**, **µg/µl** and **pmol/µl**.

11. If the units are **µg/ml**, **ng/µl**, **µg/µl**, enter the **Factor** using the keypad numbers.
    The available range is from 0.01 to 9999.
    OR

    If the units are **pmol/µl**, the factor changes to a selection table listing the ratios of the four bases in the structure. Enter the proportions of the bases **A**, **C**, **G** and **T** present using the keypad numbers and using the up and down arrows to move between boxes.
    The available range is from 0 to 9999.

<table>
<thead>
<tr>
<th>Oligo - Method Settings</th>
</tr>
</thead>
<tbody>
<tr>
<td>Pathlength</td>
</tr>
<tr>
<td>5 mm</td>
</tr>
<tr>
<td>Units</td>
</tr>
<tr>
<td>pmol/µl</td>
</tr>
<tr>
<td>Dilution Factor</td>
</tr>
<tr>
<td>1.000</td>
</tr>
<tr>
<td>Background</td>
</tr>
<tr>
<td>Off</td>
</tr>
</tbody>
</table>

12. Press **OK** to start measurements.
    The Oligo results screen is displayed.

<table>
<thead>
<tr>
<th>Oligo</th>
</tr>
</thead>
<tbody>
<tr>
<td>A230</td>
</tr>
<tr>
<td>A260</td>
</tr>
<tr>
<td>A280</td>
</tr>
<tr>
<td>A320</td>
</tr>
<tr>
<td>A260/A280</td>
</tr>
<tr>
<td>A260/A230</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Sample</th>
</tr>
</thead>
</table>

<table>
<thead>
<tr>
<th>Concentration</th>
</tr>
</thead>
</table>

<table>
<thead>
<tr>
<th>Units</th>
</tr>
</thead>
<tbody>
<tr>
<td>µg/ml</td>
</tr>
</tbody>
</table>

13. Insert the reference sample and press to start measurements.
    This reference measurement will be used for all subsequent samples until repeated.

<table>
<thead>
<tr>
<th>Oligo</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>A260</td>
<td>0.390 A</td>
</tr>
<tr>
<td>A280</td>
<td>0.140 A</td>
</tr>
<tr>
<td>A320</td>
<td>0.010 A</td>
</tr>
<tr>
<td>A260/A280</td>
<td>2.785</td>
</tr>
<tr>
<td>A260/A230</td>
<td>2.123</td>
</tr>
</tbody>
</table>

The absorbances at 260 nm and 280 nm are measured, corrected by the background wavelength value (320 nm) if selected, and the ratio of the two absorbances is calculated. The concentration is calculated based on the absorbance at 260 nm.

15. Repeat Step 14 for each sample.

- Press to display the available options, which you can select using the keypad numbers:

| 1 | Method Settings | Returns to the Method Settings screen. |
| 2 | Print           | Prints using the printer selected in the Utilities folder. |
| 3 | Show Graph      | Toggles the graph on and off. The graph shows a spectrum across the range 220 nm to 320 nm with cursors denoting 230 nm, 260 nm, 280 nm and (if background correction selected) 320 nm. |
| 7 | Sample Number   | Adds a prefix to the sample number and resets the incrementing number to the desired value. |
| 8 | Save Method     | Use the left and right arrows to select the folder you want to store the method in (Favorites/Methods 1–9/SD Memory Card), then press the down arrow and enter a name for the method. Press to save the method. |
| 9 | Auto-Print      | Toggles Auto-Print on and off. |

- Press or , or wait 20 seconds to exit the method options.

- Press to return to the Nucleic Acids folder (Lambda Bio+) or the home page (Lambda Bio).
Protein Determinations

The Lambda Bio/Bio+ includes five methods for assaying proteins (Figure 13).

<table>
<thead>
<tr>
<th>Life Science - Protein</th>
</tr>
</thead>
<tbody>
<tr>
<td>1 PROTEIN Protein UV</td>
</tr>
<tr>
<td>2 BCA</td>
</tr>
<tr>
<td>3 Bradford</td>
</tr>
<tr>
<td>4 Lowry</td>
</tr>
<tr>
<td>5 Biuret</td>
</tr>
</tbody>
</table>

Figure 13 Protein methods screen

Protein Determination at 280 nm

Protein concentration can be determined in the near UV at 280 nm by the absorbance of the amino acids tyrosine, tryptophan and phenylalanine. The absorbance at 280 nm varies greatly for different proteins with their amino acid content. Consequently, the specific absorbance 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 for by measuring the absorbance at 260 nm (A260), and applying the equation of Christian and Warburg for the protein crystalline yeast enolase (Biochemische Zeitung, 1941, 310, 384):

\[
\text{Protein (mg/ml)} = 1.55 \times A_{280} - 0.76 \times A_{260}
\]

That is:

\[
\text{Protein concentration} = (\text{Factor 1} \times A_{280}) - (\text{Factor 2} \times A_{260})
\]

This equation can be applied to other proteins if the corresponding factors are known. Your instrument determines the 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 customize the equation for a particular protein, the absorbance values at 260 nm 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 UV protein measurement at 280 nm. Factor 1 is based on the extinction coefficient of the protein. If bovine serum albumin (BSA) is an acceptable standard, setting Factor 1 = 1.115 will give linear results from 0 to 0.8 mg/ml protein.

\[
\text{Protein (mg/ml)} = 1.115 \times A_{280}
\]

Rapid measurements such as this at 280 nm 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 bovine serum albumin (BSA).

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 color obtained from the reaction of Folin-Ciocalteu phenol reagent with the tyrosine residues of an unknown protein and comparing with those derived from a standard curve of a standard protein at 750 nm, usually BSA.

- 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 fit.
**Protein Methods**

*Protein UV*

This method uses the Christian and Warburg assay.

The procedure is as follows:

1. From the home page, press 2 to open the Life Sciences folder (Lambda Bio+ only).

2. If the instrument is a Lambda Bio, from the home page press 6 to open the Proteins folder.

   OR

   If the instrument is a Lambda Bio+, press 2 to open the Proteins folder.

3. Press 1 to open the Protein UV method.  
   The Protein UV – Method Settings screen is displayed.

<table>
<thead>
<tr>
<th>Protein UV - Method Settings</th>
</tr>
</thead>
<tbody>
<tr>
<td>Pathlength</td>
</tr>
<tr>
<td>10 mm</td>
</tr>
<tr>
<td>A280 Factor</td>
</tr>
<tr>
<td>0.760</td>
</tr>
<tr>
<td>Dilution Factor</td>
</tr>
<tr>
<td>1.000</td>
</tr>
<tr>
<td>A280 Factor</td>
</tr>
<tr>
<td>1.500</td>
</tr>
<tr>
<td>Background</td>
</tr>
<tr>
<td>0 on</td>
</tr>
<tr>
<td>Units</td>
</tr>
<tr>
<td>µg/ml</td>
</tr>
</tbody>
</table>

4. Select the **Pathlength** using the left and right arrows, and then press the down arrow.  
   The options are **0.5 mm, 5 mm or 10 mm** (Lambda Bio) or **5 mm or 10 mm** (Lambda Bio+).

5. If the **Dilution Factor** is known, enter a dilution factor by using the keypad numbers, press the down arrow, and then go to Step 9.  
   The available range is from 1.00 to 9999.

   OR

   If the dilution factor is unknown, press **Options** to display the Dilution Factor screen.
6. Enter the **Volume** of the sample using the keypad numbers, and then press the down arrow.
   The available range is from 0.01 to 9999.

7. Enter the volume of the **Diluent** using the keypad numbers.
   The available range is from 0.01 to 9999.

8. Press **OK** to calculate the dilution factor and return to the Method Settings screen.

9. Select whether the **Background** correction at 320 nm is used (ON) or not (OFF) with the left and right arrows, and then press the down arrow.

10. Enter **A260 nm Factor** using the keypad numbers, and then press the down arrow.
    The available range is from 0 to 9999.

11. Enter **A280 nm Factor** using the keypad numbers, and then press the down arrow.
    The available range is from 1.00 to 9999.

12. Select the **Units** of measurement using the left and right arrows.
    The options are µg/ml, ng/µl and µg/µl.

13. Press **OK** to start measurements.
    The Protein UV results Screen is displayed.
14. Insert the reference sample and press \( \text{A} \). This reference measurement will be used for all subsequent samples until repeated.

15. Insert your first sample and press \( \text{B} \).
   The absorbances at 260 nm and 280 nm are measured, corrected by the background wavelength value (320 nm) if background correction is selected, and the protein concentration is calculated.

<table>
<thead>
<tr>
<th>Protein UV</th>
</tr>
</thead>
<tbody>
<tr>
<td>A260</td>
</tr>
<tr>
<td>0.036 A</td>
</tr>
<tr>
<td>A280</td>
</tr>
<tr>
<td>0.435 A</td>
</tr>
<tr>
<td>A320</td>
</tr>
<tr>
<td>0.002 A</td>
</tr>
</tbody>
</table>

16. Repeat Step 15 for each sample.

- Press \( \text{C} \) to display the available options, which you can select using the keypad numbers:

<p>| | | | | | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Method Settings</td>
<td>Return to Method Settings screen (step 1 above).</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>Print</td>
<td>Print result using the printer selected in the Utilities folder.</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>Show Graph</td>
<td>Toggles the graph on and off. The graph shows a spectrum across the range 250 nm to 330 nm with cursors denoting 230 nm, 260 nm, 280 nm and (if you selected background correction) 320 nm.</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>7</td>
<td>Sample Number</td>
<td>Add a prefix to the sample number and reset the incrementing number to the desired value.</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>8</td>
<td>Save Method</td>
<td>Use the left and right arrows to select the folder you want to store the method in (Favorites/Methods 1–9/SD Memory Card), then press the down arrow and enter a name for the method. Press ( \text{Save} ) to save the method.</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>9</td>
<td>Auto-Print</td>
<td>Toggles Auto-Print on and off.</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

- Press \( \text{D} \) or \( \text{E} \), or wait 20 seconds to exit the method options.

- Press \( \text{F} \) to return to the Protein folder after you have taken all your measurements.
**BCA, Bradford, Lowry and Biuret**

**NOTE:** Only the BCA method is described here. The procedure for the Bradford, Lowry and Biuret methods is identical – only the measurement wavelength is different. See *Protein Determination at 595, 546, 562 and 750 nm* on page 86 for more details.

The procedure is as follows:

1. From the home page, press 2 to open the Life Sciences folder (Lambda Bio+ only).

2. If the instrument is a Lambda Bio, from the home page press 6 to open the Proteins folder.

   OR

If the instrument is a Lambda Bio+, press 2 to open the Proteins folder.

3. Press 2 to open the BCA method.

   The BCA - Method Settings screen is displayed.

   ![BCA - Method Settings](image)

   The **Wavelength** for this method is set at 562 nm.

4. Enter the number of **Standards** (1-9) to be used in the curve using the keypad numbers or the left and right arrows, and then press the down arrow.
5. Enter the **Units**, and then press the down arrow.

You can enter text up to 8 characters long using the keypad, or press Options ☰ to display the Units screen and access a list of pre-defined units.

![Units screen](image)

In the Units screen, use the left and right arrows to select from the available options. The options are 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.

The Units screen also enables you to select the number of displayed decimal points (DP). The options are Auto, 0, 1 and 2.

**NOTE:** The result will always be fixed to 5 significant figures, regardless of how many decimal points are selected (so 98768.2 is displayed as 98768, even with 1 decimal point selected).

Press **OK** ✅ to save your options and return to the Method Settings screen.

You can still edit the units.

6. Select the type of **Curve Fit** using the left and right arrows, and then press the down arrow.

The options are **Regression** (straight-line regression), **Zero Regression** (this forces the straight line through the origin), **Interpolation** (linear interpolation) or **Cubic Spline**.

7. Select the **Calibration** mode.

The options are **Standards** (to measure prepared standards) or **Manual** (entering absorbance values by keypad) or **New Standards** (to replace any standards that have already been collected).

8. If you selected **Standards**, press the down arrow and enter the number of **Replicates**.

This determines the number of standards to be measured and averaged at each standard concentration point.

The options are **OFF** (1), 2 or 3.

**NOTE:** If you selected **Manual** in Step 7, you do not enter Replicates.

<table>
<thead>
<tr>
<th>BCA - Standards</th>
</tr>
</thead>
<tbody>
<tr>
<td>Conc. Std. 1</td>
</tr>
<tr>
<td>0.200</td>
</tr>
<tr>
<td>Conc. Std. 2</td>
</tr>
<tr>
<td>0.400</td>
</tr>
<tr>
<td>Conc. Std. 3</td>
</tr>
<tr>
<td>0.600</td>
</tr>
</tbody>
</table>

10. Enter the concentration values by using the keypad numbers, and the up and down arrows to move between the different standard boxes. The available range is from 0.001 to 9999.

11. Press Next. The BCA – Calibration screen is displayed.

<table>
<thead>
<tr>
<th>BCA - Calibration</th>
</tr>
</thead>
<tbody>
<tr>
<td>Standards</td>
</tr>
<tr>
<td>0.200</td>
</tr>
<tr>
<td>0.400</td>
</tr>
<tr>
<td>0.600</td>
</tr>
<tr>
<td>0.800</td>
</tr>
<tr>
<td>1.000</td>
</tr>
<tr>
<td>1.400</td>
</tr>
</tbody>
</table>

**NOTE:** If any duplicate or non-monotonic entries are entered on the Standards page, when Next is pressed the instrument will beep and highlight the incorrect entry.

12. If you selected **Standards**, insert the reference sample and then press Next. This reference measurement will be used for all subsequent samples until repeated.

OR

If you selected **Manual**, enter the known absorbance value for each concentration using the keypad. Go to Step 15.
The available range is from 0.001 to 9999.
13. Insert your first standard and press $\text{Insert}$. If there are any replicates, press $\text{Replicates}$ to view them, and then press $\text{Measure}$ to measure each replicate.

14. Repeat Step 13 for all your standards. A graph will display the results and the curve fit (for example, zero regression) as the measurements are made.

NOTE: You can use the up and down arrows to select a standard to be repeated if a poor reading has been obtained. Press $\text{Clear}$ to clear the previous reading before measuring.
If you selected Replicates, when all replicates have been measured, press **Next** to return to the Standards screen.

If you selected **Manual**, insert the reference sample and then press **OK**. This reference measurement will be used for all subsequent samples until repeated.

**OR**

If you selected Standards, go to Step 17.
17. Insert your first sample and press \( \rightarrow \).

The absorbance of the sample is measured and its concentration are calculated and displayed.

![Sample properties table](image)

18. Repeat Step 17 for each sample.

- Press \( \square \) to display the available options, which you can select using the keypad numbers:

<p>| | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Method Settings</td>
</tr>
<tr>
<td>2</td>
<td>Print</td>
</tr>
<tr>
<td>3</td>
<td>Show Graph</td>
</tr>
<tr>
<td>7</td>
<td>Sample Number</td>
</tr>
<tr>
<td>8</td>
<td>Save Method</td>
</tr>
<tr>
<td>9</td>
<td>Auto-print</td>
</tr>
</tbody>
</table>

- Press \( \square \) or \( \square \), or wait 20 seconds to exit the method options.

- Press \( \square \) to return to the Protein folder after you have taken all your measurements.
Measuring Absorbance and Concentration

NOTE: This method is available on the Lambda Bio only.

The Measuring Absorbance and Concentration method has two functions:

- To make absorbance (A) measurements on samples, by measuring the amount of light that has passed through a sample relative to a reference (this can be air).

- To make 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). The 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 standards of known concentration.

The procedure is as follows:

1. Press 4 to select Absorbance Concentration mode.
   The Absorbance Concentration – Method Settings screen is displayed.

   **Absorbance Concentration - Method Settings**

   - **Wavelength**: 260 nm
   - **Mode**: Absorbance

2. Set the **Wavelength** by using the keypad numbers or left and right arrows, and then press the down arrow.

3. Select the **Mode** using the left and right arrows.
   The options are **Absorbance**, **Factor** or **Standard**.
   Absorbance mode simply measures the absorbance. Factor mode measures the absorbance and then calculates the concentration using a known factor. Standard mode enables you to determine the factor by measuring a solution of known concentration, and then to calculate the concentration.
4. If you selected **Absorbance**, go to Step 7.

   OR

   If you selected **Factor**, enter the Factor using the keypad numbers. The available range is from 0.001 to 9999.

   OR

   If you selected **Standard**, enter the Concentration using the keypad numbers. The available range is from 0.01 to 9999.

5. Enter the **Units**, and then press the down arrow.

   You can enter text up to 8 characters long using the keypad, or press Options to display the Units screen and access a list of pre-defined units.

   ![Units](image)

   In the Units screen, use the left and right arrows to select from the available options. The options are **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.

   The Units screen also enables you to select the number of displayed decimal points (DP). The options are **Auto, 0, 1 and 2**.

   **NOTE:** The result will always be fixed to 5 significant figures, regardless of how many decimal points are selected (so 98768.2 is displayed as 98768, even with 1 decimal point selected).

   Press **OK** to save your options and return to the Absorbance Concentration – Method Settings screen.

   You can still edit the units.
6. Press OK to start measurements. The Absorbance Concentration results screen is displayed. The results screen for Factor mode is:

![Absorbance Concentration Table]

```
<table>
<thead>
<tr>
<th>Wavelength</th>
<th>Sample</th>
</tr>
</thead>
<tbody>
<tr>
<td>260 nm</td>
<td></td>
</tr>
<tr>
<td>Absorbance</td>
<td>Concentration</td>
</tr>
<tr>
<td>Factor</td>
<td>Units</td>
</tr>
<tr>
<td>1,000</td>
<td></td>
</tr>
</tbody>
</table>
```

7. Insert the reference sample and press OK. This reference measurement will be used for all subsequent samples until repeated.

8. For Absorbance and Factor mode measurements, insert the sample and press OK, and then go to Step 11. The absorbance or concentration of the sample is displayed.

```
<table>
<thead>
<tr>
<th>Wavelength</th>
<th>Sample</th>
</tr>
</thead>
<tbody>
<tr>
<td>260 nm</td>
<td>6</td>
</tr>
<tr>
<td>Absorbance</td>
<td>Concentration</td>
</tr>
<tr>
<td>0.178 Å</td>
<td>0.178</td>
</tr>
<tr>
<td>Factor</td>
<td>Units</td>
</tr>
<tr>
<td>1,000</td>
<td>μg/ml</td>
</tr>
</tbody>
</table>
```

OR

For Standard measurements, insert the standard and press OK.

```
<table>
<thead>
<tr>
<th>Wavelength</th>
<th>Sample</th>
</tr>
</thead>
<tbody>
<tr>
<td>260 nm</td>
<td>6</td>
</tr>
<tr>
<td>Absorbance</td>
<td>Concentration</td>
</tr>
<tr>
<td>0.178 Å</td>
<td>0.178</td>
</tr>
<tr>
<td>Factor</td>
<td>Units</td>
</tr>
<tr>
<td>1,000</td>
<td>μg/ml</td>
</tr>
</tbody>
</table>
```
The Run Standard screen is displayed.

9. Press Run to run the standard.
The Factor is calculated and displayed.

10. Insert your first sample and press .
The concentration of the sample is displayed.

11. Repeat Step 10 for each sample.
Press Options to display the available options, which you can select using the keypad numbers:

<table>
<thead>
<tr>
<th></th>
<th>Method Settings</th>
<th>Returns to the Method Settings screen.</th>
</tr>
</thead>
<tbody>
<tr>
<td>2</td>
<td>Print</td>
<td>Prints using the printer selected in the Utilities folder.</td>
</tr>
<tr>
<td>4</td>
<td>Run Standard</td>
<td>Returns to the Run Standard screen.</td>
</tr>
<tr>
<td>7</td>
<td>Sample Number</td>
<td>Adds a prefix to the sample number and resets the incrementing number to the desired value.</td>
</tr>
<tr>
<td>8</td>
<td>Save Method</td>
<td>Use the left and right arrows to select the folder you want to store the method in (Favorites/Methods 1–9/SD Memory Card), then press the down arrow and enter a name for the method. Press <strong>Save</strong> to save the method.</td>
</tr>
<tr>
<td>9</td>
<td>Auto-Print</td>
<td>Toggles Auto-Print on and off.</td>
</tr>
</tbody>
</table>

Press or , or wait 20 seconds to exit the method options.

Press to return to the home page.
**Bacterial Cell Culture Measurement (OD 600)**

Bacterial cell cultures are routinely grown until the absorbance at 600 nm (known as OD 600) reaches approximately 0.4 A before induction or harvesting. A linear relationship exists between the cell number (or density) and OD 600 up to approximately 0.6 A.

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 normalized 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 = $8 \times 10^8$ cells/ml for E. Coli.

Your Lambda Bio/Bio+ 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, but can be altered.

The use of 10 mm pathlength disposable cells is recommended for optical density measurements of cell culture solutions. Glycerol should be added to the sample to prevent the suspension settling too quickly and giving an OD that changes with time.

The procedure is as follows:

1. Press 2 to open the Life Science folder (Lambda Bio+ only).
2. If the instrument is a Lambda Bio, press 5 to select the OD 600 mode.

   OR

   If the instrument is a Lambda Bio+, press 3 to select the OD 600 mode.
The OD 600 – Method Settings screen is displayed.

3. Set the **Wavelength** by using the keypad numbers or left and right arrows, and then press the down arrow.
   The default value is 600 nm.

4. Enter the **Correction** factor to compensate for different optical configurations between this and other instruments, and then press the down arrow.

5. Select the **Units**.
   The options are **OD** or **cells/ml**.

6. If you selected **cells/ml**, enter the **Factor** used (0.000–9999) and the **Multiplier** (× 1000 or × 1000,000).

7. Press **OK** to start measurements.
   The OD 600 results screen is displayed.
   The results screen for **cells/ml** units is:

8. Insert the reference sample and press **OK**.
   This reference measurement will be used for all subsequent samples until repeated.
9. Insert your first sample and press \[\text{Play} \].
The wavelength, absorbance and OD 600 or cells/ml value are displayed.

![DD 600 Table]

10. Repeat Step 9 for each sample.

- Press \[\text{View} \] to display the available Options, which you can select using the keypad numbers:

<p>| | | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Method Settings</td>
<td>Returns to the Method Settings screen.</td>
</tr>
<tr>
<td>2</td>
<td>Print</td>
<td>Prints using the printer selected in the Utilities folder.</td>
</tr>
<tr>
<td>7</td>
<td>Sample Number</td>
<td>Adds a prefix to the sample number and resets the incrementing number to the desired value.</td>
</tr>
<tr>
<td>8</td>
<td>Save Method</td>
<td>Use the left and right arrows to select the folder you want to store the method in (Favorites/Methods 1–9/SD Memory Card), then press the down arrow and enter a name for the method. Press [\text{Save} ] to save the method.</td>
</tr>
<tr>
<td>9</td>
<td>Auto-Print</td>
<td>Toggles Auto-Print on and off.</td>
</tr>
</tbody>
</table>

- Press \[\text{Play} \] or \[\text{Stop} \], or wait 20 seconds to exit the method options.

- Press \[\text{Home} \] to return to the home page.
Accessories
Supplies, accessories, and replacement parts can be ordered directly from PerkinElmer. See the PerkinElmer website at http://www.perkinelmer.com for more information.

<table>
<thead>
<tr>
<th>Part Number</th>
<th>Accessory/Consumable</th>
</tr>
</thead>
<tbody>
<tr>
<td>L7110230</td>
<td>Lambda Bio/XLS Printer Module</td>
</tr>
<tr>
<td>L7110231</td>
<td>Lambda Bio/XLS Print Utility and Cable</td>
</tr>
<tr>
<td>L7110232</td>
<td>Lambda Bio/XLS Spare Printer Paper (20 Rolls)</td>
</tr>
<tr>
<td>L7110233</td>
<td>Lambda Bio/XLS Bluetooth Accessory</td>
</tr>
</tbody>
</table>

A range of cells and microcells are also available from PerkinElmer that are suitable for use with the Lambda Bio/Bio+ instrument.
Printer Installation and Configuration

The Printer Accessory (L7110230) is an optional accessory that allows you to print your data as you run your samples, directly from your instrument.

Printer installation

1. Turn off the line power supply and disconnect the power cable.

2. Turn the instrument over and remove the two cap head screws using the 3 mm hexagonal wrench provided.

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

4. Invert the instrument and replace the cap head screws.
5. Plug the accessory cable into the printer.

6. Lower the printer onto the locating bosses and push down firmly.

7. Reconnect the power cable.

**Printer configuration**

1. Switch the instrument on and then open the Utilities folder.

2. Press 3 to open the Printer folder.

3. Select **Built-in** as the **Printer** option using the arrow keys.

4. Press **OK** to save the settings.
**Loading or 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.
   Sometimes it helps if the platen lock is released.

4. Replace the cover.
Bluetooth Accessory Installation

1. Remove the power cable from the instrument.

2. Turn the instrument over and remove the two cap head screws using the 3 mm hexagonal wrench provided.

3. Turn the instrument back over and lift the accessory cover vertically upwards to remove it.

4. Remove the tie-wrap from the cable.
5. Plug the accessory cable into the Bluetooth module.

6. Plug the two lugs on the Bluetooth module into the innermost slots in the base of the case.

7. Lower the accessory cover vertically downwards onto the instrument, engaging the PCB in the innermost slots in the accessory cover.

8. Invert the instrument and replace the two cap head screws.

9. Connect the power cable.
10. Switch the instrument on and open the Utilities folder.

11. Press 3 to open the Printer folder.

12. Select **Computer (Bluetooth)** as the **Printer** option using the arrow keys.

13. Press **OK** to save the settings.
**Lambda Bio/XLS Print Utility**

There are two software applications comprising the Lambda Bio/XLS Print Utility.

The Lambda Bio/XLS Report Utility is an application running separately under Windows XP that enables you to connect via a USB cable to a PC onto which the software has been installed. You can connect to several instruments simultaneously. Once your data is on the PC it can be printed directly to any printer that is connected to that PC or saved. The Report Utility can save data as an Enhanced Metafile (.emf) graphics file, a comma delimited (.csv) data file, a tab delimited (.txt) data file or as an Excel file, or in print utility (.pvc) format for viewing using the Lambda Bio/XLS Report Viewer.

**NOTE:** An internal printer is also available for the instrument. This is either supplied pre-installed in the instrument or as an optional accessory (L7110230).

If you have this option, please see the *Lambda Bio/XLS Print Utility User’s Guide* (L6050015) on the *Lambda Bio/XLS User Manuals CD* (L6050018) for more information.
Maintenance
General Maintenance

Unauthorized Adjustments and Servicing

Do not attempt to make adjustments, replacements or repairs to this instrument. There are no user-serviceable parts in this instrument. If you have any problems, access the Troubleshooting Guide on the PerkinElmer website and work through the process there:

http://www.perkinelmer.com/LambdaBioXLSSupport

If you do not have access the Troubleshooting Guide, or have any further problems, contact Customer Care (see Appendix 2: Customer Care on page 121 for more information).

Cleaning the instrument

External Cleaning

Switch off the instrument and disconnect the power cord before cleaning your instrument.

Clean the outside of the instrument using a damp cloth. A mild liquid detergent may be used, if necessary. Always test an inconspicuous area of the instrument before you clean the entire instrument.

Clean all spilled materials from the affected area immediately and wipe it dry with lint-free paper or cloth.

Removing the cell holder for cleaning

To remove the sample cell holder for cleaning:

1. Loosen the thumbscrews on the sample-holder cover on the base of the instrument by turning them anticlockwise.
   The thumbscrews remain attached to the plate.
2. Lower the sample holder out of the instrument.

Figure 14 Position of cell holder thumbscrews
**Storage and Shipping**

This unit should be stored or shipped in its original packaging, which should be kept for this purpose. The unit should be kept in its packaging in a dry, non condensing environment, free from dust or dirt, in the range −10 to 50 °C.

Should you need to return your instrument to PerkinElmer, a decontamination certificate is required before the instrument is shipped. Decontamination certificates can be obtained from PerkinElmer. The Troubleshooting Guide, which will help you work through the returns process, can be accessed at:

http://www.perkinelmer.com/LambdaBioXLSSupport

If you do not have access to the Troubleshooting Guide, you can also contact Customer Care (see Appendix 2: Customer Care on page 121 for more information).

It is the responsibility of the user to carry out appropriate risk assessments and, if applicable, decontamination procedures before returning the instrument.
Appendices
## Appendix 1:Specifications

Specifications are measured after the instrument has warmed up at a constant ambient temperature and are typical of a production unit.

<table>
<thead>
<tr>
<th>Specification</th>
<th>Lambda Bio</th>
<th>Lambda Bio+</th>
</tr>
</thead>
<tbody>
<tr>
<td>Wavelength range</td>
<td>190–1100 nm</td>
<td></td>
</tr>
<tr>
<td>Wavelength scanning range</td>
<td>200–950 nm</td>
<td></td>
</tr>
<tr>
<td>Monochromator</td>
<td>Flat grating</td>
<td></td>
</tr>
<tr>
<td>Wavelength calibration</td>
<td>Automatic when the instrument is switched on</td>
<td></td>
</tr>
<tr>
<td>Spectral bandwidth</td>
<td>5 nm</td>
<td>3 nm</td>
</tr>
<tr>
<td>Wavelength accuracy</td>
<td>±2 nm</td>
<td></td>
</tr>
<tr>
<td>Wavelength reproducibility</td>
<td>±1 nm</td>
<td></td>
</tr>
<tr>
<td>Light sources</td>
<td>Pulsed xenon lamp</td>
<td>1024 element CCD array</td>
</tr>
<tr>
<td>Detector</td>
<td>1024 element CCD array</td>
<td></td>
</tr>
<tr>
<td>Absorbance range</td>
<td>−0.300 to 2.500 A (0 to 199%T)</td>
<td></td>
</tr>
<tr>
<td>Photometric linearity</td>
<td>±0.005 A or 1% of the reading, whichever is the greater at 546 nm</td>
<td></td>
</tr>
<tr>
<td>Photometric reproducibility</td>
<td>±0.003 A (0–0.5 A), ±0.007 A (0.5–1.0 A)</td>
<td></td>
</tr>
<tr>
<td>Stray light</td>
<td>&lt;1% at 220 nm and 340 nm using NaNO₂</td>
<td>&lt;0.5% at 220 nm and 340 nm using NaNO₂</td>
</tr>
<tr>
<td>Zero stability</td>
<td>±0.01 A/hour after 20 minutes warm up at 340 nm</td>
<td></td>
</tr>
<tr>
<td>Noise</td>
<td>0.005 peak-to-peak 0.002 rms</td>
<td></td>
</tr>
<tr>
<td>Digital output</td>
<td>USB port standard, Bluetooth option</td>
<td></td>
</tr>
<tr>
<td>Dimensions</td>
<td>340 × 310 × 170 mm (340 × 420 × 170 mm with printer attached)</td>
<td></td>
</tr>
<tr>
<td>Weight</td>
<td>Approximately 4.5 kg</td>
<td></td>
</tr>
<tr>
<td>Power input</td>
<td>100–250 V, 50/60 Hz, Max 30 VA</td>
<td></td>
</tr>
</tbody>
</table>
## Appendix 2: Customer Care Contacts

**NOTE:** If you experience any problems with your instrument, please refer to the Troubleshooting Guide at http://www.perkinelmer.com/LambdaBioXLSSupport before contacting Customer Care.

<table>
<thead>
<tr>
<th>Customer Care</th>
<th>Phone Number</th>
<th>Location</th>
</tr>
</thead>
<tbody>
<tr>
<td>Customer Care USA</td>
<td>1 00 762 4000</td>
<td>(In the USA)</td>
</tr>
<tr>
<td></td>
<td>(+1) 203 925 4602</td>
<td>(Outside USA)</td>
</tr>
<tr>
<td>Customer Care EU</td>
<td>0800 40 858</td>
<td>(Belgium)</td>
</tr>
<tr>
<td></td>
<td>0805 111 333</td>
<td>(France)</td>
</tr>
<tr>
<td></td>
<td>0800 0 00 66 79</td>
<td>(Germany)</td>
</tr>
<tr>
<td></td>
<td>0800 90 66 42</td>
<td>(Italy)</td>
</tr>
<tr>
<td></td>
<td>800 099 164</td>
<td>(Spain)</td>
</tr>
<tr>
<td></td>
<td>0800 896 046</td>
<td>(UK)</td>
</tr>
<tr>
<td>Customer Care Brazil</td>
<td>11 38 68 6200</td>
<td></td>
</tr>
<tr>
<td>Customer Care Canada</td>
<td>800 561 4646</td>
<td></td>
</tr>
<tr>
<td>Customer Care China</td>
<td>10 5820 8166</td>
<td></td>
</tr>
<tr>
<td>Customer Care India</td>
<td>022 6760 1700</td>
<td></td>
</tr>
<tr>
<td>Customer Care Japan</td>
<td>45 339 5889</td>
<td></td>
</tr>
<tr>
<td>Customer Care Singapore</td>
<td>67799 539</td>
<td></td>
</tr>
</tbody>
</table>
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