GE Healthcare

Getting Started with
UNICORN 5.1

UNICORN for ÄKTAoligopilot

UNICORN™

Table of Contents

1 Introducing UNICORN

About this chapter

This chapter contains:

- An overview of the UNICORN™ system and general information that you need before you can start.
- Information about the user documentation for UNICORN and how to use it.
- A Quick Start Guide that can be used as a shortcut for experienced users that want to start right away.

In this chapter

This chapter contains the following sections

Topic	See
About UNICORN	1.1
About this manual	1.2
About the UNICORN user documentation	1.3
Quick Start Guide	1.4

1.1 About UNICORN

Introduction

This section is a general overview of the UNICORN system.

What is UNICORN?

UNICORN is a complete package for control and supervision of synthesis and chromatography systems. It consists of control software and a controller card for interfacing the controlling PC to the liquid handling module.

Operating environment

UNICORN runs on a PC under Microsoft® Windows® 2000 or Microsoft Windows XP. It is designed to run under English keyboard settings.

Windows functions

Most Windows functions are also available in UNICORN, including:

- cut and paste
- right-click short-cut menus

Note: Drag and drop is not available. File and folder handling in UNICORN also differs from the general Windows file manager standard.

Compatible chromatography systems

UNICORN can be used with a number of systems including

- ÄKTA™ design systems
- OligoProcess™ systems
- BioProcess™ systems

Note: All examples in this guide are based on an ÄKTA oligopilot™ 100 system that operates with the AKOPc100 strategy. If you use another system you may find that the descriptions and instructions do not match your system on every point. In that case you also need to refer to the user documentation for your specific system.

System networks

UNICORN can be installed on a stand-alone computer to control only a single, locally attached system. However, a stand-alone computer can control up to a maximum of four separate systems. In a network installation each computer workstation can operate many systems regardless if they are locally connected or not. Each system can only be operated by one workstation at a time, but several may view the output data.

Software modules

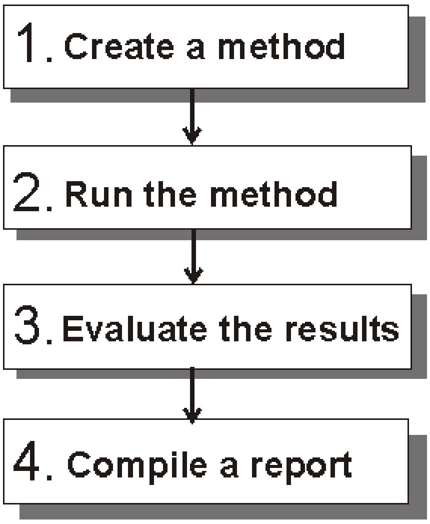
The UNICORN control software consists of four integrated modules:

Module	Function
UNICORN Manager	File handling and administration, e.g. definition of systems and user profiles etc.
Method Editor	To create and edit methods for pre-programmed control of oligonucleotide synthesis systems.
System Control	To control and monitor the synthesis processes online, through method-based or manual control.
Evaluation	To evaluate and present stored results from synthesis processes.

Note: All modules are active when the program is operating, and are not closed when they are minimized. A minimized **System Control** unit may control a process.

Work flow

The work flow in UNICORN can be divided into four distinct stages. Each stage is described in separate chapters in this manual. The flow chart below shows the work flow stages.



Help functions

An online help utility is included in the UNICORN software. The table below describes how to access the help utility.

If you want to access...	Then...
the general help utility.	open the **Help** menu in any of the software modules.
context-specific help topics.	• click the **Help** button in the dialog box. *or* • press the **F1** key on your keyboard.

Security

The table below describes the main security functions in UNICORN:

Feature	Function
Access Security	Only authorized users can access UNICORN. Each user is assigned an access level, which defines the functions that the user is permitted to use.
Connection Security	A running system can only be controlled from one connection. Systems may be locked with a password to prevent other, un-authorized users from changing parameters.

Feature	**Function**
Data Security	Result files from an ongoing synthesis run can be saved automatically at preset intervals to minimize data loss if the system fails. The results are saved locally if the network communication fails.
Electronic Signatures	Method and result files can be signed electronically for enhanced security and accountability.

1.2 About this manual

Introduction

This section provides a general description of the manual, the contents and the pre-requisites for the examples and instructions that are presented in the Getting Started guide.

The purpose of Getting Started

The purpose of Getting Started is to present a quick and easy guide to the system for a user with limited or no experience of UNICORN. The work flow is presented in the form of practical instructions for how to operate a model system. These instructions form a basic framework that the reader can expand on by reading selected parts in the other manuals.

The model system

UNICORN software can be used in numerous possible system variations. For practical reasons the user documentation is based on a model system that consists of:

- **ÄKTAoligopilot 100**
- Strategy **AKOPc100**

Note: If you use another system you may find that the descriptions and instructions do not match your system on every point. In that case you also need to refer to the user documentation for your specific system.

Refer to other manuals

The examples and instructions that are presented in this manual are deliberately limited to a minimum to reduce the number of pages that you will need to read. In almost all cases you will find additional information about each topic in the User Reference Manual.

Document structure

The manual is divided into chapters. Each chapter starts with a brief overview that presents the contents and the headings for the sections that the chapter contains. The section begins with an introduction that summarizes the content.

A section is divided into blocks of information with separating lines. The blocks are identified by labels in the margins. This makes it easier for you to quickly scan a page to find the exact topic you are looking for.

The manual contents

Getting Started contains nine chapters that can be sorted logically into 4 major topics:

Topic	Chapter
Background information.	1. Introducing UNICORN 2. UNICORN concepts

Topic	Chapter
How to prepare the system.	3. How to start your system 4. How to create a method
How to run the system.	5. How to perform method runs
How to use the results.	6. How to view results 7. How to print chromatograms 8. How to create and print reports

Typographical representations

Menu commands, field names and other text items from the software are quoted exactly as they appear on the screen, in a bold typeface:

- *Example*: **Run Setup**

Search paths are shown in a bold typeface with a separating colon between each level:

- *Example*: **View:Windows:Customise** (i.e. the menu command **Customise** in the sub-menu **Windows** from the **View**-menu).

Text entries that UNICORN generates or that the user must type are represented by a monotype typeface:

- *Example*: `Connection change`

Pre-requisites

The following pre-requisites must be fulfilled before you can use this manual the way it was intended:

- You need to have a general understanding of how your PC and Windows works. In most cases universal computer functions will not be explained.
- UNICORN must be installed and configured correctly on your computer.
- You need to understand the concepts of oligonucleotide synthesis. Terminology and functionalities will be explained only when they differ from normal practise.
- Before you try to operate a synthesis system based on the instructions in this manual you need to study and understand the safety information that is part of the system documentation.

1.3 About the UNICORN user documentation

Introduction

The user documentation for UNICORN is divided into three separate manuals. This section is an overview of the contents and the relationship between the manuals.

The manuals

The three manuals are:

- Getting Started with UNICORN for oligonucleotide synthesis (See section **1.2 About this manual** on page 8)
- UNICORN User Reference Manual for oligonucleotide synthesis
- UNICORN Administration and Technical Manual

User info about Getting Started

The questions and answers in the table below describe the features of the Getting Started manual.

Question	Answer
Who should read Getting Started?	Users that are new to the UNICORN system and with limited experience from other systems for oligonucleotide synthesis.
What do I need before I start?	A basic knowledge of PC and Windows functions and an understanding of the concepts and terminology of oligonucleotide synthesis.
What are the contents of Getting Started?	Basic descriptions of UNICORN and its use, based on a model system.
How should I use Getting Started?	Read in front of your computer and test the instructions at the same time.
When do I need to refer to the User Reference Manual?	When you need: • more in-depth information, • alternative ways to perform a task.

Question	Answer
When do I need to refer to the Administration and Technical Manual?	When you need: • general information about the network functions of UNICORN, • to set up and configure a UNICORN workstation in a network, • to trouble-shoot a workstation with network problems.

User info about the User Reference Manual

The questions and answers in the table below describes the features of the User Reference Manual.

Question	Answer
Who should read the User Reference Manual?	• Users that are experienced with previous UNICORN system versions. • Users with vast experience from other systems for oligonucleotide synthesis.
What do I need before I start?	• Knowledge of PC and Windows functions. • An understanding of the concepts and terminology of oligonucleotide synthesis. • Preferably some previous experience with UNICORN.
What are the contents of the User Reference Manual?	• Detailed descriptions of UNICORN. • Instructions on how to use the system, with suggested alternatives. *Note:* Most instructions are based on a model system.
How should I use the User Reference Manual?	Depending on your previous experience you can either read • whole chapters from the beginning to the end • only selected sections for reference.

Question	Answer
When do I need to refer to Getting Started?	When you need brief, step-by-step instructions for a selected task.
When do I need to refer to the Administration and Technical Manual?	When you need • general information about the network functions of UNICORN. • to set up and configure a UNICORN workstation in a network. • to trouble-shoot a workstation with network problems.

User info about The Administration and Technical Manual

The questions and answers in the table below describes the features of the Administration and Technical Manual.

Question	Answer
Who should read the Administration and Technical Manual?	System administrators.
What do I need before I start?	• General knowledge of UNICORN. • Knowledge of PC, Windows and general network administration functions. • An understanding of the concepts and terminology of oligonucleotide synthesis.
What are the contents of the Administration and Technical Manual?	Detailed instructions of • how to install and maintain UNICORN in a network environment. • how to create and administrate user profiles. *Note:* Most instructions are based on a model system.

Question	**Answer**
How should I use the Administration and Technical Manual?	• If you are an experienced administrator of previous UNICORN versions you can read selected sections for reference. • If this is your first experience of UNICORN administration we recommend that you study the manual in detail.
When do I need to refer to Getting Started?	When you need brief, step-by-step instructions for a selected task.
When do I need to refer to the User Reference Manual?	When you need more information about the basic functions of UNICORN.

1.4 Quick Start Guide

Introduction

This guide is intended for users who are fully familiar with the safety precautions and operating instructions that are described in all manuals, i.e. experienced users of previous versions of UNICORN. The instructions applies to an ÄKTA oligopilot 100 and assume that all installations were made according to the instructions.

Quick Start instructions

The table below describes how to create a Synthesis method, run the Synthesis and generate a printed report. The instruction is based on an **Instant Run**.

Step	Action
1	Click the **Instant run** icon in the **UNICORN Manager**. *Result*: The **InstantRun** dialog box opens.
2	• Select a system (if necessary). • Select a template. • Click the **Run** button. Result: The **Start Protocol** opens in the **System Control** module with the **Variables** page displayed.
3	• Verify that the **Weight_of_Support** value is correct. • Verify that the **Loading_of_Support** value is correct. • Verify and change all other values as required. • Click **Next** to proceed through several pages.
4	• Type appropriate values on the **Questions** page. *Note*: You must select **type of support** and a **Column**. • Click **Next** to proceed through several pages.
5	Select **Print_SyntData_AKTA** in the **Evaluation procedures** page for a printed report after the run.
6	Click the **Start** button on the last page. *Result*: The run starts.

Note: The system can be set up so that you must confirm and close two message dialog boxes before the run starts.

2 UNICORN concepts

Introduction

This chapter contains definitions and descriptions of some of the specific concepts that are presented in this manual and in the other UNICORN manuals. General concepts and common oligonucleotide synthesis terminology are not explained here.

In this chapter

This chapter contains the following section

Topic	See
Concept definitions	2.1

2.1 Concept definitions

Introduction

- This section contains explanations and definitions of a number of UNICORN concepts that are used in this manual.
- The concepts are sorted in alphabetical order.

Note: The section also lists some concepts that are described only in the User Reference Manual. These concepts are included for reference since they may be found in menus and dialogs that you will use while working with this manual.

Alarms

Systems settings or method instructions specify acceptable limits for monitor signals during a synthesis run. An **Alarm** dialog box will be displayed on the screen and an optional alarm can sound if a specified limit is exceeded. The system will be paused.

Note: Refer to the User Reference Manual for information about **Alarms**. The topic is not covered in this manual.

Batch run

You can perform a **Batch run** of a number of result files in the **Evaluation** module. The files do not have to be open and the run operates in the background. The procedure is useful if you want to print a number of results with the same settings, or if you want to perform integration with the same parameter settings on many results.

Note: Refer to the User Reference Manual for information about **Batch runs**. The topic is not covered in this manual.

Chromatogram

A chromatogram is a collection of data represented by a number of curves that have been created during a synthesis run, e.g. UV and conductivity etc. The original raw data curves cannot be deleted or modified. They can be used as a basis for evaluation procedures and subsequent creation of new curves.

A chromatogram can also contain curves that have been created and saved during an evaluation session.

Curves

The monitor signals from the synthesis run are displayed graphically as curves.

Method

The program instructions for a synthesis run are defined in a **Method**. A **Method** is normally divided into blocks that represent steps in the synthesis process. Each block consists of a series of instructions that request specific operations in the system.

MethodQueue

MethodQueues are used to link several methods (different columns) together, on the same or on different systems.

Example: A **MethodQueue** can be set up to conduct a CIP study of a number of columns, through a controlled series of scouting runs.

Note: A method can be placed in a **MethodQueue** if the system is busy when the operator wants to run the method. Refer to the User Reference Manual for information about **MethodQueues**. The topic is not covered in this manual.

Result files

UNICORN creates **Result files** when a method is run. The **Result files** contain:

- Run data from the monitors in the oligonucleotide synthesis system.

Example: UV absorbance, flow rate, conductivity etc.

- Documentation from the run.

Example: Logbook entries, settings, text method etc.

- Saved results from evaluations of the run data.

Example: Peak integrations, synthesis data etc.

Strategy

Part of the UNICORN software is specific for the system that it is set up to operate. The system specific part is usually referred to as the **Strategy**. The **Strategy** defines available method and manual instructions, system settings, run data, curves and method templates.

Note: The examples in this guide are generally based on the **AKOPc100** strategy.

Synthesis Data

Synthesis Data is a spreadsheet that can be displayed over the **System Control** module. It contains online integrated trityl data. The row corresponding to the cycle that is in progress is marked.

Template

Templates are basic methods that can be used as a starting point for developing customized methods and sequences. The method variables in a suitable **Template** is adjusted to create a method for another application.

Variable	Values at breakpoints in the **Method** and instruction parameters may be defined as **Variables**. **Variables** makes it easy to adapt a method to a particular synthesis run. • A framework **Method** with default parameters can be changed to create variants.
Warnings	Systems settings or method instructions specify acceptable limits for monitor signals during a synthesis run. A **Warning** dialog box may be displayed on the screen if a specified limit is exceeded. The system will still continue to run after a **Warning**. *Note*: Refer to the User Reference Manual for information about **Warnings**. The topic is not covered in this manual.

3 How to start your system

Introduction

The first step when you begin your work with UNICORN is to start the system. This chapter describes how to start the program and log on as a user.

In this chapter

This chapter contains the following section

Topic	See
How to start UNICORN and log on	3.1

3.1 How to start UNICORN and log on

Introduction

This section describes how to start the UNICORN program and how to log on as a user.

Username and password

The system administrator creates and defines users and may also create your initial password. (You may change the initial password to another later). The program can also be set up so you can logon without a password.

How to start the program

Note: If UNICORN is already started by a previous user, proceed to "How to log on".

There are two ways to start the program:

If you start with...	then...
a UNICORN icon on your desktop,	double-click the icon. 
the Windows Start menu,	locate the program under **Programs:Unicorn** and click **UNICORN**.

The Logon dialog box

This is an illustration of the **UNICORN Logon** dialog box:

Note: The **Logon** dialog has a **Password** text box only if a password is required.

How to log on

The table below describes how to log on to UNICORN.

Step	Action
1	• Select **Tools:Logon**. *or* • Click the **Logon/Logoff** icon in the **UNICORN Manager**.
2	Select your username in the list.
3	Type your password (optional).
4	Click **OK**.

The four program windows

The program has four windows or modules. When you start the program and log on you work in the **UNICORN Manager**. UNICORN also automatically opens the **Method Editor**, the **System Control** and the **Evaluation** modules. These modules are minimized until you activate them.

Log off after you are finished

Always log off when you leave the computer to prevent others from accidentally changing or deleting your files, or disturbing your synthesis runs. There are two ways to log off:

- Select **Tools:Logoff**.

or

- Click the **Logon/Logoff** icon.

4 How to create a method

Introduction

Synthesis runs are programmed as **Methods** in UNICORN. Before you can proceed with a chromatography run you need either to use an existing method or create a new method. This chapter describes two different ways to create new methods.

In this chapter

This chapter contains the following sections

Topic	See
How to use method templates	4.1
How to use text instructions	4.2

4.1 *How to use method templates*

Introduction

This section describes how to create methods based on an existing template.

Note: The synthesis template methods are provided in two different versions, one for **Recirculation amidite coupling technique** and one for **FlowThrough amidite coupling technique**. Recirculation is the recommended technique.

Open the New Method dialog

Open the **New Method** dialog in the **UNICORN Manager**.

- Select **File:New:Method.**

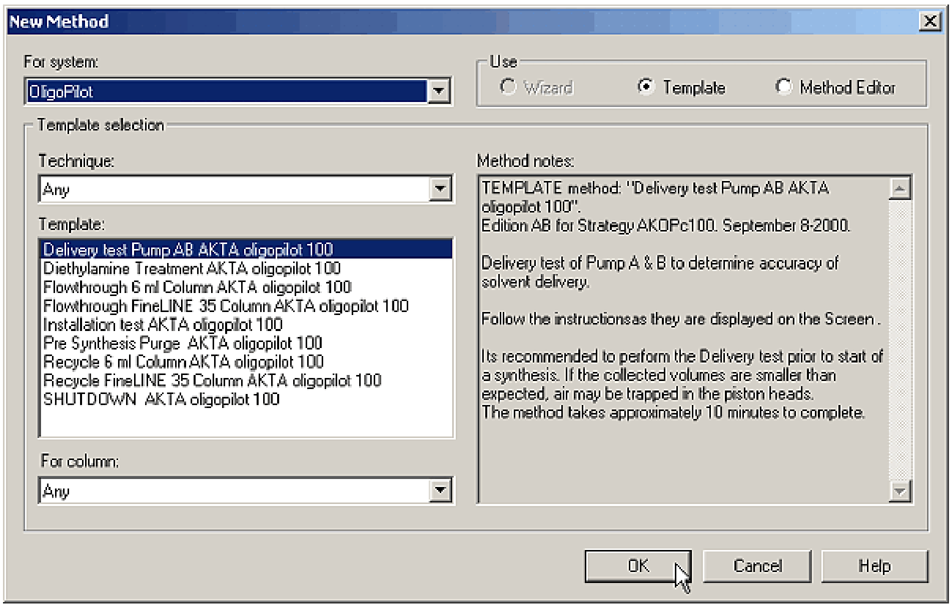
  or

- Click the **New Method** icon.

(You can also select **File:New** in the **Method Editor** module.)

The New Method dialog box

The illustration below shows the **New Method** dialog box:



For system: OligoPilot

Use: Template

Technique: Any

Template:

- Delivery test Pump AB AKTA oligopilot 100
- Diethylamine Treatment AKTA oligopilot 100
- Flowthrough 6 ml Column AKTA oligopilot 100
- Flowthrough FineLINE 35 Column AKTA oligopilot 100
- Installation test AKTA oligopilot 100
- Pre Synthesis Purge AKTA oligopilot 100
- Recycle 6 ml Column AKTA oligopilot 100
- Recycle FineLINE 35 Column AKTA oligopilot 100
- SHUTDOWN AKTA oligopilot 100

For column: Any

Method notes:

TEMPLATE method: "Delivery test Pump AB AKTA oligopilot 100".
Edition AB for Strategy AKOPc100. September 8-2000.

Delivery test of Pump A & B to determine accuracy of solvent delivery.

Follow the instructionsas they are displayed on the Screen .

Its recommended to perform the Delivery test prior to start of a synthesis. If the collected volumes are smaller than expected, air may be trapped in the piston heads.
The method takes approximately 10 minutes to complete.

How to create a new method

The table below describes how to create a method in the **New Method** dialog box.

Step	Action
1	Select **Template** in the **Use** field.
2	Select the system you want to create the method for.

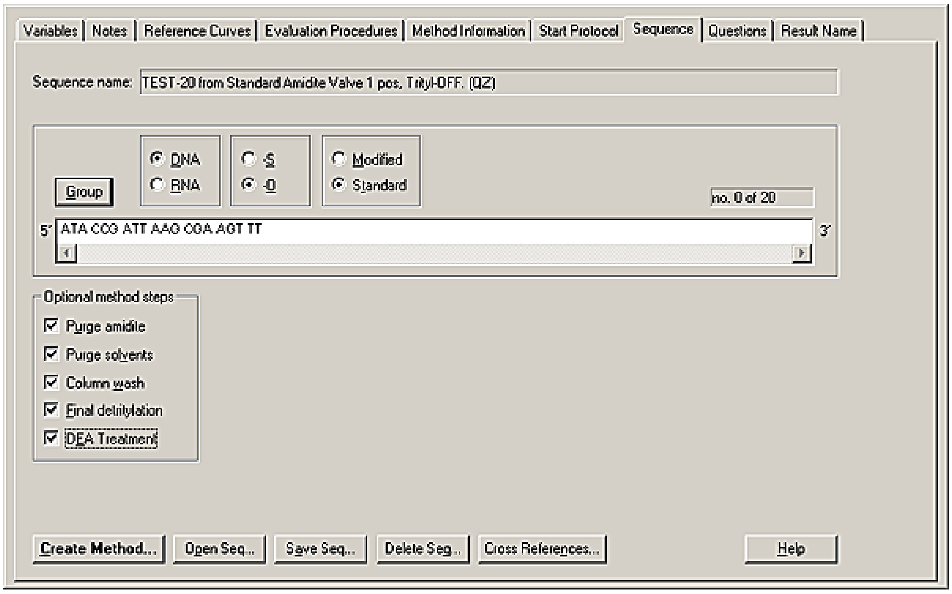
Step	Action
3	Select a template in the **Template** list.
4	Click **OK**. This opens the method template as an untitled method in the **Run Setup** in the **Method Editor** module.

Note: The **Technique** and **Column** droplists are not used in oligonucleotide applications. Both should be set to **Any**.

The Sequence tab

Click the **Sequence** tab in the **Run Setup**. The sequence name and actual sequence are displayed.

- All **Optional method steps** check boxes should be checked when making your first run.



Sequence name: TEST-20 from Standard Amidite Valve 1 pos, Trityl-OFF. (QZ)

● DNA ○ RNA

○ -S ● -O

○ Modified ● Standard

no. 0 of 20

5' ATA CCG ATT AAG CGA AGT TT 3'

Optional method steps

☑ Purge amidite

☑ Purge solvents

☑ Column wash

☑ Final detritylation

☑ DEA Treatment

How to change variables

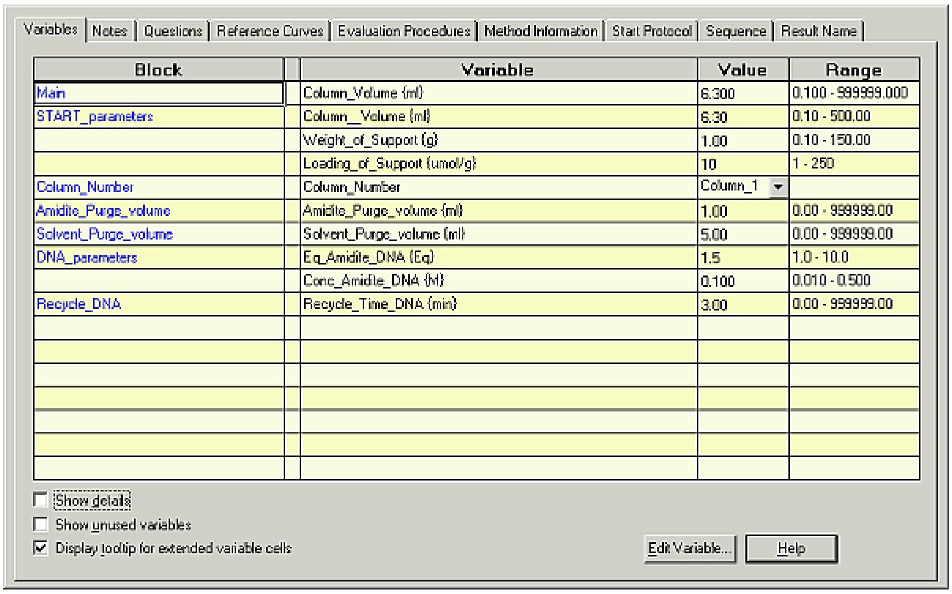
The method is represented by a number of blocks on the **Variables** tab. Each variable can be changed to a new value.

If the value is...	then...
a numerical value,	click the **Value** box and enter a new value.
OFF or a numerical value in blue,	• right-click the box to toggle between **OFF** and numerical values. • enter a new value.
in a box with a droplist arrow,	click the arrow and select a new value from the droplist.

The Variables tab

The illustration below shows the **Variables** tab.

- Verify that the **Weight_of_Support** and **Loading_of_Support** boxes are set correctly.
- Scroll down to the **Conc_Amidite_DNA** box and verify that it is set to the concentration of the amidites in the amidite bottles.



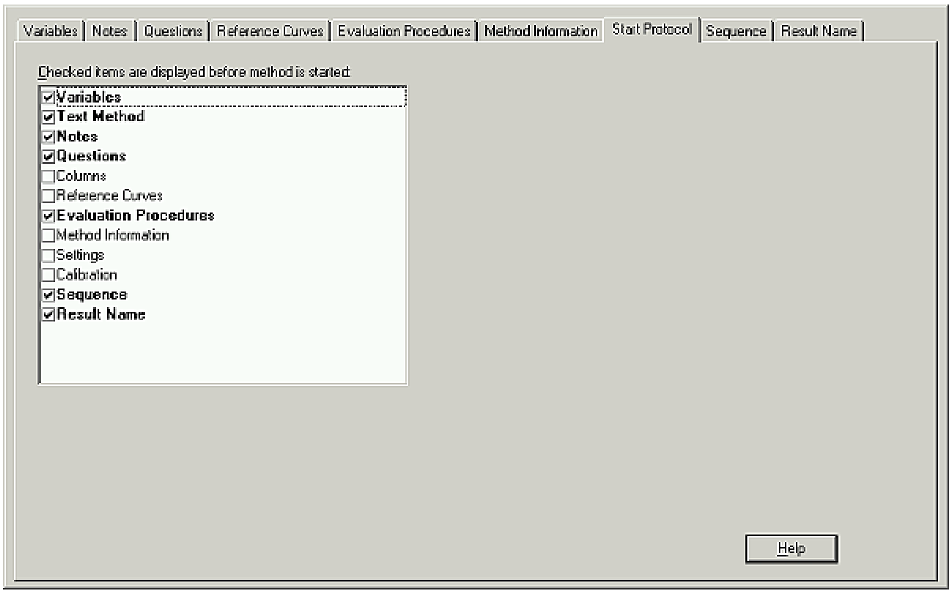
Block	Variable	Value	Range
Main	Column_Volume (ml)	6.300	0.100 - 999999.000
START_parameters	Column__Volume (ml)	6.30	0.10 - 500.00
	Weight_of_Support (g)	1.00	0.10 - 150.00
	Loading_of_Support (umol/g)	10	1 - 250
Column_Number	Column_Number	Column_1	
Amidite_Purge_volume	Amidite_Purge_volume (ml)	1.00	0.00 - 999999.00
Solvent_Purge_volume	Solvent_Purge_volume (ml)	5.00	0.00 - 999999.00
DNA_parameters	Eq_Amidite_DNA (Eq)	1.5	1.0 - 10.0
	Conc_Amidite_DNA (M)	0.100	0.010 - 0.500
Recycle_DNA	Recycle_Time_DNA (min)	3.00	0.00 - 999999.00

☐ Show details
☐ Show unused variables
☑ Display tooltip for extended variable cells

The Start Protocol

The **Start Protocol** tab shows the items that will be displayed as pages in the **Run Setup** sequence.

- Click the check boxes for the items that you want to select.



Checked items are displayed before method is started:

☑ **Variables**
☑ **Text Method**
☑ **Notes**
☑ **Questions**
☐ Columns
☐ Reference Curves
☑ **Evaluation Procedures**
☐ Method Information
☐ Settings
☐ Calibration
☑ **Sequence**
☑ **Result Name**

How to finalize and save your method

The table below describes how to finalize the creation of your method, and how to save it.

Step	Action
1	• Click the **Sequence** tab. • Click the **Create Method...** button. *Result*: The **Save As** dialog box opens.
2	• Type a name for the method. • If necessary, select the system the method is created for. • Click **OK**. *Result*: The method is saved and available in the **Methods** window in the **UNICORN Manager**. The method remains open in the **Method Editor** so you can continue editing if you wish.

4.2 How to use text instructions

Introduction

Sometimes you need more advanced editing facilities, which are available when you work directly in the **Text Instructions Editor** in the **Method Editor**. This section is a brief description of this process.

The Text Instructions Editor

You can use the **Text Instructions** in the **Method Editor** to build your method step by step. You can also use the editor to modify instructions in methods based on templates.

When do I use Text Instructions?

Use text instructions when you want to:

- change selected instructions in the method, e.g. the outlet valve position,
- add blocks or instructions, e.g. **Watch** instructions,
- change method instructions to adapt to non-standard system configurations,
- create new methods for applications not covered by the supplied templates.

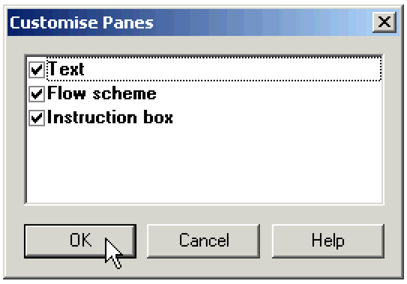
Valid instructions

The system strategy determines the available instructions. A method that is developed for one system may not be valid for another.

How to open the Editor

The table below describes how to open the **Text Instructions Editor**.

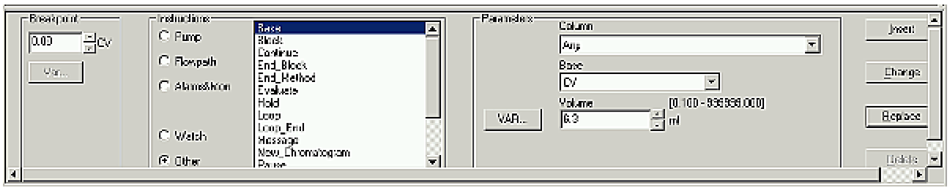
Step	Action
1	Select the **Method Editor** module.
2	Select **File:New**. *Result*: The **New Method** dialog opens.
3	• Select a system (if more than one is available) • Select **Method Editor** and click **OK**. *Result*: The Method Editor module opens in text edit mode.
4	Proceed with step 5 and 6 if the screen is blank.
5	Click the **Customise Panes** icon.

Step	Action
6	Select **Text** and **Instruction Box** and click **OK**.  Customise Panes ☑ Text ☑ Flow scheme ☑ Instruction box

How to enter Text Instructions

The text instructions are selected in the **Instruction box** in the lower part of the **Method Editor**. Applicable parameters can be edited for each selection. Use the buttons to **Insert**, **Change**, **Replace** or **Delete** the selected instructions. All text entries are shown in the **Text** pane.

The illustration below shows the **Instruction box**:



How to save your method

Before you can run your method you must save it.

- Select **File:Save**.

or

- Click the **Save** icon.

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5 How to perform method runs

Introduction

Once you have a defined synthesis in place you can perform a synthesis run. You can monitor its progress in the **System Control** module. This chapter describes how to perform the method run, the data display, how you can focus on the information you are interested in and make adjustments while the method run is in progress.

In this chapter

This chapter contains the following sections

5.1 *How to run your method*

Introduction

Follow the instructions in this section if you want to start a synthesis run based on the method you created and saved in the previous chapter. Also use this procedure if you want to run other methods.

Connect to the system

Before you can start a run, you must connect to the system. Open the **System Control** window and look at the **Connection** panel in the **Run Data** section. If you are not connected the panel will show the text **NO**. Once you are connected the text changes to **YES**. Refer to the User Reference Manual if your system is not connected.

Instruments: Ready
Connection: YES
Run Status: End

Prepare the system

After the system is connected it must be prepared. Verify that this already has been done or refer to your system documentation for the correct procedure.

How to start a method run

You initiate the synthesis run in a series of dialog boxes in the **Run Setup** in the **System Control** module. The **Start Protocol** for the method decides which pages you need to fill in. The steps in the table below is an example of a **Run Setup** sequence. When you are finished in one dialog box you click **Next** to proceed.

Step	Action
1	• Select the **File:Run** menu command *or* • click the **Run** toolbar icon. Run *Result*: The **Run Setup** opens.
2	In the **Variables** dialog box: • Verify that the value for **Weight_of_support** is equal to what was calculated when the column was packed. • Verify that the **Loading_of_support** value is appropriate.

Step	Action
3	• Proofread the sequence in the **Text method** dialog box. *Note*: The sequence cannot be modified at this time.
4	In the **Notes** dialog box some information can already be present. Click the **Start Notes** tab and add your own comments.
5	In the **Questions** dialog box some questions may be mandatory and must be answered before you can start.
6	In **Evaluation Procedures** you select the automated operations you want the system to perform after the synthesis run, e.g. a printed synthesis report.
7	The **Sequence** page displays the sequence and Optional method steps. This cannot be changed at this point Click **Next** to proceed to name your result file and define where it should be stored.

How to name the result file

The final step before starting is to name your result file and define where it should be stored. The default file name is defined in the **Result Name** page of the **Run Setup**. By default the result file name will either be the same name as the method, the date of the run or a pre-defined name. The name is followed by a three-digit sequence number starting with 001. You can change this name and select a new directory by clicking **Browse**.

You can also select to have the software add a unique identifier to the file name.

How to start the method run

- Click the **START** button in the **Result Name** dialog box.

The result depends on how UNICORN is configured:

- The synthesis run starts

or

- The synthesis run is set to **Pause** and a couple of message dialog boxes open.

If the system is set to **Pause**, continue with the following steps:

- Read the messages and confirm by clicking the **Close** buttons.
- Click the **Continue** icon.

Result: This will initiate the method run and you can follow its progress in the **System Control** module.

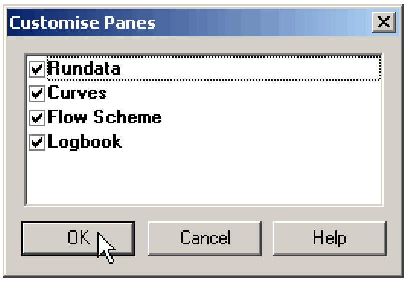
5.2 *The System Control module*

Introduction

All data on your synthesis run are displayed in the **System Control** module. You have a choice of four different panes that can be open one at a time or all at once in separate parts of the window.

How to select displays

The table below describes how to select the panes that are displayed in the **System Control** module.

Step	Action
1	• Select the **View:Panes** menu command. *or* • Click the **Customise Panes** icon.
2	Click the check boxes for the panes that you want to display.  Customise Panes ☑ Rundata ☑ Curves ☑ Flow Scheme ☑ Logbook
3	Click **OK.**

The Run Data pane

The **Run Data** pane shows the current values for the running parameters. When the system is running, the text **Run** is displayed in the **Run Status** panel. If the system is operated manually the text **Manual** is displayed. The illustration below shows only part of the **Run Data** pane.

Run Data

Acc. Volume 626.31 ml

Block Volume 1.46 ml

Acc. Time 89.58 min

Block Time 0.72 min

FlowA 0.00 ml/min

FlowB 2.00 ml/min

Pressure 1.8 Bar

Cond 160 uS/cm

UV1_436nm 91 mAU

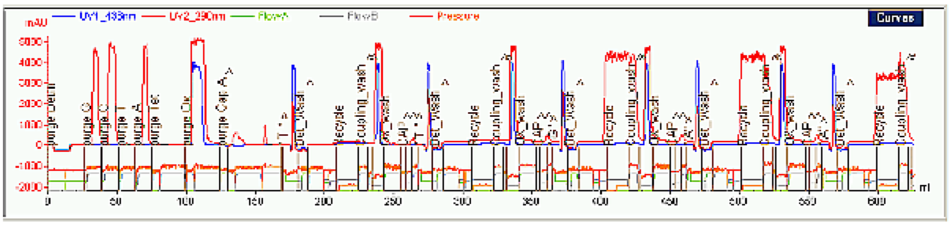
UV2_290nm 298 mAU

Integrate Inactive

Scale 27.9 umol

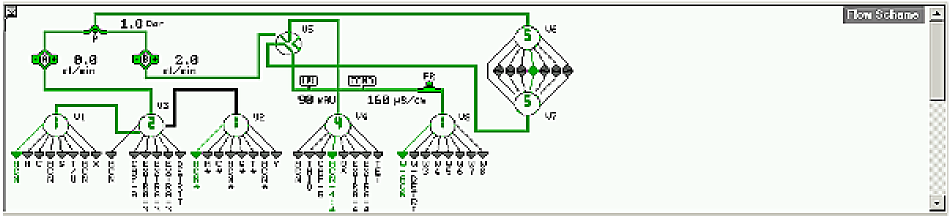
The Curve Data pane

The **Curve Data** pane shows selected monitor signals as curves during your method run. All curves are stored in the result file. Normally the curves are scaled with auto scaling, i.e. the scale is adjusted continually to the highest and lowest values for each curve.



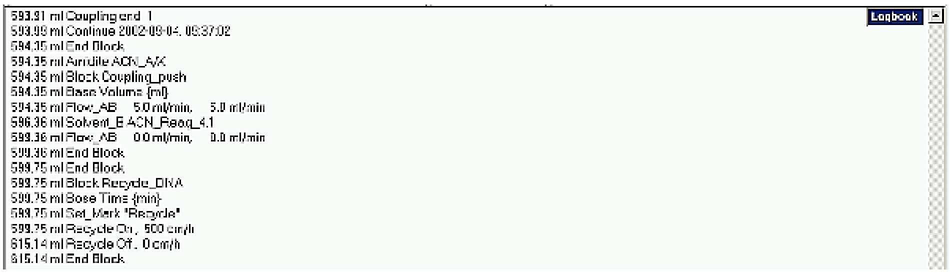
The Flow Scheme pane

The **Flow Scheme** pane shows a schematic view of your system configuration.



The Logbook pane

The **Logbook** pane is shown at the bottom. The **Logbook** shows exactly when the instructions in the method were executed during the run. It also shows all manual instructions that were performed and all alarms and warnings that were registered.



```
593.91 ml Coupling end 1
593.99 ml Continue 2002-09-04, 09:37:02
594.35 ml End Block
594.35 ml Amidite ACN_A/K
594.35 ml Block Coupling_push
594.35 ml Base Volume (ml)
594.35 ml Flow_AB     5.0 ml/min,     5.0 ml/min
596.36 ml Solvent_B ACN_Reaq_4.1
599.36 ml Flow_AB     0.0 ml/min,     0.0 ml/min
599.36 ml End Block
599.75 ml End Block
599.75 ml Block Recycle_DNA
599.75 ml Base Time (min)
599.75 ml Set_Mark "Recycle"
599.75 ml Recycle On , 500 cm/h
615.14 ml Recycle Off , 0 cm/h
615.14 ml End Block
```

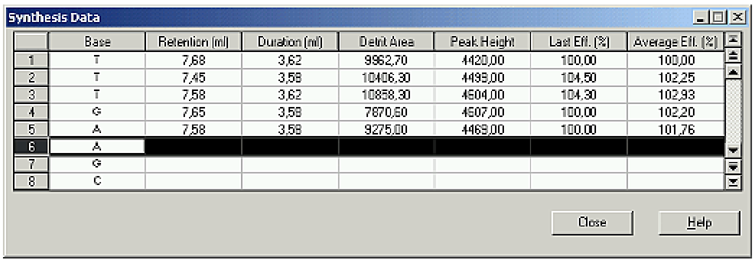
How to view a single pane

If you want....	then....
to enlarge a pane	right-click and select **Maximize**.
to return to the original size	right-click and select **Restore**.

How to view Synthesis Data

- Select the **View:Synthesis Data** menu command.

This will open the **Synthesis Data** dialog box where the online integrated trityl values are displayed. The highlighted row displays the cycle that is running currently.



	Base	Retention (ml)	Duration (ml)	Detrit Area	Peak Height	Last Eff. (%)	Average Eff. (%)
1	T	7,68	3,62	9962,70	4420,00	100,00	100,00
2	T	7,45	3,58	10406,30	4499,00	104,50	102,25
3	T	7,58	3,62	10858,30	4504,00	104,30	102,93
4	G	7,65	3,58	7870,60	4507,00	100,00	102,20
5	A	7,58	3,58	9275,00	4469,00	100,00	101,76
6	A						
7	G						
8	C						

5.3 How to change the way your run is displayed

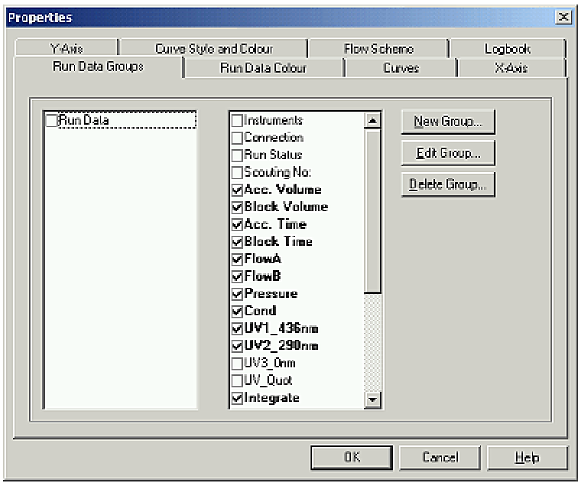
Introduction

There are a number of ways to change the way your method run data is displayed in the **System Control** module. This section describes a few of the options.

How to edit the pane displays

The table below describes how to open the **Properties** dialog box to edit the way the panes are displayed.

Step	Action
1	Right-click in the pane you want to edit.
2	Select **Properties** from the menu.
3	Click the tab for the pane you want to edit. *Result*: The page shows all the options that you can select in this particular pane. You also have a choice of different styles, colors and axis layouts for your curves.



☐ Run Data

☐ Instruments
☐ Connection
☐ Run Status
☐ Scouting No:
☑ Acc. Volume
☑ Block Volume
☑ Acc. Time
☑ Block Time
☑ FlowA
☑ FlowB
☑ Pressure
☑ Cond
☑ UV1_436nm
☑ UV2_290nm
☐ UV3_0nm
☐ UV_Quot
☑ Integrate

How to change the Y-axis scale display

You can select which curve the Y-axis scale refers to in two different ways:

- Click the curve name at the top of the **Curve Data** pane.

or

- Click the Y-axis scale to toggle between the curve scales.

How to set fixed values for the Y-axis

The table below describes how to set a fixed value range for the Y-axis for a selected curve in the **Properties** dialog box.

Step	Action
1	Click the Y-axis tab.
2	Click the curve you want to edit.
3	Click the **Fixed** radio button.
4	Type a minimum and a maximum value. The maximum range values allowed are shown above the entry boxes.
5	Repeat steps 2 to 4 for all other curves you want to edit.
6	Click **OK**.

5.4 *Manual control*

Introduction

In some applications you may want to change some parameters manually during a run. This section exemplifies how you can change the pump flow manually.

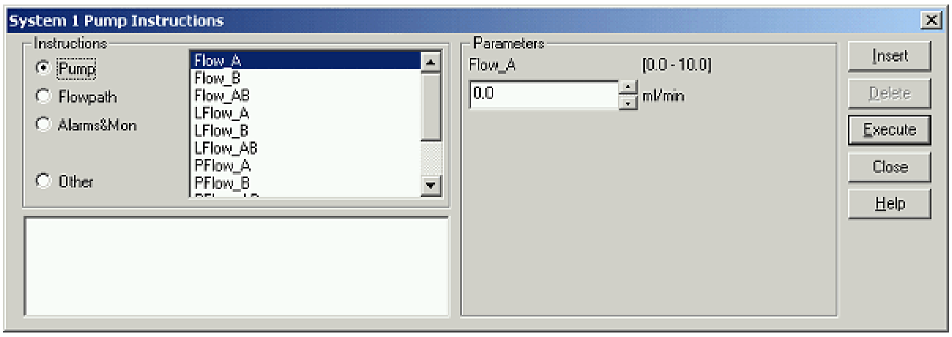
How to change the pump flow

The table below describes how to change the pump flow.

Step	Action
1	Select **Manual:Pump**. *Result*: the **System Pump Instructions** dialog box opens The **Pump** radio button is selected.
2	Click the function you want to change, i.e. **Flow_A**.
3	Enter a new value (**Flow_A**) under **Parameters**. You can use the arrows to step the value up or down.
4	• Click **Execute** to execute the instruction immediately. *or* • Click **Insert** to add the instruction to the list below the instructions menu. *Note*: If there are instructions on the list, the **Execute** button will execute all instructions on the list at the same time.
5	Click **Close** to close the dialog box.

The System Pump Instructions box

The illustration below shows the **System Pump Instructions** dialog box:



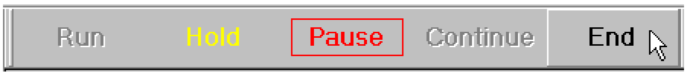
Flow_A [0.0 - 10.0]

0.0 ml/min

Note: The parameter values will be updated continually during the run if the **Auto update** checkbox is selected.

How to end your run manually

Click the **End** button to end the method run before it is finished. You can save the partial result the same way that you save a completed run.



6 How to view results

Introduction

This chapter describes how to view the results from your method run in the **Evaluation** module.

In this chapter

This chapter contains the following sections

Topic	See
How to view and edit your result layout	6.1
How to view the run documentation	6.2
How to compare curves	6.3

6.1 *How to view and edit your result layout*

Introduction

This section describes the basics of how to view and edit the layout of your results in the **Evaluation** module.

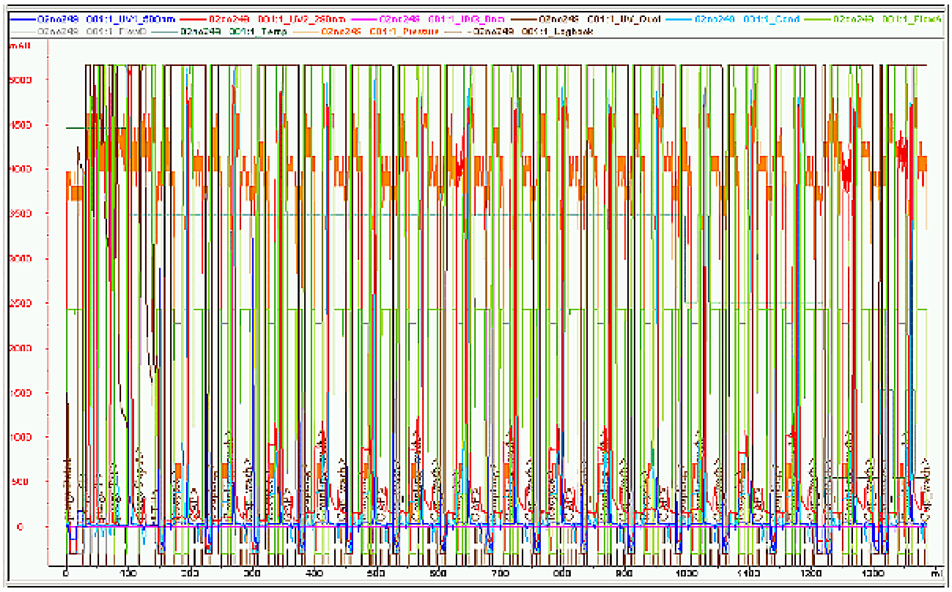
How to open the result file

The table below describes how to view the results.

Step	Action
1	Complete the method run.
2	Locate the result file in the **Results** pane in the **UNICORN Manager** module.
3	Double-click the file. *Result*: The file opens in the **Evaluation** module.

The Raw Chromatogram Data

The result file is opened in a **Chromatogram** window. The default view shows all the curves as in the illustration below.



How to change the chromatogram layout

The table below describes how to change the layout of the **Chromatogram** display.

Step	Action
1	Right-click in the **Chromatogram** window and select **Properties**. *Result*: The **Chromatogram Layout** dialog box opens.

Step	Action
2	Click the **Curve** tab.
3	Click the check-boxes to de-select the curves that you do not want to display.
4	Click **OK**.

Raw data curves are saved

Your selections determine the curves that are displayed in the **Chromatogram** window and shown on printouts.

Note: The original raw data curves can never be modified, renamed or deleted from the result file.

How to change the Y-axis scale

Normally the curves are auto scaled, i.e. the highest and lowest values for each curve set the scale. The table below describes how to change auto scaled Y-axis scales to fixed values in the **Chromatogram Layout** dialog box.

Step	Action
1	Click the Y-axis tab.
2	Click the curve you want to edit.
3	Click the **Fixed** radio button.
4	Enter new minimum and maximum values.
5	Repeat steps 2 to 4 for all other curves you want to edit.
6	Click **OK** to execute the changes and close the window.

How to change the Y-axis scale display

You can select which curve the Y-axis scale refers to in two different ways:

- Click the curve name at the top of the **Curve Data** window.

or

- Click the Y-axis scale to toggle between the curve scales.

How to view curve details

The table below describes how you can zoom in on a curve to view more details.

Step	Action
1	Place your cursor in a corner of the area you want to enlarge.

Step	Action
2	Press and hold the left mouse button and drag diagonally over the area. *Result*: A rectangle appears.
3	Release the mouse button. *Result*: The area within the rectangle is enlarged.
4	Repeat steps 1 - 3 to enlarge the selected area further.
5	Right-click and select **Undo Zoom** to zoom out one step.
6	Right-click and select **Reset Zoom** to return to the full window view.

How to save a layout

You can save your edited layout. It can be applied later to any result file. Follow the steps in the table below.

Step	Action
1	Right-click and select **Properties** to open the **Chromatogram layout** dialog box.
2	Select the **Layout library** tab.
3	Click the **Save current layout as...** button.
4	Enter a name for the layout and click **OK**.

How to apply a saved layout

Select a layout from the **Saved layouts** list in the **Layout library**. Click the **Apply selected layout** button.

6.2 *How to view the run documentation*

Introduction

The full documentation of a method run is stored in the result file. You can view this information in the **Documentation** dialog box in the **Evaluation** module. This section gives an example of how to view the **Logbook**.

How to open the run documentation

Maximize the **Evaluation** module and either:

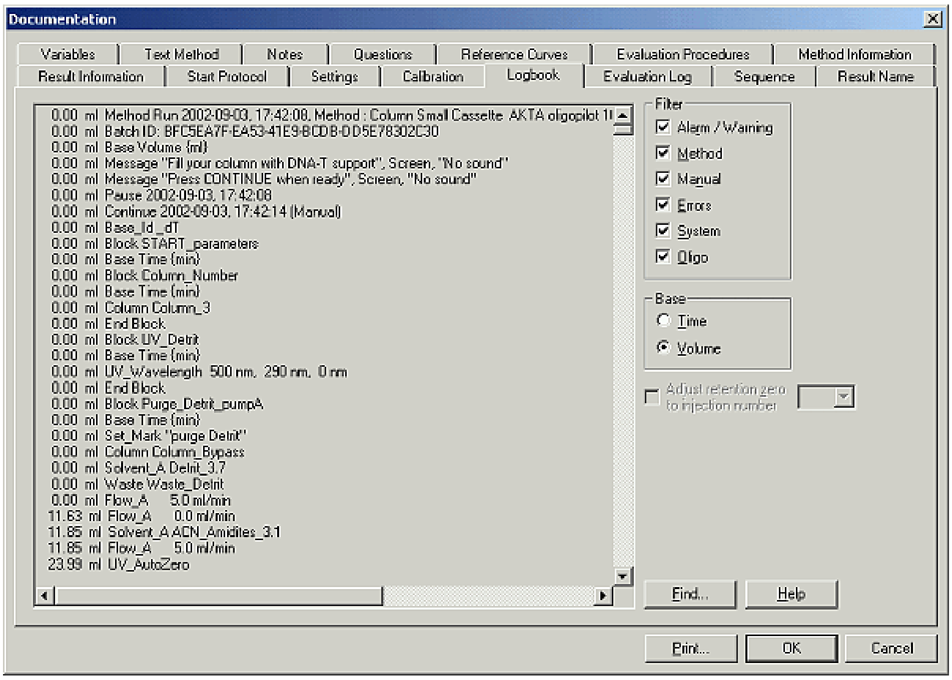
- Select the **View:Documentation** menu command

or

- Click the **View Documentation** icon.

The documentation window

This is an illustration of the **Documentation** dialog box with the **Logbook** tab selected. Click the tabs to view other information.



```
 0.00 ml Method Run 2002-09-03, 17:42:08, Method : Column Small Cassette  AKTA oligopilot 1I
 0.00 ml Batch ID: BFC5EA7F-EA53-41E9-BCDB-DD5E78302C30
 0.00 ml Base Volume {ml}
 0.00 ml Message "Fill your column with DNA-T support", Screen, "No sound"
 0.00 ml Message "Press CONTINUE when ready", Screen, "No sound"
 0.00 ml Pause 2002-09-03, 17:42:08
 0.00 ml Continue 2002-09-03, 17:42:14 (Manual)
 0.00 ml Base_Id_dT
 0.00 ml Block START_parameters
 0.00 ml Base Time {min}
 0.00 ml Block Column_Number
 0.00 ml Base Time {min}
 0.00 ml Column Column_3
 0.00 ml End Block
 0.00 ml Block UV_Detrit
 0.00 ml Base Time {min}
 0.00 ml UV_Wavelength  500 nm,  290 nm,  0 nm
 0.00 ml End Block
 0.00 ml Block Purge_Detrit_pumpA
 0.00 ml Base Time {min}
 0.00 ml Set_Mark "purge Detrit"
 0.00 ml Column Column_Bypass
 0.00 ml Solvent_A Detrit_3.7
 0.00 ml Waste Waste_Detrit
 0.00 ml Flow_A     5.0 ml/min
11.63 ml Flow_A     0.0 ml/min
11.85 ml Solvent_A ACN_Amidites_3.1
11.85 ml Flow_A     5.0 ml/min
23.99 ml UV_AutoZero
```

Filter
☑ Alarm / Warning
☑ Method
☑ Manual
☑ Errors
☑ System
☑ Oligo

Base
○ Time
● Volume

☐ Adjust retention zero to injection number

6.3 *How to compare curves*

Introduction

You can import or copy curves from different method runs into one chromatogram for comparison. This section is an example of how you can use the function **Open to compare** to import curves.

Open the dialog box

First open the dialog box **Open Curves to Compare**. You can either:

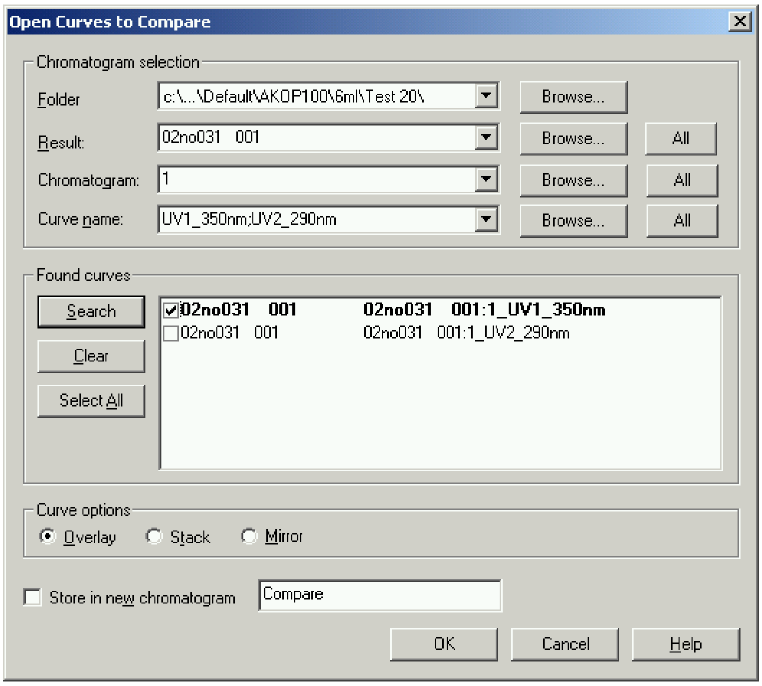
- Select **File:Open to compare:Curves**.

or

- Click the **Open curves to compare** icon.

The Open curves to compare dialog box

The illustration below shows the dialog box **Open Curves to Compare**.



Folder: c:\...\Default\AKOP100\6ml\Test 20\
Result: 02no031 001
Chromatogram: 1
Curve name: UV1_350nm;UV2_290nm

☑ **02no031 001 02no031 001:1_UV1_350nm**
☐ 02no031 001 02no031 001:1_UV2_290nm

● Overlay ○ Stack ○ Mirror

☐ Store in new chromatogram: Compare

How to import the curves

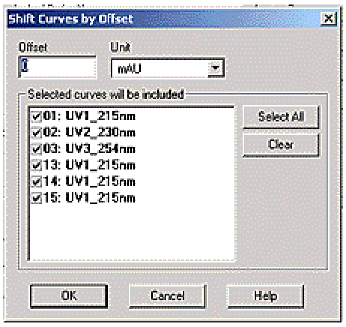
The table below describes how to import curves and store them in a new chromatogram.

Step	Action
1	Define search criteria for the folder, result, chromatogram and/or curve name. Use the **Browse** command buttons.

Step	Action
2	Click **Search**. *Result*: A list of found curves is displayed.
3	Repeat step 1 - 2 to add more curves to the list.
4	• Select the individual curves that you want to import. *or* • Click **Select all** to import all curves.
5	Click the checkbox **Store in new chromatogram** and enter a name in the text box (**Compare** is default). *Note*: You can also save the curves in the active chromatogram.
6	Select one of the **Curve options**: **Overlay**, **Stack** or **Mirror**. *Result*: This will decide how the curves are displayed.
7	Click **OK**.

How to set the stack offset

If you selected the **Stack** option the **Shift Curves by Offset** dialog box is opened automatically. Adjust the offset distance between the curves to a suitable value.



Offset: 0

Unit: mAU

Selected curves will be included

☑ 01: UV1_215nm
☑ 02: UV2_230nm
☑ 03: UV3_254nm
☑ 13: UV1_215nm
☑ 14: UV1_215nm
☑ 15: UV1_215nm

---

7 How to print your chromatograms

Introduction

This chapter describes how to print open chromatograms. Proceed to **8 How to create and print reports** on page 49 if you want to add text information to your prints or create a complete report.

In this chapter

This chapter contains the following section

Topic	See
How to print active chromatograms	7.1

7.1 *How to print active chromatograms*

Introduction

This section describes how to print the chromatograms that are open in the **Evaluation** module.

Before you print

Open all chromatograms that you want to print in the **Evaluation** module before you proceed.

How to print

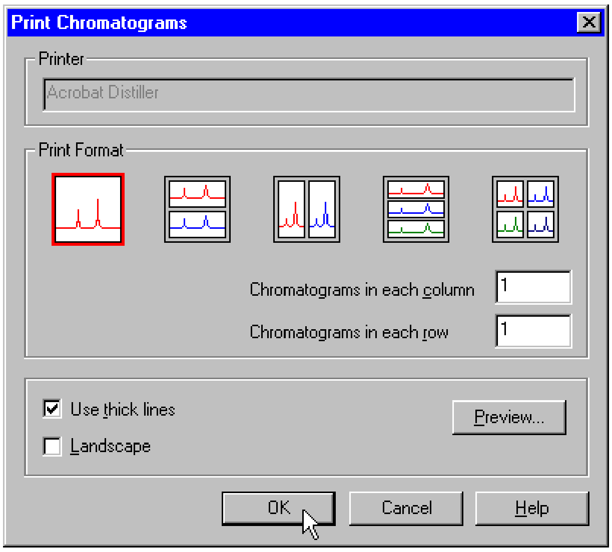
The table below describes how to print active chromatograms.

Step	Action
1	• Select the **File:Print** menu command. *or* • Click the **Print** icon. *Result*: The **Print Chromatograms** dialog box opens.
2	Select print formats and layout options.
3	Click **Preview**. Result: The **Customise Report** window opens.
4	• Verify that the layout is correct. • Click **Edit Mode** to make changes, e.g. change the order of the chromatograms. Click **Preview** to return to preview mode. • Click **Exit** to return to the **Print Chromatograms** dialog box.
5	Click **OK**.

The Print Chromatograms dialog box

This is an illustration of the **Print Chromatograms** dialog box.

Note: The selected print format is outlined in red.



Printer: Acrobat Distiller

Chromatograms in each column: 1

Chromatograms in each row: 1

☑ Use thick lines

☐ Landscape

8 How to create and print reports

Introduction

The **Evaluation** module provides extensive tools to create detailed reports. This chapter describes how to create reports.

In this chapter

This chapter contains the following sections

Topic	See
How to print an existing report format	8.1
How to edit an existing report format	8.2
How to create and print a customized report format	8.3

8.1 How to print an existing report format

Introduction

This section describes how to use an existing report format to print a basic report with a chromatogram and text.

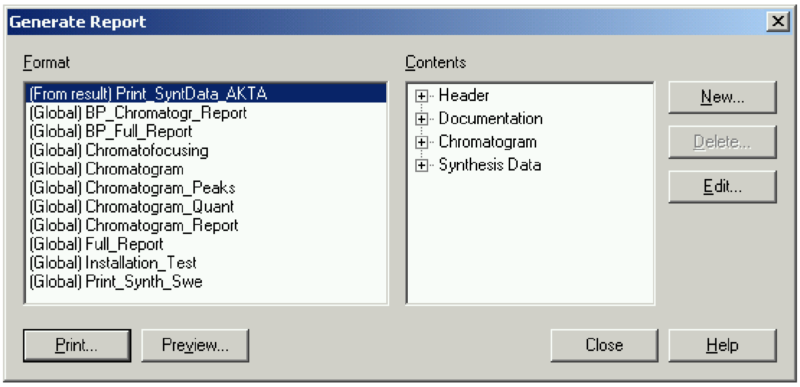
How to print a report

The table below describes how to print a report.

Step	Action
1	• Choose **File:Report**. *or* • Click the **Report** icon. *Result*: The **Generate Report** dialog box opens.
2	Select format **(From result) Print_SyntData_AKTA**. *Result*: This creates a report containing the chromatogram and the answers to the questions from the **Run Setup Questions** page.
3	Click **Print**. *Result*: The **Print** dialog box opens.
4	Click **OK**.

The Generate Report dialog box

This is an illustration of the **Generate Report** dialog box.



Format

(From result) Print_SyntData_AKTA
(Global) BP_Chromatogr_Report
(Global) BP_Full_Report
(Global) Chromatofocusing
(Global) Chromatogram
(Global) Chromatogram_Peaks
(Global) Chromatogram_Quant
(Global) Chromatogram_Report
(Global) Full_Report
(Global) Installation_Test
(Global) Print_Synth_Swe

Contents

Header
Documentation
Chromatogram
Synthesis Data

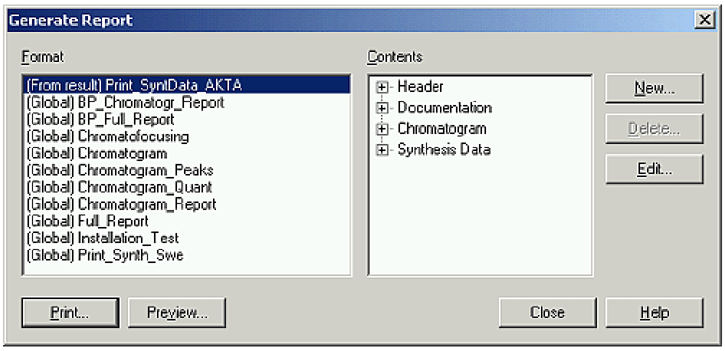
8.2 *How to edit an existing report format*

Introduction

This section describes how to open an existing report format to edit the items that are included in the report.

How to open and edit a report format

The table below describes how to open and edit a report format.

Step	Action
1	• Choose **File:Report** *or* • Click the **Report** icon. *Result*: The **Generate Report** dialog box opens.  Format (From result) Print_SynIData_AKTA (Global) BP_Chromatogr_Report (Global) BP_Full_Report (Global) Chromatofocusing (Global) Chromatogram (Global) Chromatogram_Peaks (Global) Chromatogram_Quant (Global) Chromatogram_Report (Global) Full_Report (Global) Installation_Test (Global) Print_Synth_Swe Contents ⊞ Header ⊞ Documentation ⊞ Chromatogram ⊞ Synthesis Data
2	Select a report format.
3	• Click **Edit**. *Result*: The **Customize Report** window opens in edit mode.
4	• Double-click an item that you want to edit in the report. *Result*: A **Setup** dialog box specific for the item opens.
5	• Edit the item. • Repeat step 4 for all other items you want to edit.

How to apply the report format

Once you have finished editing the report items you can apply the format.

If you want to...	then...
to print the report	• click the **Print** icon. 🖨
to preview the changed report layout	• click the **Preview** button.
to save the format	• choose **File:Save As** and enter a name for the report format.

8.3 *How to create and print a customized report format*

Introduction

You can select a number of different objects (including chromatograms, methods, images, free text etc.) and create a customized report format. The objects can be aligned, re-sized and positioned to fit your specific layout. This section describes only some of the formatting options.

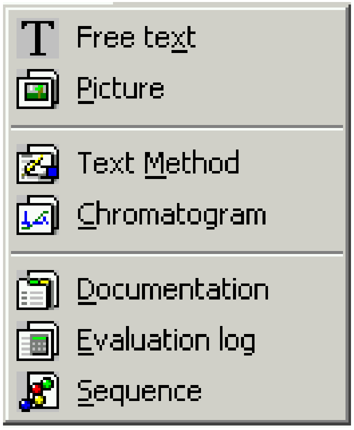
How to create a new report format

The table below describes how to create a new customized report format.

Step	Action
1	• Choose **File:Report**. *or* • Click the **Report** icon. *Result*: The **Generate Report** dialog box opens.
2	Click the **New** button. *Result*: The **Create New Report Format** dialog box opens.
3	Choose **Customised Format** and click **OK**. *Result*: The **Customise Report** window opens.
4	Proceed to "How to add items to the empty report".

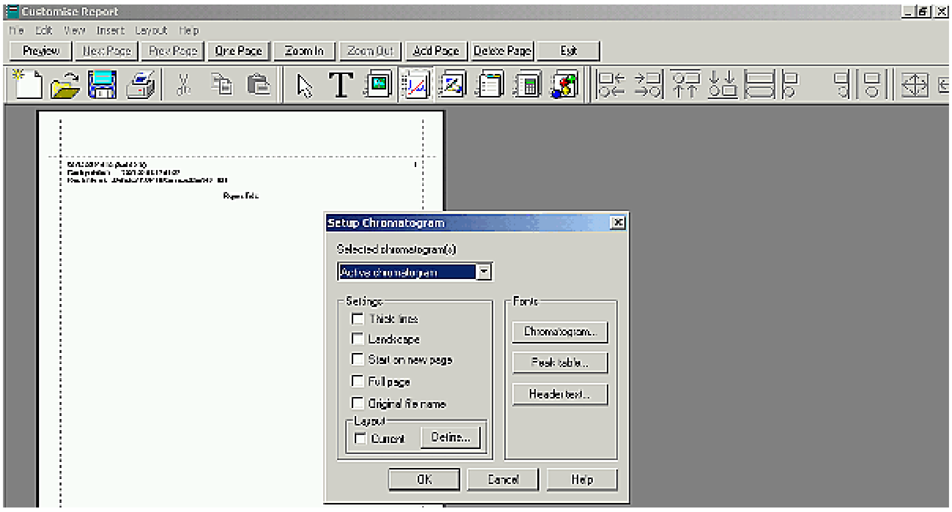
How to add items to the report

The table below describes how to add items to your empty report format.

Step	Action
1	Select an information item. • Click one of the item icons in the toolbar. *or* • Select an item from the **Insert** menu. 
2	Press and hold down the left mouse button, and drag out a box to the size of the item you want to insert. *Note*: The mouse pointer shows a symbol for the type of item you have selected.
3	Release the mouse button. *Result:* A **Setup** dialog box opens. The dialog box is specific to the type of item that you want to insert.
4	Select the options you want.
5	Click **OK**.
6	Repeat steps 1 to 5 for each new item you want to insert.
7	Click **Preview** to view the final results.

The Setup Chromatogram dialog box

The illustration below shows the **Setup Chromatogram** dialog box in the **Customise Report** window.



Selected chromatogram(s): Active chromatogram

☐ Thick lines
☐ Landscape
☐ Start on new page
☐ Full page
☐ Original file name

Layout: ☐ Current

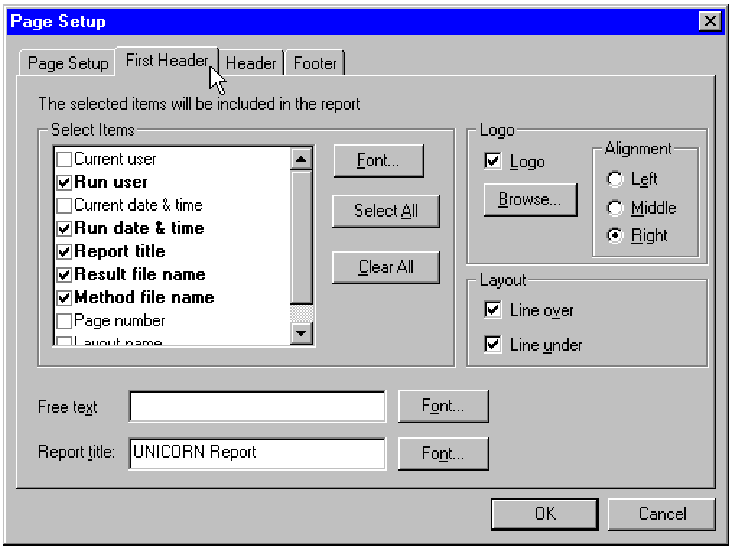
How to set up the page format

The table below describes how to set up the page formatting.

Step	Action
1	Double-click anywhere in the **Customise Report** window. Result: The **Page Setup** dialog box opens.
2	Click the **Page Setup** tab and enter values for all **Margins**.
3	Click the **First Header** tab and select the items that you want to include in the first page header.
4	Click the **Footer** tab and select the items that you want to include in the footer.
5	Click the **Header** tab and select the items that you want to include in the header. *Note*: This tab is not available if you selected **Same header on all pages** in the **Page Setup** tab.

The Page Setup dialog box

The illustration below shows the **First Header** tab in the **Page Setup** dialog box.



The selected items will be included in the report

Select Items
- ☐ Current user
- ☑ **Run user**
- ☐ Current date & time
- ☑ **Run date & time**
- ☑ **Report title**
- ☑ **Result file name**
- ☑ **Method file name**
- ☐ Page number
- ☐ Layout name

Logo
- ☑ Logo

Alignment
- ○ Left
- ○ Middle
- ● Right

Layout
- ☑ Line over
- ☑ Line under

Free text:

Report title: UNICORN Report

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