GE Healthcare

UNICORN 5.1 User Reference Manual



UNICORN for ÄKTAoligopilot



● UNICORN[™]

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Table of Contents

1	Introducing UNICORN	
Introduction	This chapter contains:	
	 A general overview of the UNICORN™ system. Information about the user documentation for UNICORN and how 	to use it.
In this chapter	This chapter contains the following sections	
	Торіс	See
	About UNICORN	1.1
	About this manual	1.2
	About the UNICORN user documentation	1.3

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About UNICORN 1.1 Introduction This section is a general overview of the UNICORN system. What is UNICORN is a complete package for control and supervision of chromatography/oligo **UNICORN?** systems. It consists of control software and a controller card for interfacing the controlling PC to the chromatography liquid handling module. Oligonucleotide Synthesis is used to make synthetic oligonucleotides in the column that is attached to the system controlled by UNICORN. UNICORN is a trademark of GE Healthcare. **Operating environ-** UNICORN runs on a PC under Microsoft® Windows® 2000 or Microsoft Windows XP. It is designed to run under English keyboard settings. ment Windows func-Most Windows functions are also available in UNICORN, including tions • 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. Bar code reader You can connect a bar code reader to the PC and use the reader to enter information instead of using the keyboard. This can be useful for example when entering information like batch IDs. Compatible chro-UNICORN can be used with a number of systems including matography sys- ÄKTA™ design systems tems 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 chromatography 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 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 profile etc.
Method Editor	To create and edit methods for pre- programmed control of 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. All modules will normally open when the program is started. However, a user profile may be set up so that not all modules are available. Only the available modules will be displayed.

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.
the online manuals.	open the Help menu in any of the software modules and select Manuals .

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 ac- cess level, which defines the functions that the user is permitted to use.

Feature	Function
Connection Security	A running system can only be con- trolled from one connection. Systems may be locked with a password to pre- vent other, un-authorized users from changing parameters.
Data Security	Result files from an ongoing synthesis run can be saved automatically at pre- set intervals to minimize data loss if the system fails. The results are saved loc- ally 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

This section is a general description of the manual, the contents and the pre-requisites
for the examples and instructions that are presented in the User Reference Manual.
The purpose of the User Reference Manual is to present a comprehensive guide to the UNICORN system for a user either with previous experience of this system or from other, similar oligosynthesis or chromatography systems. The system is presented in detail, along with practical instructions of how to operate a model system.
This manual and the corresponding version of Getting Started with UNICORN for ÄKTAoligopilot covers the following systems: • ÄKTA™ oligopilot™ • OligoPilot™ • OligoProcess™





Note: A general version of this manual is available for use with most ÄKTA design instruments. Adapted versions of the manual are available for ÄKTAxpress™ and BioProcess™ systems.

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

Refer to other manualsThe User Reference Manual does not contain information about the installation procedure or network configuration. You will find this information in the Administration and Technical Manual.Sometimes you may find it more convenient to refer to the Getting Started with UNICORN guide for a linear, step-by-step instruction how to perform a task. Note: When you install the UNICORN software you choose which manuals you wish to install. You can also install the manuals after the program installation.Document structure tureThe 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. Most sections begin with an introduction that summarizes the content. Some sections are divided into blocks of information with separating lines. The blocks are identified by a label in the margin. This makes it easier for you to quickly scan a page to find the exact topic you are looking for.Typographical representationsMenu 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:Panes:Customize (i.e. the menu command Customize in the sub-menu Panes from the View-menu). Text entries that UNICORN generates or that the user must type is represented by a monotype typeface: Example: Connection change		<i>Note</i> : 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.
Sometimes you may find it more convenient to refer to the Getting Started with UNICORN guide for a linear, step-by-step instruction how to perform a task. Note: When you install the UNICORN software you choose which manuals you wish to install. You can also install the manuals after the program installation. 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. Most sections begin with an introduction that summarizes the content. Some sections are divided into sub-sections. A section is divided into blocks of information with separating lines. The blocks are identified by a label in the margin. This makes it easier for you to quickly scan a page to find the exact topic you are looking for. 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:Panes:Customize (i.e. the menu command Customize in the sub-menu Panes from the View-menu). Text entries that UNICORN generates or that the user must type is represented by a monotype typeface: Example: Connection change	Refer to other manuals	The User Reference Manual does not contain information about the installation procedure or network configuration. You will find this information in the Administration and Technical Manual.
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Example: Connection change		Text entries that UNICORN generates or that the user must type is 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.

About the UNICORN user documentation 1.3 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 UNICORN User Reference Manual for oligonucleotide synthesis (See 1.2 About this manual on page 12). UNICORN Administration and Technical Manual User info about The questions and answers in the table below describe the features of the Getting **Getting Started** 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. Basic descriptions of UNICORN and its What are the contents of Getting Staruse, based on a model system. ted? How should I use Getting Started? Read in front of your computer and test the instructions at the same time. User info about The questions and answers in the table below describes the features of the User the User Refer-Reference Manual. ence 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.

Question	Answer
What do I need before I start?	Knowledge of PC and Windows func- tions and an understanding of the con- cepts and terminology of oligonuc- leotide synthesis. Preferably 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.
	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, or only selected sections for reference.

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 Adminis-	Detailed instructions of:
tration and Technical Manual?	• How to install and maintain UNICORN in a network environment.
	• How to create and administrate user profiles.
	Most instructions are based on a model system.

Question	Answer
How should I use the Administration and Technical Manual?	• If you are an experienced adminis- trator of previous UNICORN versions you can read selected sections for reference.
	 If this is your first experience of UNICORN we recommend that you study the manual in detail.

2 UNICORN concepts

Introduction This chapter contains:

- Definitions and descriptions of some of the specific concepts that are presented in this manual and in other UNICORN manuals.
- An overview of the UNICORN user interface.
- A Quick Start Guide that can be used as a shortcut for experienced users that want to start right away.

Note: General concepts and common terminology for oligonucleotide synthesis are not explained here.

In this chapter

This chapter contains the following sections

Торіс	See
Concept definitions	2.1
The UNICORN user interface	2.2
Quick Start Guide	2.3

2.1	Concept definitions
Introduction	This chapter contains explanations and definitions of a number of UNICORN concepts that are used in this manual.
	The concepts are organized in alphabetical order.
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 if the monitored values exceed or fall below specified limits. The system will be paused.
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.
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 can be 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.
	<i>Example</i> : A MethodQueue can be set up to conduct a CIP study of a number of columns, through a controlled series of scouting runs.

Result files UN

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.

StrategyPart 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 definesavailable 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	 Instruction parameters and values at breakpoints in the Methodmay 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.

WarningsSystems settings or method instructions specify acceptable limits for monitor signals
during a separation 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.

2.2 The UNICORN user interface

Introduction

This section is an overview of the four UNICORN modules with descriptions of some of the elements of the user interface. The section also contains a description of the search functions in UNICORN.

Note: A user profile can be set up so that the user only has limited access to the modules described in this chapter. Only the available modules will open when the program is started.

In this section

This section contains the following sub-sections

Торіс	See
UNICORN Manager	2.2.1
The Method Editor module	2.2.2
The System Control module	2.2.3
The Evaluation module	2.2.4
Search functions	2.2.5
Help functions and manuals	2.2.6
Snapshots	2.2.7

2.2.1 **UNICORN** Manager

Introduction The UNICORN Manager is mainly used for file and folder administration.

The UNICORN Manager windows

The module is divided into two windows, the **Methods** window and the **Results** window. See the illustration below:

UNICORN Main Menu				
File View Administration Tools Window Help				
💵 🕪 🍈 🏦 🚯 🇯				
Methods		B Results	Marian Constanting of the	
n/L./Default		a.\\Defaul\\AKDP100\Bm\\	Optimication	
Name System	Size Type Mod	Name	Size Type	Applified 🔺
2	Prev Folder		Frev Falder	
az1003	Method Quaue Folder 200	🛂 02no247 - 001	2215KB Result File	2002-00-04 11:48
Queues	User Folder 200	💾 02no248 🛛 001	2287ft8 Result File	2002-09-04 11:47
🚉 Per - Jumal metoder	User Folder 2000	🛃 02no245 🛛 003	2252KD Result File	2002-09-02 20:27
02no298 System 2	292KB Method File 200	🛛 02no240 C01	2149KB Result File	2002-09-02 11:54
🖬 02no297 System 2	292K3 Method File 200	💾 02no241 🛛 001	2315KB Result File	2002-08-31-04:02
🖸 02no296 System 2	292K9 Method Me 2000	🛃 02no219-001	204188 Result file	2002-08-26 11:15
🖬 GEA Col4 LmL column System 1	269K9 Method File 2000	💹 02no233 001	21398B Result File	2002-08-23 21:28
CEA Col5 System 2	260KB Method File 2000	💹 02no230 001	2317KB Result File	2002-08-23 14:04
DEA Col7 System 2	268K8 Method File 2000	12:02:29 001	212508 Result File	2002-08-23 14:04
GEA Col5 System 2	269K9 Method File 2000	🛃 02no220 - 001	2122K0 Result File	2002-00-23 14:00
🖬 Little Bertha System 2	S27KB Method File 200	💹 02no225_001	2369KB Result File	2002-08-23 09:03
🖬 flos through 65 pdfr 🥼 System 2	S30K8 Method File 2000	💹 0200224 - 600	2355KB Result File	2002-08-22 09:02
test akop10 System 1	326K8 Method File 2000	💾 02no226 🛛 001	212288 Result File	2002-08-22 07:15
🖬 PS classic verification 🦳 System 1	326K9 Method File 2000	🕺 02no223 🛛 00L	2369KB Result File	2002-08-21 08:07
🖬 kee System I	S28KB Method File 200	02no222 00L	2371KB Result File	2002-08-20 29:09 🖉
🖬 optimisation 🦳 System 2	293KB Method File 200	💾 02m218-001	233488 Result File	2002-08-19 25:14 💍
captest 293953 System 1	327K0 Method Me 2000	🛃 02no217 🛛 001	223080 Result file	2002-00-19 00:55 📄
🖬 Cap Test coupling System I	B31K9 Method File 2000	💹 02no214 001	2201XB Result File	2002-08-19 08:55
		🛛 02no216 🛛 001	2237KB Result File	2002-08-16 22:10 🖉
		💾 02no213 🛛 001	211088 Result File	2002-08-16 08:44 🚫
		💹 02no211 00L	1057KB Result File	2002-00-15 09:00 🔡
		🛛 02no210 🛛 001	2144KB Result File	2002-08-14 21:25
		💾 02no193 🛛 001	2325K8 Result File	2002-07-12 07:28 🚬
		🔮 02no192 🛛 001	215088 Result file	2002-07-12 07:27
		💹 02no191 🛛 001	2316KB Result File	2002-07-11 15:50 👘
		🛛 02no190 001	2176KB Result File	2002-07-11 08:12 📓
		💾 02no189 🛛 001	229688 Result File	2002-07-11 08:11 🖹
		🛃 02no100 🛛 001	2013K0 Result file	2002-07-10 10:32 📗
1		💆 02no187 🛛 001	21.15KB Result File	2002-07-09 16:03 🚫
1		💾 02no186 🛛 001	2325KB Result File	2002-07-09 09:49 🕃
1		🛃 02no185 🛛 001	2264K8 Result File	2002-07-09 09:49 🔡
T		W 02mp104 001	219688 Realt File	2002-07-00.07-51
2 ant		Matheod	l trans defende	

dow

The Methods win- The Methods window contains all the saved methods, MethodQueues and all the folders containing methods that are available to the user. See the illustration below:

c:\\Default					
Name	System	Size	Туре	Modified	Crea
2			Prev Folder		
Demo 1			User Folder	12/7/2001 11:0	12/7
Demo 2			User Folder	12/7/2001 11:0	12/7
🔰 Test Meth	ods 1		User Folder	12/7/2001 11:0	12/7
🧕 Test Meth	ods 2		User Folder	12/7/2001 11:0	12/7
🧃 Test Queu	e		Method Queue Folder	12/13/2001 9:4	12/1
Test5	system	579KB	Method File	11/21/2001 4:2	11/2

Note: The icons for **MethodQueue** folders are different from the regular folder icon.

The Results win-The **Results** window contains all the saved results and all the result folders.

dow

💾 Results			_ 🗆	×
c:\\Default\AK0P100\6ml\0ptimisatic	n			
Name	Size	Туре	Modified	
		Prev Folder		
🔟 02no247 001	2215KB	Result File	2002-09-04 11:48	
🛄 02no248 001	2287KB	Result File	2002-09-04 11:47	
🔟 02no245 001	2252KB	Result File	2002-09-02 20:27	
🔟 02no240 001	2149KB	Result File	2002-09-02 11:54	
📕 02no241 001	2319KB	Result File	2002-08-31 04:02	
🔟 02no219 001	2341KB	Result File	2002-08-26 11:15	
🔟 02no233 001	2119KB	Result File	2002-08-23 21:28	
III 1772				

Toolbar icons in the UNICORN Manager

The table below describes the toolbar icons in the module.

lcon	Function
•	The Logon/Logoff icon is used to log on or log off the system.
	<i>Note</i> : The arrow in the Logoff icon points away from the door.
	The Instant Run icon immediately starts a run from a selected template or from a wizard.
	The New Method icon opens the Method Editor module and displays the New Method dialog box.
	The System Control icon activates the first connected System Control module and displays the Manual instruction dialog box.
	The Evaluation icon opens the Open Result dialog box. Select a result file and click OK to start the Evaluation module.
	The MethodQueue icon opens the MethodQueue Editor .
	The Existing MethodQueue icon opens the Running MethodQueue dialog box to display MethodQueues in progress.

Limited access to the UNICORN Manager Some user groups may be defined to have only a limited access to the **UNICORN Manager** functions. The available functions in the limited version are:

- Log off
- Change User Attributes
- Change Password
- Quit Program
- Help

There is also a **Cancel** button which minimizes the dialog box. The illustration below shows the limited access version of the **UNICORN Manager**.

UNICORN Manager			×
	UNICORN Logon Ir	nformation	
	Logoff	Change User Attributes	Help
Mi.	Quit Program	Change Password	Cancel

Note: For more information about how to change passwords and user attributes please refer to **3.4 How to change your passwords and user attributes** on page 57. For more information about how to log off and quit the program, please refer to **3.1 Log on routines and log off routines** on page 46.

2.2.2 The Method Editor module

Introduction The **Method Editor** module provides complete facilities for advanced editing of the methods.

Two modes

The Method Editor interface operates in two modes:

- Run Setup
- Text Instructions

Run Setup

Run Setup is a dialog box with a number of tabs that define the method properties. See the illustration below:

Variables Notes Questions Reference	Cu	ves Evaluation Procedures Method Information Start Proto	al Sequence I	Result Name
Block	Π	Variable	Value	Range
Main		Column_Volume (ml)	6.300	0.100 - 959999.000
START_parameters		ColumnVolume {mB	6.3D	0.10 - 500.00
		Weight_of_Support {g}	1.00	0.10 - 150.00
		Loading_of_Support {umol/g}	10	1 - 250
Calumn_Number		Calumn_Number	Column_1 📼	
Amidite_Purge_volume		Amidite_Purge_volume {ml}	1.00	0.00 - 999999.00
Solvent_Purge_volume		Salvent_Purge_volume {m}	5.00	0.00 - 995999.00
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 toollip for extended variable cells				

Text Instructions Text Instructions are used for advanced editing. Up to five different display panes can be open at the same time:

- The **Block** pane (not used for oligonucleotide synthesis).
- The Flow Scheme pane.
- The Gradient pane (not used for oligonucleotide synthesis).
- The **Text** pane.
- The Instruction box pane.

See the illustration below:



The Flow SchemeThe Flow Scheme pane displays the configuration of the system components. Thepanepane is static and for information only. See the illustration below:



The Text pane

The **Text** pane displays the method as a list of text instructions. The instructions can be organized in blocks, denoted by blue square symbols. The blocks can be expanded to show the instructions within the block. See the illustration below:

Teat



The Instruction box pane

The Instruction box pane is used to enter, edit or delete instructions. See the illustration below:



Toolbar icons in t

The table below describes the toolbar icons in the module.

he	Method	Editor	

lcon	Function
*	The New icon opens the New Method dialog box. The dialog box is used to create a new method.
	The New Block icon opens the New Block dialog box, which is used to add blocks to a method.
	The Open icon displays all available method files and method folders in the Open dialog box.
	The Save Method icon saves the edited method.
	The Print icon opens the Print dialog box. Select the method elements that you want to print.
	The Customise Panes icon opens the Customise Panes dialog box, which is used to select the panes that are open in Text Instructions mode.
	·

lcon	Function
1	The Text Instructions icon opens the Method Editor in Text Instruc- tions mode.
	The Run Setup icon opens the Method Editor in Run Setup mode.
	The Log Format icon opens the Log Format dialog box, which is used to display the accumulated time or volume for a method.
×.	The Method Wizard icon opens the Method Wizard , which is used to create new chromatography methods. This is not used for oligonuc-leotide synthesis methods.

2.2.3 The System Control module

Introduction	The System Control module is used to perform and monitor synthesis runs.		
The System Con- trol panes	 Con- The System Control module contains four different display panes that can be opened all at once or in any combination: The Run Data pane. 		
	The Claves pane.		
	Ine Flow Scheme pane.		
	The Logbook pane.		
The Run Data pane	The Run Data pane displays the current values for the selected run parameters. The values are updated at regular intervals, which are defined in the system strategy. See the illustration below:		
	Instruments Connection Run Status Acc. Volume Block Volume Block Volume Acc. Time Block Time 0.00 min 0.00 min 0.00 min		
The Curves pane	The Curves pane displays monitor signal values graphically. See the illustration below:		
	Null UV1_550n UV2_220nn Card Pressure 40X 40X		

The Flow Scheme pane

The **Flow Scheme** is a graphical representation of the oligonucleotide synthesis system. During a run, the **Flow Scheme** displays open flow paths in color. Monitor signals can be displayed numerically. See the illustration below:



The Logbook pane	The Logbook pane displays all actions during a synthesis run, e.g. method start and end, base instruction, method instructions and manual instructions such as Pause or Hold. See the illustration below: 0.00 ml Method Run 2002-10-29, 16:19:30, Method : 02no337, Result : c:\\Default\AKOP10 0.00 ml Batch ID: 75B85179-3670-4E46-A0E6-1864CC13BC96 0.00 ml Base CV, 6.30 (ml) 0.00 ml Base_Id_dT 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_5 0.00 ml Block UV_Detrit 0.00 ml Base Time {min} 0.00 ml Base Time {min}		
The Status bar	The Status bar in the bott status of the separation ru	om of the System Control module displays the current un. See the illustration below:	
	For Help, press F1	Run Block	
	The current system status is represented by the colored dot:		
	 A green dot represents a running system. 		
	 A red dot represents a system in Pause state. 		
	 A yellow dot represents a system in a Hold state. 		
	• A white dot represents a system in an End state.		
Toolbar icons in	Toolbar icons in The table below describes the toolbar icons in the module:		
trol	lcon	Function	
	Run	The Run icon opens the Run dialog box, which shows all available methods. If a method is loaded, Run Setup opens.	
	Hold	The Hold icon suspends execution of the method, while liquid is still pumped at the current flow rate and eluent concentration.	
	Pause	The function of the Pause icon depends on the strategy. The Pause icon suspends execution of the method and stops all pumps so that the system comes to a stand- still.	
	Continue	The Continue icon resumes the execution of a paused or held method.	

lcon	Function
End	The End icon terminates the method execution and puts the system into an End state.
	The Customise Panes icon opens the Customise Panes dialog box, which is used to select the display panes that are open.
	The View Documentation icon opens the documenta- tion pages. Run notes can be entered in the Notes page and settings can be changed.
	The View Properties icon opens the Properties dialog box, which is used to control the data display in the System Control panes.
	The Connect System icon is used to connect a system.
11	The Disconnect System icon is used to disconnect the system.
*	The Take Control of the System icon is used to leave the view mode for the system and change into a con- trol mode.
I	The Leave Control of the System icon is used to leave the control mode for the system and change into a view mode.

2.2.4 The Evaluation module

Introduction The Evaluation module provides extensive facilities to present and to evaluate curve data.

The module win-
dowOpened result files are displayed in the Evaluation module window. See the illustration
below:



Toolbar icons in
the Evaluation
module

The table below describes the toolbar icons in the module:

lcon	Function
*	The New icon opens an empty chromatogram.
	The Open icon displays all available result files and result folders in the Open Result dialog box.
	The Open Curves to Compare icon opens the Open Curves to Com- pare dialog box, which is used to select and open curves for compar- ison.
	The Save icon saves the edited result file.

lcon	Function
	The Print icon opens the Print Chromatograms dialog box.
	The Report icon opens the Generate Report dialog box, which is used to select a report format.
	The View Documentation icon opens the Documentation dialog box, which is used to view and edit the result documentation.
fir	The Peak Integrate icon opens the Integrate dialog box, which is used to select peaks to integrate in a modified peak table.
	The Chromatogram Layout icon opens the Chromatogram Layout dialog box, which is used to select and format curves and display items in the chromatogram.
N.	The Multifile Peak Compare icon opens the Multifile Peak Compare Wizard , which is used to compare peak data from different result files.
2.2.5	Search functions
-----------------------------------	--
Introduction	This section describes the general search functions that can be used to locate for example chromatograms, curves and text strings in UNICORN. These functions can be used in several program modules, dialog boxes and wizards.
Search the Folder list	The search will take place in the displayed folder only. To select another folder, click the Browse button and open the desired folder.
Search the Result list	• The search will take place in <i>all</i> result files within the selected folder as denoted by the asterisk (*). To select specific result file(s), click the Browse button and select the result file(s).
	• You can use wildcard characters to search for chromatograms within result files with a specific name profile.
	- * represents any number of characters
	- ? represents any single character
	Wildcard character examples:
	iex will search files named "iex"
	iex* will search all files with names that begin with "iex"
	*iex will search all files with names that end with "iex"
	<code>?iex</code> will search only 4-character names that end with iex
Search the Chro- matogram list	The asterisk (*) indicates that all chromatograms within a result file will be selected. Click Browse to select one or several specific chromatograms.
Search the Curve name list	The UV curves are identified by number and sometimes wavelength. For example, UV1_280, UV2_280 and UV1_254 are all different curves. To search for all UV curves, select *UV* in the Curve name text field.
Searches for Sample ID	A Sample ID can be used as a search criteria if it has been defined as a variable. The Sample ID can be entered in searches for result files both in the UNICORN Manager and in the Evaluation module.

Find a text string The Find command is used to search for text strings:

Find		×
Find what:		0K.
 Match whole word only Match case Search from top of document 	Olifection Ol∐p Olipown	Cancel

Field	Description
Find what	Type the text string you want to find.
Match whole word only	Select the check-box if you only want complete string matches, not partial matches.
Match case	Select the check-box if you only want matches which correspond according to upper-case and lower-case letters.
Search from top of document	Select the check-box to start the search from the top of the document, otherwise the search will start from the cursor position.
Direction	Choose whether to search upwards or downwards in the document.

Commands

Use the commands below to find more occurrences of a text string after you have found the first one:

- Press F3 to search for the next occurrence of the string or right-click and choose Find next.
- Right-click and choose **Find previous** to search for a previous occurrence.

General information about searches

- The default setting is to search in all result files or chromatograms. • User-entered search filters (to a maximum of 10) will be saved in the drop-down
- menus for both **Result** and **Chromatogram** selections. More than one string can be used as a search delimiter (insert ";" between strings), and search filters are automatically saved and stored within user profiles.
- Click All to return to the default setting to search in all result files or chromatograms.

	•
Introduction	There are different ways to get help and instructions in the UNICORN application:
	From the Help menu in each module
	From the context-sensitive help in each dialog box
	• By selecting the Online Manual from the Help menu
	• By pressing the <f1> key</f1>
	 By right-clicking an instruction in the Method Editor and selecting the What's This? menu item
The Help menu	From the Help menu in each module you can access the Help file.
	 From the Help menu of the UNICORN Manager module you can also access the installed manuals.
	The illustration below shows the Help menu of the UNICORN Manager module:
	Help



The Help file

The table below describes how to open and use the Help file:

Step	Action
1	Choose Help:Index .
	Result: The Help file is displayed
2	 Type a word you want help on in the text box in the left pane. <i>Result</i>: The closest matches are displayed in the list. Select a match and click the Display button. <i>Result</i>: The associated help text is displayed in the right pane.
3	 You can also click the Contents tab to view the contents of the Help file divided into sections. Click the plus signs to expand the tree structure. Click a topic to read the associated help text.

Manuals

When UNICORN was installed, the administrator selected which manuals to install. Therefore the available manuals may be different on your system than in the illustration below.

Note: Manuals can be added after the UNICORN installation. See the Administration and Technical manual for more information.

How to open a manual

To open a manual

• choose Help:Manuals in the UNICORN Manager module.

Result: The **Manuals** dialog box is opened.

M	anuals	×
1	Select a Manual and press OK.	
	 UNICORN Online User Manual AKTA oligopilot User Manual 18-1142-20 Getting Started UNICORN 4 oligo 18-1168-97AA2002-10 Installation Guide 18-1142-21 Making Your First Run 18-1142-23 Monitor pH_C-900 - User Manual 18-1120-06.ac Monitor UV-900 - User Manual 18-1120-05.ab Pump P-900 - User Manual 18-1120-04.ab Unicorn 4 oligo 18-1168-99AA2002-10 UNICORN 4-10 - Administration Manual 56-3207-98.aa Valve INV-907 - Instructions 56-8101-01.ac Valve IV-908, PV-908 - Instructions 56-8101-02.ac 	
,	OK Cancel <u>H</u> elp	

• Select the manual and click the **OK** button.

Note: Some manuals are only available in PDF format.

Context-sensitiveIn each dialog box there is a Help button. If you press that button, either of thehelpfollowing will be displayed:

- A message box with relevant information, for example the dialog box options.
- The Help file, with relevant information displayed in the right pane.

2.2.7 Snapshots

IntroductionA Snapshot provides information about a method run at a certain point in time. It
contains information about the values of all the variables at the selected point.Snapshot functionality is available in

- the **Method Editor**, where Snapshot instructions can be inserted in a method to be recorded during the method run.
- the **Evaluation** module, where you can take Snapshots from a result file using the Marker.
- the **System Control** module, where you can take Snapshots during a run using the Marker.

How to view recor-
ded SnapshotsThe table below describes how to view Snapshots which have been recorded during
a method run using the Snapshot text instruction.

Note: How to insert the **Snapshot** text instruction in a method is described in **5.3 How to use Text instructions** on page 90.

Step	Action
1	In the Evaluation module,
	choose View:Documentation
	or
	click the View Documentation icon.
	<i>Result</i> : the Documentation dialog box is displayed.
2	Select the Result Information tab.
	Select the Snapshots sub-tab.
	<i>Result</i> : The recorded Snapshot information for a chromatogram is displayed in a list.
3	You can
	• select other chromatograms in the Select chromatogram drop- down box.
	• select the Rows or Columns radio button to display each Snapshot as a row or a column.
	 select the Time or Volume radio button depending on which quantity you want as a base.

Step	Action
4	To print the Snapshot information
	click the Print button
	 select the Snapshot check box in the Print dialog box.
	• click OK .
5	Click OK (or the Cancel button) to exit the Documentation dialog box.

How to take Snapshots in the Evaluation module

How to take Snap- The table below describes how to take Snapshots in the Evaluation module:

Step	Action
1	 Open a result file in the Evaluation module. Right-click and select Marker in the menu. <i>Result</i>: A vertical line indicating a certain point is displayed.
2	Click the marker line and drag it to the desired point where you want to take a Snapshot.
3	Right-click and select Snapshot in the menu. <i>Result</i> : The Snapshot is displayed in the Snap Shot dialog box.
	Curve Retention Amplitude Unit 01: 02no297 001:1_UV1_350nm 2557.89 2713.00 mAU 02: 02no297 001:1_UV2_290nm 2557.89 3301.00 mAU Save to File Bint Close Help

Step	Action
4	• Click the Save to File button if you want to save the information as an Excel file (.xls) or a tabbed text file (.txt).
	 You can also copy the information to the clipboard:
	- Click and drag the mouse in the table to select the information you want to copy.
	- Press CTRL+C.
	The information can now be pasted in a text editor.
	Click the Print button if you want to print the information.
	Click the Close button.
5	Repeat steps 2 to 4 if you want to view more Snapshots.

How to view Snapshots during a method run

The table below describes how to view Snapshots in the **System Control** module during a method run:

Step	Action
1	A method is running and the System Control is displayed:
	• Right-click in the Curves pane and select Marker in the menu.
	<i>Result</i> : A vertical line is displayed.
2	Click the marker line and drag it to the desired point where you want to take a Snapshot.
3	Right-click in the Curves pane and select Snapshot in the menu. <i>Result</i> : The Snapshot is displayed in the Snap Shot dialog box.
	Curve Retention Amplitude Unit 01: 02no297 001:1_UV1_360nm 2557.89 2713.00 mAU 02: 02no297 001:1_UV2_290nm 2557.89 3301.00 mAU Save to File Bint Close Help

Step	Action
4	• Click the Save to File button if you want to save the information as an Excel file (.xls) or a tabbed text file (.txt).
	You can also copy the information to the clipboard:
	- Click and drag the mouse in the table to select the information you want to copy.
	- Press CTRL+C.
	The information can now be pasted in a text editor.
	Click the Print button if you want to print the information.
	Click the Close button.
5	Repeat steps 2 to 4 if you want to view more Snapshots.

2.3 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 assume that all installations were made according to the instructions, that the model system is used and is connected.

Quick Start in-
structionsThe table below describes the easiest way to create a Synthesis method, run the
Synthesis and generate a printed report. The instruction applies to the ÄKTA oligopilot
100 system and is based on an Instant Run.

Step	Action	
1	Click the Instant run icon in the UNICORN Manager module.	
	<i>Result</i> : 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.	
	<i>Note</i> : It is mandatory to select type of support and a Column .	
	Click Next to proceed through several pages.	
5	Select Print_SyntData_AKTA in the Evaluation procedures page.	
	<i>Result</i> : A printout will automatically be generated after the run.	
6	Click the Start button on the last page.	
	<i>Result</i> : 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.

3 General system operations

IntroductionThis chapter describes how to start the program, assign user properties and set up
the system.Refer to the Administration and Technical Manual for installation and network
configuration instructions.

In this chapter This chapter contains the following sections

Торіс	See
Log on routines and log off routines	3.1
How to create a new user	3.2
How to assign user properties	3.3
How to change your passwords and user attributes	3.4
How to connect to the oligo synthesis system	3.5
How to set up a printer	3.6

3.1 Log on routines and log off routines

IntroductionThis section describes how to start and quit the UNICORN program, and how to log
on and log off.

Username and
passwordNormally the system administrator defines the users and creates your first password.
The program can also be set up so you can log on without a password.
Note: The first time after UNICORN has been installed, you may need to log on as a
default user and create a user profile. This process is described in 3.2 How to create
a new user on page 51.

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 in Windows 2000	locate the program under Programs:Unicorn and click the UNICORN logo	
the Windows Start menu in Windows XP	locate the program under All programs:Unicorn and click the UNICORN logo	

How to log on	The table below describes how to log on to UNICORN.		
	Step Action		
	1	Select Tools:Logon in the UNICORN Manager module	
		or	
		• Click the Logon/Logoff icon in the UNICORN Manager module	
		▶ □	
		<i>Result</i> : the Logon dialog box is displayed.	
		<i>Note</i> : You do not have to perform this step if you start up UNICORN. When you start UNICORN the Logon dialog box is automatically displayed.	
	2	Select your username from the list.	
	3	Type your password (optional).	
	4	Click OK .	
The four program modules	The progra the UNICC Editor, the until you o UNICORN Note: If the not open.	am has four modules. When you start the program and log on you work in DRN Manager module. UNICORN also automatically opens the Method System Control and the Evaluation modules. These modules are minimized activate them. Up to four System Control module windows may open if was set up to control more than one system at the installation. e access rights are limited to only some modules, the other modules will	
Log off after you are finished	Always log changing to log off i • Select	g off when you leave the computer to prevent others from accidentally or deleting your files, or disturbing your UNICORN runs. There are two ways n the UNICORN Manager : Tools:Logoff	
	or • Click th	ne Logon/Logoff icon.	

▶]

Note: In case your access to the **UNICORN Manager** is restricted you will still be able to log off.

Processes can run The process will continue even if you log off while a synthesis run is in progress. You after log off can leave the process locked and set a password to protect it from interference. The table below describes how to log off and set a password for a running process.

		-
	Step	Action
	1	Select Tools:Logoff in the UNICORN Manager module.
		or Click the Logoff icon.
		Result: A confirmation box opens.
	2	Click Yes to confirm that you want to log off. <i>Result</i> : The Leave Control of system dialog box opens.
	3	Click the Locked radio button.
	4	Type a password in the Password text box.
	5	Click OK .
Unlocked Log off	It is not recommended that you log off and leave a running system unlocked. This means that the run is in progress without a user that is responsible for the process	
Automated work- station lock or logout	ated work- The system administrator may set an automatic workstation lock or log off after specified time for a user. If there are no keyboard entries or mouse movements with the time limit, the workstation will be locked or logged off.	
	Note: A loc	cked workstation can be activated again only by the previous user if the

regular log in password is entered. If another user wants to log on and use the workstation the previous user can be logged off without entering the correct password. The previous user's files will be closed and the new user will only have access to his own files. Automated logout will not happen while a MethodQueue or a Scouting scheme is operating.

How to log on and When you log on again after leaving the system locked with a process running or unlock the system after an automated workstation lock, you will be asked to unlock the system.

Step	Action
1	Log on to the system.
	<i>Result</i> : The System Unlock Confirmation dialog box opens.

Step	Action
2	Type your login password or the password that the system was locked with in the Password text box.
3	Click OK

Note: You can connect in view mode only without providing the password.

Systems lockedYou can unlock a system that has been locked by another user if you have the correctby other userspassword.

You may still be able to unlock a system even if you do not have the password. Any user with **Unlock locked systems** authorization can override another user's lock by entering his or her own logon password. However, it is recommended that this authorization is limited to only a few users.

How to quitUNICORN will still be open after you have logged off. To close the program you mustUNICORNlog in again and quit UNICORN (you cannot quit the program if you are not loggedin). The table below describes how to do this.

Step	Action	
1	Select the File:Quit Program menu command in the UNICORN Manager module.	
	or	
	• Click the close icon in the top right-hand corner of the program window.	
	<i>Result</i> : A confirmation box opens.	
2	Click Yes to confirm that you want to quit.	
3	A Warning opens if you have any unsaved data in the Method Editor or Evaluation module.	
	• Click Yes to continue to close the program. Your unsaved data will be lost when the program is closed.	
	Click No to return to the program and save your data.	
4	The Leave Control of system dialog box opens. Select the locked or unlocked option as in the logoff procedure.	
	Note: This step only happens when a system is connected.	
5	Click OK .	

Note: Do not shut down Windows 2000/XP or turn off the computer if you quit UNICORN with a separation run in progress. If you are performing a **MethodQueue run** you cannot quit the program at all.

In case your access to the **UNICORN Manager** is restricted you will still be able to quit the program.

3.2 How to create a new user

Introduction This section describes how to create a new user and assign a home folder for the user's methods and results.

Default user A default user is created when the system is installed. The default user has unrestricted access to all UNICORN functions. You log on with this profile when you access a newly installed system for the first time.

 Step
 Action

 1
 Select user default from the user drop-list.

 2
 Type password default if necessary.

 Note: The default user is the only user that is allowed to use the user name as password.

 3
 Click OK or press the Enter key.

The table below describes how to log on as the default user.

Logon		×
	ORN logon	
User name:		
default		•
Password:		

,		
ОК	Cancel	Help

Note: We recommend that the default user is deleted when regular user profiles are created.

How to open UserAll user administration is performed in the User Setup dialog box in the Main MenuSetupmodule. It is accessible only to authorized users (and the default user).

User Setup is found on the **Administration** menu.

• Choose Administration:User Setup.



The User Setup dialog box

The illustration below shows the **User Setup** dialog box.

Each user is assig different functions assigned to that g	ned to an access group. in UNICORN. When ch roup are affected.	This group defines access to anging a group, all users	Access groups
Jsers Name	Full name	Group	
🥥 default	default	Administrator	New
UPC-user	OPC-user	Administrator	<u>E</u> dit Delete <u>P</u> rint

How to create a new user

The table below describes how to create a new user.

Step	Action	
1	Click the New button in the User Setup dialog box.	
	<i>Result</i> : The Create New User dialog box opens.	
2	Enter a user name in the User name text box.	
3	Enter the full name of the user in the Full name text box.	
4	Enter the position of the user in the Position text box.	
5	Select or create a Home folder :	
	• Select a Drive and a folder from the Name drop-list and proceed to step 9.	
	or	
	• If you need to create a new home folder, proceed with step 6.	
6	Click New .	
	<i>Result</i> : the Create New Folder dialog box opens.	
7	Select a Drive and type a folder name.	
8	Click OK to create the folder and return to the Create New User dialog box.	
9	Click OK .	
	<i>Result</i> : The new user is created and added to the User Setup list.	
10	Click Close.	
	or	
	• Click the New button and repeat steps 1 - 8 to create more users.	

Home folders

Each user must be assigned to a home folder. The **Default** folder can be used if you do not want to assign an individual home folder.

Note: If you create a home folder on the C: (local) drive it will not be accessible from other computers. If you select a network, make sure that is addressed by the same drive letter from all computers in the network.

3.3 How to assign user properties

IntroductionA user is assigned properties that define password rules, and the folders,
chromatography and oligonucleotide systems that the user can access. This section
describes how to assign properties.

How to open UserThe user properties are defined in the User Setup dialog box in the UNICORN Managerpropertiesmodule. The table below describes how to open User Setup.

Step	Action	
1	Select Administration:User Setup.	
2	Select a user in the Users list.	
3	Click the Edit button. <i>Result</i> : The User properties dialog box opens.	

The **User properties** dialog box is used to edit the user definition and assign properties for passwords, folder and system access, and available manual instructions.

How to edit the user definition

The table below describes how to edit the user definition in the **User properties** dialog box.

Step	Action
1	Select the User item.
2	Select an access group from the Group drop-down box. <i>Note</i> : A pre-defined access group is assigned a certain level of access to UNICORN.
3	Select a folder from the Home folder drop-down box.
4	Click the check boxes to select Administrator Attributes .
5	Click OK to finalize or select another definition to edit.

How to edit theThe table below describes how to edit the attributes in the User Attributes windowuser attributespane.

Step	Action
1	Select the Attributes item.

Step	Action
2	Select applicable attribute items in the User Attributes pane:
	Use large toolbar icons
	Show unused variables
	Show variable details
	Default overwrite of baselines and peak tables
	Prompt for column before manual runs
3	Type which curve to display in the Quick view dialog box.
4	• Select a size definition and type a value for the Logbook mark height.
5	Click OK to finalize or select another definition to edit.

The Advanced dialog page

The **Advanced** window pane is used to define password policies for the user. Normally this is only used by the system administrator.

User properties	×
User properties Eric (Eric Lemming) User Attributes Advanced Password age V Expires in 90 Password uniqueness V Remember 5 Account lockout V After 3 Automatic workstation V Lock after Logoff after Signature Password Indexed Signature Password Indexed Signature Signatur	Aays passwords bad logons minutes
СК	Cancel Help

Note: This dialog page is only available if a required password was selected when the software was installed.

How to define ac- cess to folders	The Access dialog page is used to define the folders and systems that the user has access to. Click the check box for each selected folder and system.
and systems	Up to 20 folders can be set up to be shared. The user has access to all files and sub-folders in the selected folders. Only selected folders will be visible in the methods or results panels of the UNICORN Manager module.
	<i>Note</i> : All users should have access to the Failed folder on each local station in a network installation. This will ensure that users can access results that were saved in the Failed folder in case of a network communication error.
How to define available manual instructions	The Instructions dialog page is used to define the manual instructions and system sounds that are available to the user as well as which monitors the user is allowed to calibrate. Click the check box for each selected instruction, sound or monitor.
Access groups	The level of access to UNICORN functions for each user is determined by the Access group that the user is assigned to. The access authorizations can be edited for each group, normally by the systems administrator. Refer to the Technical and Administration Manual if you need to edit an Access group .
	<i>Note</i> : User access can be limited to only some UNICORN modules. If that is the case the unavailable modules will not be displayed. E.g. if the UNICORN Manager is unavailable you will only have access to a dialog box with the basic functions to change limited user attributes, passwords and to log out and quit the program.

3.4 How to change your passwords and user attributes

Introduction Every user can change his or her passwords and some user attributes even if user administration is handled exclusively by the system administrator. The changes are made in the **UNICORN Manager**.

How to change
passwordsThe table below describes how to change your logon and signature passwords.

Step	Action
1	Select Administration:Change Password . <i>Result</i> : The Change Password dialog box opens.
2	Type your old logon password in the Old text box. <i>Note</i> : Your passwords will only be shown as asterisks.
3	Type a new password in the New text box.
4	Repeat the new password exactly in the Confirm text box.
5	Repeat steps 2 to 4 in the Signature password section if necessary.
6	Click OK .

About passwords The list below is a summary of facts and advice about UNICORN passwords:

- The system can be set up to operate without required passwords.
- The minimum number of password characters is set up at installation.
- Passwords can be any combination of letters and numbers.
- Passwords are case sensitive.
- Avoid using obvious passwords, e.g. your username, your telephone number, etc.
- The settings in the **User properties** determine the expiration for a password. Change passwords regularly even if your user profile is set up without password expiration.

How to change	The table b	below describes how to change your user attributes.
	Step	Action
	1	Select Administration:Change User Attributes.
		<i>Result</i> : The Change user attributes dialog box opens.
		Change User Attributes Image: Change toolbar icons Image: Use large toolbar icons Show unused variables Image: Show variable details Show variable details Image: Default overwrite of baselines and peak tables Quick view curve Quick view curve 1 Fraction mark height 2 Injection mark height 50 Percent of window height Image: Percent of window height
		Logbook mark height 3 Character heights OK Cancel Help
	2	Dialog check box options
		The dialog check box options are described below:
		Use large toolbar icons
		Display large toolbar icons in all modules.
		Show unused variables
		Show variables that are not used in the method on the Variable page of the Start Protocol .
		Show variable details
		Show detailed method variables on the Variable page of the Start Protocol .
		Default overwrite of baselines and peak tables
		When new baselines and peak tables are created, the old ones are overwritten.
	3	Mark heights
		Select a size definition and type the height for the following marks:
		Fraction mark
		Injection mark
		Logbook mark
	4	Click OK.

3.5 How to connect to the oligo synthesis system

Introduction A computer can have up to four oligonucleotide systems connected at a time. This section describes how to connect to the systems, and different connection modes.

How to establishThe table below describes how to connect an oligonucleotide system that is locallya connectionconnected to your computer.

Step	Action
1	Open a System Control module.
	<i>Note</i> : Each UNICORN installation may have up to four System Control modules. The number of modules are selected when the software is installed.
2	Select the System:Connect menu command.
	or
	Click the Connect to system toolbar icon.
	<i>Result</i> : The System Connect dialog box opens.
3	Select the system you want to connect.
4	Click OK .

Remote connec-
tionsEach computer workstation may have up to fouroligonucleotide systems connected
locally. In a network installation you may connect a system that is physically
connected to another computer, the local station. Your system is then a remote
station.

The local station that is connected to the chromatography system must be logged on to the network and the UNICORN drivers must be running. However, the connection will work even if the UNICORN program is not running on the local station.

Network log on Ensure that your workstation is logged on to the network before you start an

oligonucleotide system that is directly connected to the station. You can operate a local system without logging on to the network, but there are several disadvantages to this:

- Files stored on network drives are not accessible.
- Changes made to global files, e.g. user settings files, will apply only locally and will be lost the next time you log on to the network.
- Result files that are directed to a network drive will be stored in the **Failed** folder on the local station.

Connection modes

Several workstations can connect to a singleoligonucleotide system at the same time but only one workstation can be in control mode. The other connections are in view mode and the connected workstations can only monitor the system activity, but not issue any commands.

The system status is indicated on the status bar at the bottom of the **System Control** window. The table below describes the different connection modes, the corresponding status texts and some of the various actions you can take to change the connection mode.

Connection mode	Status Text	Possible action to change connection mode
Not connected	Not Connected	Connect to a system.
Control mode.	Controlled By: default	Disconnect from or leave control of the system. (The system is controlled by you.)
View mode	Controlled By: Eric	No connection possible. (The system is controlled by another user.)
View mode	Locked By: Eric	Click the Connect to sys- tem icon and supply a password. (The system is locked by another user.)

Connection mode	Status Text	Possible action to change connection mode
View mode	System is available	Connect to the system. (The system has been left unlocked.)

trol of a system

How to leave con- The table below describes how to leave control of a system so that it is available to be controlled by other users.

Step	Action
1	Select System:Leave Control.
	or
	Click the Leave control of system icon.
	- Correction of the second sec
	Result: The Leave Control of system dialog box opens.
2	Click the radio buttons to select to leave the system unlocked or locked.
3	Enter a password (if the system is to be locked).
4	Click OK .

How to disconnect The table below describes how to disconnect from a system.

a system

Step	Action
1	Select System:Disconnect.
	or Click the Disconnect from system icon.

Step	Action
2	Result:
	If the system is in view mode
	the system is disconnected.
	If the system is in control mode
	• the Leave Control of System dialog box opens.
3	Select to leave the system locked or unlocked.
4	Click OK .
	Result: The system is disconnected.
Note: If yc be conne You can v Summarı The table systemth	au disconnect from a system in control mode and re-connect to it, you may cted in view mode. Another user may have taken control in the meantime iew and print a total summary of a selected system from the System Table dialog box. below describes how to view and print an information summary of a selected e systems:
Note: If yc be conne You can v Summary The table systemth Step	Action
Note: If yc be conne You can v Summary The table systemth Step 1	Action Choose Administration:System Setup in the UNICORN Manager. Result: The Sustem Setup dialog box is displayed:
Note: If yc be conne You can v Summary The table systemth Step 1	u disconnect from a system in control mode and re-connect to it, you may cted in view mode. Another user may have taken control in the meantime iew and print a total summary of a selected system from the System Table dialog box. below describes how to view and print an information summary of a selected e systems: Action Choose Administration:System Setup in the UNICORN Manager. Result: The System Setup dialog box is displayed: System Setup
Note: If yc be conne You can v Summary The table systemth Step 1	a disconnect from a system in control mode and re-connect to it, you may be taken in view mode. Another user may have taken control in the meantime diew and print a total summary of a selected system from the System Table dialog box. below describes how to view and print an information summary of a selected e systems: Action Choose Administration:System Setup in the UNICORN Manager. Result: The System Setup dialog box is displayed:

How to disconnect when quitting

How to view or print a system summary

Step	Action	
2	 Select the system you want a summary of. Click the Summary button. <i>Result</i>: The System Table Summary dialog box is displayed: 	
	System 1 The system is an oligo system. Control unit 1 at pipe (computer) SEUPPW000639 controls the system. Backup is taken every 5 minutes. Strategy in use: AKOP×100 Strategy is designed for the ÄKTA Oligo Pilot project, Standard configuration with pump head 2 Program and file versions: • Unicom V3.10 • Strategy Builder V2.51 • PH/C-900 V1.03 • Uviews V1.03 • Canserv.ini p2.303(1999-06-21) Developed by Mattias Berglund, APBiotech 2000 Components: Manual Valve Instructions, enabled UV, enabled	
3	 Click the Print button to print the information. Click the Close button to exit the dialog box. 	

3.6 How to set up a printer

Introduction UNICORN uses the default printer and printer settings that are installed on your computer. You can change your printer by changing the default Windows settings, but you can also set up a printer in UNICORN for the current working session.

How to set up a printer

The table below describes how to set up a printer in UNICORN.

Step	Action
1	Select the File:Printer Setup menu command in the UNICORN Manager module.
	Result. The Fint Setup didiog box opens.
2	Select a printer from the Name drop-down box.
3	Change all printer properties as necessary.
4	Click OK .

Note: To save created reports electronically you can select to print the files in PDF-format. To be able to do this you must have a full version of Adobe[™] Acrobat[™] installed and select PDF Writer or Distiller[™] in the **Printer Setup**.

4 Files and folders in UNICORN

Introduction All UNICORN data is organized in files and folders. Files and folders are handled like in any other Windows application, with some exceptions. This chapter describes how to work with UNICORN files and folders, with the focus on the topics that are specific for UNICORN.

In this chapter This chapter contains the following sections

Торіс	See
How to create folders	4.1
How to open and preview files	4.2
How to arrange and locate your files	4.3
How to copy, delete, rename and backup files and folders	4.4

4.1 How to create folders

Introduction This section describes how folders are organized in UNICORN and how to create a new user-specific folder for the user's methods and results.

UNICORN folders The files and folders are displayed in the two **UNICORN Manager** module windows.

- All method files and corresponding folders are listed in the **Methods** window.
- The result files and folders are listed in the **Results** window.
- You can only see folders that you have access to.
- You can only see method files that are written for systems that you have access to.

How to create a user-specific folder

The table below describes how to create a user-specific folder.

Step	Action
1	Select the window you want to create the folder in: Methods or Results .
	(<i>Result</i> : The window title bar is highlighted.)
2	Select File:New:Folder.
	or
	Right-click and select the New Folder shortcut.
	<i>Result</i> : The Create New Folder dialog box opens.
3	Type a name for the new folder.
4	Click OK .

4.2	How to	open and preview files	
Introduction	This sectio also previ	on describes how to open your saved method files and result files. You can ew your result files to identify the correct file before you open it.	
How to open a method file	You open window to	a method file in the UNICORN Manager module. Click the file in the Methods a select it and	
	 choose 	e File:Open.	
	or		
	 right-c 	lick the file and choose Open from the short-cut menu.	
	or		
	double-click the file.		
	<i>Result</i> : The file is opened for editing in the Method Editor module.		
	Note: A m	ethod file cannot be opened on two workstations simultaneously.	
How to open a result file in	You can open a result file in the UNICORN Manager module. Click the file in the Results window to select it and		
UNICORN Man-	• choose File:Open.		
ager	or		
	• right-c	lick the file and choose Open from the short-cut menu.	
	or		
	• double	-click the file.	
	Result: The	e file is opened for editing in the Evaluation module.	
How to open a result file in the	The table Evaluatio	below describes how to open a result file from the File Navigator in the n module.	
ule	Step	Action	
	1	Click the Files tab.	
	•	·	

Step	Action
2	Locate and double-click the result file Recent Runs Files Find X Example Result Example Result001 Example Result002 Example Result003 Example Result004 Example Result004
	Result: The result file opens.

Note: The **File Navigator** is opens by default in the **Evaluation** module. If it has been closed, select **View:File Navigator** in the **Evaluation** module.

Quick View Quick View is a preview function for result files to make it easier to select the correct result file.

You can preview the first curve in the first chromatogram. You can also select to view another curve as default by selecting another curve number in your **User Attributes** settings, see **3.4 How to change user attributes** on page 58.

Several files can be opened for comparison.

How to use Quick The table below describes how to preview result files in Quick View.

View

Step	Action
1	Select one or more result files in the Result window of the UNICORN Manager .

Step	Action	
2	 Choose File:Quick View. or Right-click and choose Quick View from the short-cut menu. 	
	Result: The Quick View dialog box opens. Quick View: c:\\Default\Example files\Example Result\Example Result002.res Example Result002:1_UV1_215nm	
3	• Click the Next and Previous buttons to move between the result files (if more than one is selected).	
	• Click the Open button when the right file is displayed.	
	<i>Result</i> : The result file that is displayed in the dialog box opens in the Evaluation module.	

4.3 How to arrange and locate your files

Introduction	This section describes how to arran workspace and how to locate files	ge the way the files are displayed in your UNICORN through a search.
Different view modes	You can choose how the files and windows. The options are the stan • Details • List • Large icons • Small icons.	folders are displayed in the UNICORN Manager dard Windows alternatives:
How to change the view mode	 If you want to change the view yo Select View and the option that or Right-click and select View and 	u either: : you want, the option that you want from the shortcut menu.
Sort order in de- tailed view	The files can be sorted in a differer view. The table below shows the o	nt order when a window is displayed in detailed ptions.
Sort order in de- tailed view	The files can be sorted in a differer view. The table below shows the operation Sorted by:	nt order when a window is displayed in detailed ptions. Order
Sort order in de- tailed view	The files can be sorted in a differer view. The table below shows the o Sorted by: Name	nt order when a window is displayed in detailed ptions. Order Alphabetical order or reverse alphabet- ical order.
Sort order in de- tailed view	The files can be sorted in a different view. The table below shows the operation of the source of th	nt order when a window is displayed in detailed ptions. Order Alphabetical order or reverse alphabet- ical order. Alphabetical order or reverse alphabet- ical order (Method window only).
Sort order in de- tailed view	The files can be sorted in a different view. The table below shows the operation of the solution of the soluti	nt order when a window is displayed in detailed ptions. Order Alphabetical order or reverse alphabet- ical order. Alphabetical order or reverse alphabet- ical order (Method window only). Smallest or largest files first.
Sort order in de- tailed view	The files can be sorted in a different view. The table below shows the operation of the solution of the soluti	Alphabetical order or reverse alphabetical order. Alphabetical order or reverse alphabetical order. Alphabetical order or reverse alphabetical order. Smallest or largest files first. Alphabetical order of file extension type.
Sort order in de- tailed view	The files can be sorted in a different view. The table below shows the or sorted by: Sorted by: Name System Size Type Modified	Int order when a window is displayed in detailed ptions.OrderAlphabetical order or reverse alphabet- ical order.Alphabetical order or reverse alphabet- ical order (Method window only).Smallest or largest files first.Alphabetical order of file extension type.Most recently modified files first.

How to change the sorting order

Select one of the methods below to change the sorting order:

orting order • Select View

• Select View:Sort and the option that you want,

or
• Right-click and select **Sort** and the option that you want from the short-cut menu.

or

• Click the column header for the option that you want to sort by (a second click on the same header will reverse the order).

Note: Only the currently active window is affected.

How to filter Method files

The files in the **Method** window can be filtered to show only methods for selected systems. You can also limit the displayed files by using standard Windows wildcard characters. The title bar of the **Method** window indicates if a filter has been activated.

The table below describes how to activate a filter.

Step	Action
1	Select View:Filter.
	or
	• Right-click and select Filter from the shortcut menu.
	<i>Result</i> : The Filter dialog box opens.
2	Click the check-boxes for the systems for which you want to show files.
3	Enter a file name specification (if necessary).
4	Click OK .

How to find files The table below describes how to perform a search for files.

Step	Action		
1	Click either the Methods or Results window and: Select the File:Find menu command. 		
	or		
	Right-click and select Find from the shortcut menu.		
	Result: The Find files dialog box opens.		
	Pind files michDefoult Ijomat Fgund ficking and like Ijomat		
	P Name Path File specification CCUECEADD CL. Volkak Lynk Rewittles Councestion CL. Volkak Lynk Rewittles Councestion CL. Volkak Question CL. Volkak CL. Volkak Question CL. Volkak Questin num CL. Volkak		
2	Add search criteria to the dialog box, for example:		
	• Type a name in the Name field.		
	• Select a file type from the Type drop-down box.		
	Select if the search should include subfolders.		
	Select date limits in the Date drop-down boxes.		
	• Type text strings to match Question or Answer texts.		
	Iype a variable name and, if desired, a value.		
	• Type a Batch ID .		
	<i>Note</i> : You can search for a sample ID provided the sample ID is defined as a variable.		
3	Click Find .		
	<i>Result</i> : The search results are listed in the Found folders and files field. The search is limites to either methods or results and to the folder (in- cluding its subfolders) that is currently displayed.		

Step	Action
4	Double-click a file in this list.
	<i>Result</i> : The dialog box is closed and the selected file is highlighted in the UNICORN Manager window.
	<i>Note</i> : If you click Close you will return to the UNICORN Manager win- dow with no file highlighted regardless if you have selected one in the dialog box or not.

How to copy, delete, rename and backup files and folders 4.4

Introduction UNICORN has some file and folder handling functions that are slightly different from the general Windows functions. This section focuses on the differences. *Note*: You need explicit authorization in your user profile to copy, move and delete files.

How to copy or move files and folders

There are some restrictions to how you can copy or move files and folders:

- Files and folders can only be copied or moved to folders that are specific to your user name.
- You can also copy files to and from the folders that you have access to on the network.
- Method files or folders cannot be copied to the **Results** window.
- Result files and folders cannot be copied to the **Methods** window. •

If you copy a folder you will also at the same time copy all files and folders that it contains. The table below describes how to copy files and folders.

Note: Follow the same steps but select **Move** to move files and folders.

Step	Action	
1	Select one or more files and folders in either the Methods or Results window of the UNICORN Manager .	
2	Select File:Copy.	
	or	
	Right-click and select Copy from the short-cut menu.	
	<i>Result</i> : The Copy dialog box is opened.	
3	Select a target folder or floppy disk drive.	
4	Click OK .	

to External

The function Copy Use the function **Copy to External** when you need to copy files and folders outside of your own user folders. Copy to External should be used specifically when you need:

- to copy a method to another system (the method can then be connected to the appropriate system),
- to copy to a floppy disk drive. (The files are automatically compressed into a zip-file. The file will also automatically be spanned across several disks if necessary.)

Action
Select the file you want to copy.
Select File:Copy to External.
or
• Right-click and select Copy to External from the shortcut menu.
Result: the Copy to External dialog box opens.
Select the destination drive and folder.
Click the Save button.
-

How to Copy to The table below describes how to use the function **Copu to External**. External

The function Copy

from External

The function **Copy from External** can be used to import files and folders:

- If the files were saved using the function **Copy to External** they will automatically be decompressed.
- Copied method files must be connected to the same type of system they originally were created for. This is part of the **Copy from External** procedure.
- Method files that have been copied in and connected are displayed in the designated folder in the **Methods** window.

How to use Copy from External

_

The table below describes how to use the function **Copy from External**.

Step	Action	
1	Select a destination folder in the Methods or the Results window.	
2	Select File:Copy from External.	
	or	
	Right-click and select Copy from External.	
	<i>Note</i> : Do not select a file icon.	
	Result: The Copy from External dialog box opens.	
3	Select the files you want to copy.	

Step	Action
4	Click Save .
	Result:
	• Result files are copied into the designated folder in the Results window.
	• If method files were selected, the Method-System Connection dialog box opens.

How to connect a method to a system. method to a system. Step

Step	Action		
1	Select a method and double-click a system.		
	Method - System Connection Method i file: System: Select a method file OK Cancel Help		
2			
2	Repeat step 1 until all methods are connected to a system.		
3	Click OK .		

How to renameThe table below describes how to rename files and folders in the Methods or Resultsfiles and folderswindows in the UNICORN Manager module.

Step	Action
1	Select the item that you want to rename.

Step	Action
2	Select File:Rename.
	or
	Right-click and select Rename from the shortcut menu.
	<i>Result</i> : The Rename dialog box opens.
3	Type a new name.
4	Click OK .

How to delete filesThe table below describes how to delete files and folders in the Methods or Resultsand folderswindows in the UNICORN Manager module.

Note: Home folders cannot be deleted this way.

Step	Action
1	Select the item that you want to delete.
2	 Select File:Delete. or Right-click and select Delete from the shortcut menu. or Press the Delete key.
3	Confirm the delete action in the confirmation dialog box

Backup security

rity Backup copies should be taken regularly to avoid data loss in the event of hard disk failure or accidental deletion. You can use the function **Copy to External** to save your files on the network server.

Note: GE Healthcare cannot accept responsibility for the replacement of method programs that were lost as a result of computer failure or other incidents.

5 How to create a method

Introduction Oligonucleotide synthesis runs are programmed as **Methods** in UNICORN. Before you can proceed with a synthesis run you need either to use an existing method or create a new method. This chapter describes how to create new methods. It also contains instructions for signing a method.

In this chapter This chapter contains the following sections

Торіс	
How to use the Method templates	5.1
How to create a Sequence	5.2
How to use Text instructions	5.3
How to sign the method	5.4

5.1 How to use the Method templates

IntroductionThis section describes how to create methods based on an existing template.Note: A custom system, for example a process system, requires that the users create
their own templates by saving methods as templates. Each method is written for a
specific strategy. The function of the method cannot be guaranteed on systems
having other strategies.

How to create aThe table below describes how to create a method in the UNICORN Manager module.new methodNote: The New Method dialog box is also accessible from the Method Editor module
using the same commands.

Step	Action	
1	Choose the File:New:Method menu command	
	or	
	click the New Method icon.	
	or	
	 right-click in the Methods window and select New:Method from the shortcut menu. 	
	<i>Result</i> : The New Method dialog box opens in the Method Editor module.	
2	Select Template in the Use field.	
	• Select the system for which you want to create the method.	
	Select Any from the Technique drop-down list.	
	Select a method template from the Template list.	
	Select Any as column from the For column list.	
	• Click OK .	
	<i>Result:</i> The method template will be opened as an untitled method in the Run Setup in the Method Editor .	

Note: Columns are not selected for oligonucleotide synthesis.

Method notes Click the Notes and then the Method Notes tabs in the Run Setup. The notes describe

important information about the template and how the system should be connected so that the method will work correctly.

Note: If your system does not correspond to the description on the **Method Notes** tab, either:

• rearrange the valves and tubing connections in accordance with the method notes description

or

• edit the method instructions in accordance with your system setup.

The Test Sequence Several of the templates contain a partially built method for a pre-defined 20 base sequence. This sequence can be used unmodified or be edited to create new methods. See **5.2 How to create a Sequence** on page 82 for more information on how to create and edit a sequence.

- Click the **Sequence** tab to display and edit the sequence as needed.
- Click the **Save Seq...** button to save the sequence in the sequence library only.
- Click the **Open Seq...** button to open a saved sequence.

The illustration below shows the **Sequence** tab with the default 20 base sequence:

Variables Notes Reference Curves Evaluation Procedures Method Information Start Protocol Sequence Questions Result Name
Sequence name: TEST-20 from Standard Amidite Valve 1 pos, Trityl-OFF. (QZ)
© DNA © S © Modified © ENA © Q © Sjandard
5' ATA CCO ATT AAG COA AGT TT 3'
Optional method steps
I Pyrge amidite
✓ Puige solvents
✓ Column wash
Final dehitylation
I DEA Treatment
Create Method Open Seq Save Seq Delete Seg Cross References

Note: The synthesis reaction proceeds from 3' to 5'. The 3' base position is always the first base on the solid support before the start of the synthesis procedure.

 How to save the new method
 The table below describes how to create and save a new method.

Step	Action	
1	Click the Create Method button.	
	<i>Result</i> : The Save As dialog box opens.	
2	• If required, save the method in a folder other than the default home folder.	
	• Enter a Method name for the method. The total path can be up to 256 characters long. The method name must be unique for the chosen system within the folder.	
3	 If you have more than one system connected to the computer, choose the System for which the method is intended. The method can be run on any system that uses the same strategy. Remember that different systems may have different configurations and control capabilities. Click OK. 	
	<i>Result</i> : The method is saved, but remains open in the Method Editor , so that you can continue editing if you wish.	

Note: You might want to sign your method. If you do so, you can choose to lock the method so that nobody will be able to change the method. See **5.4 How to sign the method** on page 91 for further instructions.

5.2 How to create a Sequence

Introduction

This section describes how to create a sequence and use it to create a method.

• You can create a new sequence by editing the default 20 base sequence in the **Sequence** tab when you create a new method based on a template.

or

• You can open a saved method and edit the sequence in the **Run Setup Sequence Editor**.

or

• You can open the **Sequence Editor** in the **Run Setup** in the **Method Editor** module and create a new sequence.

How to open theThe table below describes how to open the Sequence Editor in the Run Setup in theSequence EditorMethod Editor module.

Step	Action	
1	Choose the Method Editor module	
2	Click the Run Setup icon.	
	Case of the second s	

Note: If a method already is open in the **Method Editor** it will be displayed in the **Run Setup**.

 How create the
 The table below describes how to create a new sequence in the Sequence Editor.

 new sequence
 I

Step	Action
1	Use the radio buttons to select the base type for the first position:
	DNA or RNA
	 Oxidated (-O) or thiolated (-S)
	 From the Standard or Modified reagent position
	<i>Note</i> : The sequence is entered from 5' to 3'. See table below for possible combinations and how this is displayed in the Sequence Editor .
	Iype the first position base.
2	 Repeat step 1 for the subsequent positions as needed.
	Note: A maximum of 200 bases can be entered.
3	• Click the Group button if you want the sequence to be displayed in groups of three bases, beginning from the 5' end.
4	Click the Save Seq button.
	<i>Result</i> : The Save Sequence dialog box opens.
	• Type a name for the sequence in the Sequence name text box.
	• Click OK .
	<i>Result</i> : The sequence is saved and available in the Sequence list .
	<i>Note</i> : The saved sequence is only available to the current user. User logged in with other user names will not be able to display this sequence.

Note: The synthesis reaction proceeds from 3' to 5'. The 3' base position is always the first base on the solid support. This base should be taken from the standard position and should be oxidated.

How to create a new method from the sequence

You can now proceed to create a method using the new sequence. The table below describes how to create the method in the **Run Setup**.

Step	Action
1	• Select Optional method steps as needed in the Sequence Editor .
2	 Select the other tabs in the Run Setup and add information as needed.

Step	Action
3	• Select the Sequence tab again and click the Create Method but- ton.
	<i>Result</i> : The Save As dialog box opens.
	• Type a name for the method in the Method name text box.
	• Click OK .
	<i>Result</i> : The method is saved.

Note: You might want to sign your method. If you do so, you can choose to lock the method so that nobody else will be able to change the method. See section **5.4 How to sign the method** on page 91 for further instructions.

The available base combinations

The table below describes the base combinations that are available in the **Sequence Editor** and how they are displayed.

Note: There are four extra reagent positions available in **ÄKTA OligoPilot**. They are labelled **X**, **Y**, **Z** and **Q**.

Radio button combinations	Bases as represented on the screen
DNA, -O (oxidated), Standard	5 ACGTXYZQ
DNA, -O (oxidated), Modified	5' ACGT
DNA, -S (thiolated), Standard	5 ACGIXYZQ
DNA, -S (thiolated), Modified	
RNA, -O (oxidated), Standard	5´acguxyzq
RNA, -O (oxidated), Modified	5 बटेव्रेच
RNA, -S (thiolated), Standard	5

Radio button combinations	Bases as represented on the screen
RNA, -S (thiolated), Modified	5' <u>acgu</u>

The table below describes how to display and edit the cross references in the

How to edit the sequence cross references

Sequence Editor.

Step	Action
1	Click the Cross References button. Result: The Cross References List dialog box opens. Cross Reference List Coupling Purge Solvent Purge Amidite Column wash Final detrilylation DEA Treatment Result Res
	Image: Add_ONA_A 2 A Add_SDNA_A 3 A Add_DNA_A_v2 4 A Add_DNA_A_v2 5 C Add_DNA_C 7 C Add_DNA_C_v2 8 C Add_DNA_C_v2 9 G Add_DNA_C_v2 10 Q Add_DNA_G 11 G Add_DNA_G v2 12 G Add_DNA_G v2 13 T Add_DNA_G v2 W Image: Note that the second sec
2	Edit the cross references as needed: • Choose the block you want to edit
	 Click the down arrow beside the Block droplist and select a block name. Click the Insert button.
	<i>Result</i> : The block is changed to the selected block name.
3	Repeat step 2 to change other cross references as needed.Click OK.
	Result: The Cross References List dialog box closes.

Sequence options There are optional sequence settings that can be selected in the **Options** dialog box in the UNICORN Manager.

• Select Administration:Options to open the Options dialog box.

The illustration below shows the **Options** dialog box.

Options	×
Global	ı mode
Evaluation Asymmetry Ratio at 10 0 · 100 (% of peak Resolution algorithm 3	height)
Oligo Start message Sequence check Sequence paste	
OPC Cup Logon/Logoff security All Users Take Control	HDA Memory cache limit 0 HDA File cache limit 10
HDA File cache path TEMP	Browse
ОКЪ	Cancel Help

The table below describes the Oligo options:

Option	Explanation	
Start message	Enable sequence verification messages and pause before start of method run.	
Sequence check	 Enable check if the sequence is using two different bases from the same physical position if the base used in the 3' is allowed. 	
Sequence paste	Enable sequence copy and paste in the Sequence tab.	

5.5	How to use Text Instructions			
Introduction	You can use the Text Instructions editor in the Method Editor to build your method step by step. You can also use the Sequence Editor to create a method.			
	Advanced Instruction to edit me	editing facilities are available when you work directly in the Text ns editor. This section is a very brief description of this process. See 6 How thods on page 92 for detailed instructions.		
	<i>Note:</i> Each method is written for a specific strategy. The function of the method cannot be guaranteed on systems having other strategies.			
When do I use	Use Text Ir	nstructions when you want:		
Text Instructions?	• to change selected instructions in the method, for example the outlet valve position			
	 to add blocks or instructions, for example Watch instructions 			
	• to change method instructions to adapt to non-standard system configurations			
	• to creat	e new methods for applications not covered by the supplied templates.		
How to edit Text	Open the T	ext Instructions editor by following the steps in the table below.		
	Step	Action		
	1	Select the Method Editor module and click the Text Instructions icon.		
	2	Click the Customise Panes icon and select Text and Instruction Box.		
		• Click OK .		

How to use Text instructions 5 7

Step	Action		
3	Select instructions in the Instruction box in the lower part of the Method Editor , and use the Insert , Change , Replace or Delete buttons. All text entries are shown in the Text pane. Applicable variables can be edited for each selection. The illustration below shows the Instruction box :		
	Biskport Influctions Amote Parameters Bass Var Parameters Parameters Var Parameters Parameters Var Parameters Var Parameters Var Parameters Parameters Var V		

Instructions can be organized in blocks

Individual text instructions can be grouped in blocks of instructions (marked by blue square symbols) for a specific functional use, e.g. **Column Wash**, **Oxidation**, **Coupling** etc. A block may contain other blocks or individual instructions.

This is an example of text instructions in the **Text** pane:



Note: A block is only shown once even if it is used more than once in the method.

How to save the
new methodA new method is untitled, and must be saved under a method name before it can be
used.

The table below describes how to save a new method.

Step	Action
1	Click the Save Method toolbar or choose File:Save .

	Step	Action		
2		• If required, save the method in a folder other than the default home folder.		
		• Enter a Method name for the method. The total path can be up to 256 characters long. The method name must be unique for the chosen system within the folder.		
	3	 If you have more than one system connected to the computer, choose the System for which the method is intended. The method can be run on any system that uses the same strategy. Remember that different systems may have different configurations and control capabilities. Click OK. 		
		<i>Result:</i> The method is saved, but remains open in the Method Editor , so that you can continue editing if you wish.		
	Note: You r method so method or	2: You might want to sign your method. If you do so, you can choose to lock the hod so that nobody will be able to change the method. See 5.4 How to sign the hod on page 91 for further instructions.		
How to displayA dedicated strategy is available for each system in the ÄKTAdesigndescriptions of in- structionsAlthough the majority of the instructions are general, some of them of between the individual strategies.		d strategy is available for each system in the ÄKTAdesign platform. ne majority of the instructions are general, some of them differ slightly ne individual strategies.		
	The list below describes two ways to display descriptions of the instructions in yo particular strategy:			
	 Select the instruction in the Instruction Box of the Method Editor and press <f1:< li=""> or Right-click the instruction in the Text pane and choose the menu option What's This? </f1:<>			
How to print de- scriptions of in- structions	• The table below describes how to print descriptions of the instructions in your particular strategy:			
311 4010113	Step	Action		
	1	Select File:Print in the Method Editor.		
 Select the Instruction set option to print the full set of Click OK. 		 Select the Instruction set option to print the full set of instructions. Click OK. 		

How to add a Snapshot

The **Snapshot** instruction can be used to record the curve values at a specific point in the method run. The values are recorded in the result file and can be viewed in the **Snapshots** tab of the **Documentation** dialog box (See **9.7 Run documentation** on page 253). Up to 500 snapshots can be recorded in each result file. The table below describes how to add a snapshot instruction to a method:

Step	Action
1	• In the Text pane, select the instruction immediately before the po- sition where you want to insert the Snapshot instruction.
2	 Select Other in the Instructions field of the Instructions box. Select Snapshot in the instructions list.
3	Type a name in the Name text box in the Parameters field. Click the Insert button.

Note: Snapshots can also be taken in the **System Control** and **Evaluation** modules. However, these snapshots will only record the data for a specific moment. For more information about the **Snapshot** function see **2.2.7 Snapshots** on page 39.

5.4 How to sign the method

Instruction If you sign the method, you can choose to lock it so that nobody will be able to change it.

Step	Action		
1	Choose File:Sign Method in the Method Editor.		
	<i>Result</i> : The Sign the Method dialog box is displayed.		
2	Click the Signing tab and do the following:		
	• Select a user in the User drop-down list box. In most instances, you will want to use the current user shown on the list.		
	 In the Meaning field, provide a short text description explaining the meaning behind the signature (for example "Method now fully tested and approved"). 		
	• Type your signature password in the Password field. If desired, select the Lock box to lock the method permanently from further changes by other users.		
	 If needed, view a list of all signatures associated with the current method on the View Signatures tab. 		
	Click OK on either the Signing or View Signatures tab.		

The table below describes how to sign the method.

6 How to edit methods

Introduction

This chapter describes the complete facilities for editing methods in UNICORN. For many applications, suitable methods can be created by changing the sequence and create a new method from the template methods supplied with the system.

Use the more advanced editing facilities described here when you want

- to change selected instructions in the method, for example, change the outlet valve position
- to add blocks and instructions
- to change method instructions to adapt to non-standard system configurations.

In this chapter

This chapter contains the following sections

Торіс		
The Method Editor interface	6.1	
Method blocks	6.2	
Method instructions	6.3	
How to use method variables	6.4	
Run Setup		
How to use selected method instructions		
Standard Watch conditions		
How to save or delete a method template	6.8	
How to print a method		
How to export a method		

6.1 The Method Editor interface

IntroductionThis section contains a general description of the Method Editor user interface and
the editing operations that can be performed in the different parts of the module.

In this section This section contains the following sub-sections

Торіс	See
Method Editor module	6.1.1
Text Instructions editor	6.1.2

6.1.1	Method Editor module		
Two modes	The Method Editor interfa	ce operates in two modes:	
	Text Instructions edito Text Instructions edito	r for entering and editing method instructions (see 6.1.2 or on page 95)	
	• Run Setup for defining	method properties (see 6.5 Run Setup on page 122).	
How to open the The table below describe Method Editor		how to open the dialog boxes in the Method Editor :	
dialog boxes	If you want to open	then	
	the Text Instructions	click the Text Instructions icon.	
	editor		
		or	
		choose View:Text Instructions.	
	the Run Setup	click the Run Setup icon.	
		or	
		choose View:Run Setup.	
	the Log Format	click the Log Format icon.	
		or	
		choose View:Log Format.	

6.1.2 Text Instructions editor

How to select panes to be displayed

You have a choice of four panes that can be open together with the **Instruction box** in the **Text Instructions** editor, all at once or one at a time.

Follow the steps in this table to select the panes to be displayed:

Step	Action
1	In the Method Editor, choose View:Text Instructions
	or
	click the Text Instructions icon.
2	Choose View:Panes:Customize (or select additional panes here)
	or
	click the Customize Panes icon.
3	Select panes
	• Select panes in the dialog box and click the OK button.
	Customise Panes
	Deselect panes Deselect panes in the Customize Panes dialog box and click the
	OK button.
	or
	• right-click a window and select Hide .

formed in the dif- ferent panes	The pane	ls used	See section	
operations per-	panes:			

The pane	Is used	See section
Text	 to display and hide block instructions. 	6.2.1 How to view meth- od blocks on page 98
	 to select current in- struction. 	6.3 Method instructions on page 110
	• to cut, copy and paste instructions.	
	• to move instructions within a breakpoint.	
Flow scheme	 for information only. This window is not updated according to system status and changes in the meth- od. 	8.2.4 The Flow Scheme pane on page 187
Instruction box	 to specify break- points, instructions, parameters and vari- ables. to insert, change and 	6.3.2 How to add meth- od instructions on page 112
	delete instructions.	
Block	to select or display blocks.	6.2 Method blocks on page 97

Introduction This section contains a description of how to organize a method in blocks of instructions in order to make it more structured, and of how to work with method blocks.

In this section This section contains the following sub-sections

Торіс	See
How to view method blocks	6.2.1
How to call method blocks	6.2.2
How to add method blocks	6.2.3
How to delete method blocks	6.2.4
How to rename method blocks	6.2.5
How to find, copy and move method blocks	6.2.6
How to import method blocks	6.2.7

6.2.1 How to view method blocks

Instructions can	To view a method as a long list of individual text instructions can be confusing and		
be grouped into	inconvenient. Text instructions can therefore be grouped into blocks of instructions		
blocks	that define a specific functional use. For example, one block might contain the		
	instructions necessary to wash a column, and another block contains instructions		
	to do a Detritylation, etc.		

The Text pane

In the **Text** pane of the **Method Editor**, the method is shown as a list of blocks, denoted by the blue square symbols. Note that a block can also contain sub-blocks.

The figure below shows the text instructions in blocks:

()	1ain)	
-	0.00	Base CV, (6.3)#Column_Volume {ml}, Any
-	0.00	Message "Fill your column with DNA-T support", Screen, "No sound"
-	0.00	Message "Press CONTINUE when ready", Screen, "No sound"
-	0.00	Pause -1.0
	0.00	Base_Id _dT
Ē.	0.00	Block START_parameters
Ē.	0.00	Block Purge_G
Ē.	0.00	Block Purge_C
Ē.	0.00	Block Purge_T_U
	0.00	Block Purge_A
Ē- ا	0.00	Block Purge_Tetrazole
•	0.00	Block Purge_solvents_ox
•	0.00	Block Column_wash
	0.00	Block AddDNA_T
	··· (A	ddDNA_T)
	. 0.	00 Base Time
	0.	00 Set_mark '''' T ''''
E	0.	10 Block Detritylation
E	0.	20 Block Detrit_wash
	··· 0.	20 Base_Id _dT
E	0.	25 Block Coupling_Recycle_DNA_T
E	0.	30 Block Oxidation_DNA
E	J 🗌 O.	35 Block Capping_DNA
÷.	0.00	Block AddDNA_T
tit 🗖	0.00	Plack Add DNA C

The table below describes how to view or hide the instructions:

lf you want	then
to view the instructions	click the "+" symbol
	or
	double-click the block name.
to hide the instructions	click the "-" symbol
	or
	double-click the block name.

0.2.2	Ηοώ το call method blocks	
General descrip- tion	To execute the instructions contained within a block in a method, the block must be called by the program. When a block is called, the instructions in the block are executed in the order that they are written until the block is finished or the End_Block instruction is executed. Any settings made in a block are valid throughout the method until the settings are changed.	
Types of calls	There are two types of calls:	
	 Unconditional calls, which are made with a Block instruction. 	
	• Conditional calls, which are made with a Watch instruction. This makes it possible to call a specified block or an instruction when a particular monitor signal meets a given condition. As long as the condition is not met, the block is not activated.	
Watch instruc- tions	Watch instructions are indicated by a green line that show the start and duration of the watch. These instructions can use various conditions to respond to absolute signal values or to rate of signal changes.	
	The breakpoint when the Watch instruction is issued determines when the watch begins, not when the block is activated. Once set, a watch remains active until the condition is met or a new Watch instruction is issued for the same monitor. The watch is cancelled automatically when the condition is met. A watch can also be turned off with the Watch_off instruction.	

6.2.2 How to call method blocks

6.2.3 How to add method blocks

Two ways to add	You can add method blocks to a method in two ways, using either			
method blocks	• the Instruction box of the Text Instructions editor,			

or

• the **New Block** dialog box reached via the **New Block** icon.

Both these alternatives are described below.

How to add blocks with the Instruction box

How to add blocks The table below describes how to add blocks with the Instruction box:

Step	Action	
1	In the Text pane of the Text Instructions editor, select the instruction or block that you want to precede the new block.	
2	Select Other:Block in the Instruction box .	
3	 Enter a name for the block in the Block field. Click the Insert button. <i>Result:</i> The block is inserted after the block that was selected in step 1. 	

The New Block dialog box

The illustration below shows the **New Block** dialog box that can be used when adding new method blocks:

New Block
Name:
Base © Same as main © Iime © ⊻olume
© <u>C</u> olumn volume 0.10 ml
Length Length: 0.00 CV
Call
Erom: Main
<u>At</u> 0.00 CV
OK Cancel Help

with the New Block dialog box

How to add blocks The table below describes how to add blocks with the menu options of the New Block dialog box:

Step	Action		
1	Choose Block:New in the Method Editor		
	or		
	click the New Block icon.		
	Result: The New Block dialog box is displayed.		
2	Enter the relevant information in the New Block dialog box, and click OK .		
	<i>Result:</i> The new block is added to the method, and placed last of all blocks.		
	<i>Note</i> : The block can be placed in other positions by selecting something other than Main in the From droplist.		

The fields of the New Block dialog	The table below describes the fields of the New Block dialog box:		
box	Field	Description	
	Name	Block names can be up to 30 characters long, and can contain letters (A-Z), digits (0-9) and the underscore character.	
Block names must be unique within the meth retained but not significant (the names Colu COLUMN_WASH are treated as identical).		Block names must be unique within the method. The case of letters is retained but not significant (the names Column_Wash and COLUMN_WASH are treated as identical).	
	Base	One of the following options can be selected:	
		• SameAsMain : the new block will inherit the base from the Main block in the method. The corresponding Base instruction will be inserted in the block at breakpoint 0.	
		• Time: The block will be based on time.	
		• Volume : The block will be based on volume.	
		• Column volume : The block will be based on column volume.	
	Length	A block continues until the breakpoint for the End_Block instruction has been reached.	
		An End_Block instruction will automatically be inserted in the block at the defined breakpoint. This field must not be left blank.	

Field	Description		
Call	You can call the new block from an existing block (for example the Main block).		
	Select values in the two fields:		
	• From		
	The block from which the newly created block should be called.		
• At The breakpoint at which the call is to be made.			
			If you do not want to call the block (for example when the block being created is to be activated by a Watch instruction), choose the <un-used></un-used> line from the From drop-down list. Blocks using this line are placed last in the method in the Unused category.
	<i>Note</i> : You should not call a block from within itself. If you do, you will generate a potentially infinite loop that exceeds the maximum number of calls allowed in a method. A loop symbol is displayed at the beginning of the line if this occurs.		

0.2.4	 How to delete method blocks There are four ways to remove blocks from a method: To right-click a block and choose Delete from the shortcut menu To select a block and click Delete in the Instruction box To select a block and press the <delete> key on the keyboard</delete> To select a block and use the Block:Delete Block command Note: When you use the first three ways the block is only moved to the Unused section. 		
Four ways to de- lete blocks Delete options			
	Delete option Effect • Block:Delete Block command The block is totally removed from the method. If the block is called several times in the method, all the blocks will be deleted. Blocks deleted in this fashion		
	 Shortcut menu De- lete command Instruction box De- lete button <delete> key</delete> 	The block is deleted from the method and transferred to the Unused section. If the block is called several times in the method, however, only the row with the block currently marked in the Text pane will be deleted. In this case, the block will not be placed in the Unused section (since the block is still used in the method). Blocks deleted in this fashion can be called again in the method.	

How to delete method blocks 624

 How to use the
 The table below describes how to delete a block using the Block:Delete Block

 Block:Delete Block
 command:

Step	Action
1	Select the menu command Block:Delete Block in the Method Editor. Result: The Delete Block dialog box is displayed with all blocks listed in alphabetical order. Delete Block Select the block(s) to delete: Add_DNA_C_v2 Add_DNA_G_v2 Add_DNA_G_v2 Add_DNA_T Add_DNA_T Add_DNA_Y Add_DNA_Y Add_DNA_Y Add_DNA_Z_v3_4 Add_DNA_Z_v3_4 Add_RNA_a_v2 Add_RNA_A_A Add_RNA_A_A Add_RN
2	Select the blocks you want to delete and click OK .
3	Click Yes to confirm.

How to delete un- The table below describes how to delete an unused method block.

used blocks

Step	Action
1	Highlight the method block.
	Press the <delete> key</delete>
	or
	Right-click and choose Delete on the shortcut menu.
	<i>Result</i> : The Delete Block dialog box opens. Note that the Move button is not available.
2	Click the Delete button.
	<i>Result</i> : The unused block is deleted and cannot be called upon again in the method.

6.2.5 How to rename method blocks

Instruction

The table below describes how to rename blocks:

Step	Action
1	Right-click the block you want to rename in the Text pane and select Rename . Result: The Rename Block dialog box is displayed. Rename Block Select the block to rename: Coupling_Recycle_RNA_z_v3_4 Coupling_Recycle_RNA_z_v3_4 Coupling_Recycle_RNA_z_v3_4 Detrit_peak_start_UV Detrit_wash Detrit_wash Detrit_wash Dw_push Dw_push_Atart_UV Detrit_wash Dw_push_Atart_UV Detrit_wash Dw_push_Atart_UV Detrit_wash Dw_push_Atart_UV Purge_Av2 Purge_Av2 Purge_V2 Mew name: Receive Close Help
	<i>Note:</i> By default, the block that is currently selected in the Text window is automatically selected in the dialog box.
2	Enter the new name in the New name field and click Rename .
3	 If needed, repeat step 3 for other blocks. Click Close. Note: If the block you renamed is called in a Block or Watch instruction, the block name in these instructions will be changed automaticallu.

6.2.6 How to find, copy and move method blocks

Introduction By using the **Edit** options in the **Method Editor**, you can find, copy and paste and move blocks within a method.

How to find text strings in the method text

The table describes how to find text strings in the method text.
--

Step	Action
1	Choose Edit:Find in the Method Editor,
	or
	right-click an instruction or a block in the Text window and select Find .
	Result: The Find dialog box is displayed.
	Find X Find what: OK Match whole word only Direction Match gase Qp Search from top of document Down
2	 Enter the text you want to search for, search direction and case matching criteria. Click OK.

How to copy and The table describes how to copy a block.

Step	Action	
1	Right-click the block you want to copy.	
	Choose Copy.	
2	• Right-click the instruction line just above the point where you want the block to be pasted.	
	Choose Paste .	
	<i>Result:</i> A dialog box asks if you wish to rename the pasted block.	
3	Click Yes to rename the block before insertion, or No to insert the copied block directly.	
	<i>Result:</i> The pasted block is inserted with the same breakpoint value as the block or instruction selected for point of insertion.	
How to move a block	The table describes how to move a block.	
------------------------	--	--
	Step	Action
	1	Right-click the block you want to move.Choose Cut.
	2	 Right-click the instruction line just above the point where you want the block to be pasted. Choose Paste.
		<i>Result</i> : The block is now removed from its original breakpoint and pasted at the new breakpoint. The pasted block is inserted with the same breakpoint value as the block or instruction selected for point of insertion.

6.2.7 How to import method blocks

Introduction You can import method blocks from other method files. You can also use this function to copy blocks within a method. In the latter case, it is important to note that it is the *saved* version of the method that will be copied, not changes that have been made after you last saved the method.

The block is imported exactly as it appears in the source method. If the base of the imported block is defined as **SameAsMain**, the block will inherit the main base in the new method, regardless of the base in the source method. Also, the imported block is inserted with the same breakpoint value as the block selected for point of insertion.

Instruction

The table below describes how to import method blocks:

Step	Action
1	Choose Block:Import Block As in the Method Editor. Result: The Import Block dialog box is displayed.
2	 Select the method from which you want to import a block. Select the block. <i>Result:</i> The name of the selected block is displayed in the Block name field.

Step	Action
3	In the Call field, do the following:
	• On the From drop-down list, select a block into which the block will be imported.
	• In the At field, select the breakpoint value for the block to be impor- ted.
	Click the Import button.
	<i>Note</i> : The imported block cannot have the same name as an existing block in the method. If the default name is not allowed for this reason, the Import button will be gray and locked. If this occurs, change the name of the imported block so that the Import button becomes available.
4	 Repeat steps 2 and 3 if needed. Click the Close button.

6.3 Method instructions

Introduction This section describes how to work with the individual method instructions, in order to edit method blocks and methods.

In this section This section contains the following sub-sections

Торіс	See
How to read method instructions	6.3.1
How to add method instructions	6.3.2
How to delete method instructions	6.3.3
How to change or move method instructions	

6.3.1 How to read method instructions

struction markings

Description of in- Method instructions are displayed in the **Text** pane of the **Text Instructions Editor**. The table below explains the meaning of the markings:

Marking	Explanation
Blue square beside text	Valid call instructions, that is, Block and Watch instruc- tions to other blocks in the method.
Blue square with a red cross	Call instruction that contains one or more invalid in- structions.
Bold text	Valid instructions.
Red dot	Instructions with invalid syntax. All such instructions must be deleted or changed before a method can be run. See 6.3.4 How to change or move method instruc- tions on page 115.
	The instructions may be of the following types:
	• Calls to blocks which are not defined in the method
	 Instructions that apply to a different system strategy (can occur if a method is written for one system and saved for another)
	 Instructions for components that have not been selected in the System Setup.
Normal text	Instructions that will not be executed because
	 they are positioned after the end of a block or method or they constitute a block to which there is no call.
Text with a loop symbol	When a block is called from within itself this will gener- ate a potentially infinite loop, which might exceed the maximum number of calls allowed in a method.

6.3.2 How to add method instructions

Instruction

The table below describes how to add a method instruction in the **Text Instructions Editor**:

Step	Action
1	Select a block in the Text pane, and display the instructions within the block.
2	Select an instruction line in the block. Make sure that the selected in- struction line is in the block, not the call to the block.
3	 Open the Instruction box if it is not already displayed (View: Panes). Do the following: Set the desired breakpoint in the Breakpoint field. Choose the instruction type and the instruction in the Instructions field. For basic help on each instruction, click the instruction and press <f1>.</f1> Type values for instruction parameters in the Parameters fields. If a scroll bar appears at the right side of the Parameters field, additional parameters are required.
4	 Click the Insert button. <i>Result:</i> The instruction will be inserted in the block at the position of the breakpoint of the new instruction, if there are no other instructions at that breakpoint immediately after the currently highlighted instruction, if the highlight is at the same breakpoint as the new instruction as the last instruction at the breakpoint, if there are several instructions at the same breakpoint and none of these is highlighted. <i>Note:</i> Instructions that are placed at the same breakpoint are executed simultaneously, with the exception of Block instructions which are executed in the sequence in which they are written.

Pause, Hold and
Hold_until instructIf you use ÄKTA systems, the Pause, Hold, and Hold_until instructions will stop
execution at this breakpoint, that is, instructions following after Pause, Hold and
Hold_until at the same breakpoint will not be executed until a Continue instruction
is issued.

6.3.3 How to delete method instructions

Instruction

The table below describes how to delete method instructions in the **Text Instructions Editor**:

Step	Action
1	Select the instruction in the Text pane.
2	Use one of the following alternatives:
	• Right-click the instruction and choose Delete in the displayed menu,
	or
	 press the Delete button in the Instruction box,
	or
	• press the Delete key on your keyboard.

End_Block instruction

If you delete the **End_Block** instruction, the block will end at the last instruction in the block.

How to suspend
execution tempor-An instruction that has been deleted can only be recovered by re-inserting the
instruction. If you want to suspend execution of an instruction temporarily (for example
during development work), you can replace the breakpoint with a value after the
End_Block or End_Method instruction.

6.3.4 How to change or move method instructions

How to change anThe table below describes how to change an instruction in the Text pane of the TextinstructionInstructions Editor:

Step	Action
1	Select the instruction.
	<i>Result</i> : The instruction with its current parameters is displayed in the Instruction box .
2	Make the required changes to the breakpoint or parameters
	or
	select a new instruction in the Instruction Box.
3	Click the Change button
	or
	the Replace button.
	<i>Note</i> : These buttons are equivalent unless changes are made to the breakpoint. See below.

Effects of the
Change button
and the Replace
button on break-
points

The table below describes the difference in function between the **Change** button and the **Replace** button when you change breakpoints:

Button	Function
Change	This button shifts all subsequent instructions in the block according to the change in the breakpoint. Change does not affect the relative order of instruc- tions in the method. You cannot change the breakpoint of an instruction to earlier than the nearest previous breakpoint in a block.
	The illustration shows an example where Solvent A is changed from breakpoint 0 to 1:

6.3 Method instructions

6.3.4 How to change or move method instructions

Button	Function
Replace	This button moves the selected instruction but does not change the breakpoint of any other instruction. Replace can change the relative order of instructions in the method.
	The illustration shows an example where Solvent A is changed from breakpoint 0 to 1:

Effects of the Change button and the Replace button on block length

The **Length** parameter in the **Wash** instruction affects the length of a **wash_block**. Depending on which button you use, the change will have different results. The table below describes this:

Command	Function
Change	If this button is used to change the length of a wash_block, the breakpoints for any instructions issued during the progress of the wash_block will be adjusted proportionately so that they are always placed at the same relative position within the wash_block. Instruc- tions issued after the end of the wash_block will be shifted by the amount of the change. Since the wash_block works over time, any instruction that you want to insert after a wash_block should be placed after the combined breakpoint and wash_block length.
	<i>Note</i> : Moving the End_block instruction in a wash_block with the Change button does not affect the length of the wash_block .
Replace	If this button is used to change the length of a wash_block, other instructions are not affected.

How to move an Move an instruction within the same breakpoint

instruction

Select the instruction in the **Text** pane of the **Text Instructions Editor** and drag it to its new location to change the order of instructions within the same breakpoint in a block.

Move an instruction to another breakpoint

The table below describes how to move an instruction to another breakpoint:

Step	Action
1	• Select the instruction in the Text pane of the Text Instructions Ed - itor.
	Choose Edit:Cut.
2	Select the instruction line just <i>above</i> the point where you want the cut instruction to be pasted.
	Choose Edit:Paste .
	<i>Result:</i> The instruction is now removed from its original breakpoint and pasted at the new breakpoint. The pasted instruction is inserted with the same breakpoint value as the instruction selected for point of insertion.

6.4 How to use method variables

IntroductionMethod variables can be used to edit suitable methods. Variables can be assigned
to most instruction parameters including breakpoints.

Each parameter defined as a variable is also assigned a default value, which is used if no changes are made to variable values at the start of a run. Up to 500 variables can be defined in a single method.

All variables are listed on the **Variables** tab of the **Run Setup**, grouped according to the block in which they appear. See **6.5.2 The Variables tab** on page 125.

Identifying variables Parameters defined as variables can be identified in two ways:

- In the **Text** pane in **Text instructions**, the parameter is given as the default value in parentheses followed by the variable name. The illustration below shows an example of this:
 - 0.00 Block Column_wash

 (Column_wash)
 0.00 Base SameAsMain
 0.00 Block Column_Number
 0.00 Waste Waste_ACN
 0.00 Solvent_A ACN_Amidites_3.1
 0.00 Solvent_B ACN_Reag_4.1
 0.00 PFlow_AB 10.00 {Bar}
 (8.00)#CV_Column_Wash Flow_AB 0.00 {ml/min}, 0.00 {ml/min}
 8.00 End_block
- When the instruction is shown in the **Instructions** field of the **Instruction box**, the **VAR** button beside the parameter field is displayed in capital letters, that is **VAR** not **Var**.

The illustration below shows an example of the **Instruction box** where **UV1** is defined as a variable and **UV2** and **UV3** are fixed.

- Breakpoint	Instructions	ParataQuela Crastantes	Parameters	1191.700	l local 1
0.00 Sinin	C Europ	Integration_ON	VAB	350 - nn	insar
· · · · ·	C Flowpath	Integration_OFF		1102 NHTEE IN , 7001	
Vet		Caldaneta	Var	230 × nn	Qhange
		%_Tetrancle Arridite Dono	302	UV3 0-0FF [0 - 200]	Baclara
	C Wateh	DV UV Wavelendth		1 <u>0</u> 111	
	C Other	U ^{0_AuloZero}			Dolote 💌
•					

When to change variable values

Variable values can be changed immediately before the start of a method run without using the **Method Editor**, allowing one method to be used for runs under a variety of conditions.

How to change variable values	To change	default variable values, you can either		
	• edit the			
	change	the value in the Variables tab of Run Setup .		
	Changes m vice versa.	nade in the Text pane are automatically updated on the Variables tab and		
	The figure	below illustrates the relationship between variables in the Text pane and		
	0.00 Block	D CV_Detrit_Wash (CV) c DNA_parameters arameters Becycle_DNA a_Amidite (1.50)#Eq_Amidite_DNA (Eg) Becycle_DNA Becycle_DNA Conc_Amidite_DNA (M) Becycle_DNA Becycle_DNA Conc_Amidite_DNA (M) Becycle_DNA Becycle_DNA D CV_Couping_Wash D CV_Couping_Wash (CV)		
Breakpoints	If a breakpoint is defined as a variable, changing the variable value in the Variabl tab when the method run is started will shift other instruction breakpoints according This functionality is equivalent to using the Change button to alter a breakpoint (s 6.3.4 How to change or move method instructions on page 116 for how the Chan button affects instructions).			
How to define new variables	Only one v block. How block. The	variable that affects block length (breakpoint) may be defined within each vever, any number of parameters may be defined as variables within a table below describes how to define a new variable.		
	Step	Action		
	1	Select the instruction where you want to define the variable in the Text pane of Text instructions .		
		box.		
	2	Locate the breakpoint or the required parameter in the Instruction box.		
		Click the Var button.		

Result: The Variable Name Definition dialog box opens.

Step	Action
3	• Enter a name for the variable.
	 Select the Visible in details only check box if you want to set the variable as a "details" variable. Detail variables only become visible on the Variables tab if the Show details check box is selected. This option is useful for hiding less important variables. Click OK.
	<i>Result:</i> The Var button changes to VAR to confirm the new variable. The variable is displayed in the Text pane.

Variable names

Variables are defined with names that can be explicit descriptions of the variable function, for example **Column_wash**. Suitable choices of variable names can make the method easier to read and understand, and also help the operator in setting variable values at the start of a method run.

The names can be up to 32 characters long and the following characters can be used:

- Letters (A-Z)
- Digits (0-9)
- The underscore character (_)

The case of letters is retained, but not significant. The names **Flow_Rate** and **FLOW_RATE** are treated as identical.

How to rename a The table below describes how to rename a variable:

variable

Step	Action
1	Select the instruction that includes the variable you wish to rename in the Text pane of Text instructions .
	<i>Result:</i> The parameters for the instruction are shown in the Instruction box .
2	 Locate the required parameter in the Parameters field. Click the VAR button.
3	Enter a new variable name in the dialog box and click OK .

Note: Variables can also be renamed in the **Edit Variables** dialog box in the **Method Editor**. See **6.5.2 The Variables tab** on page 126 for more information.

How to remove aThe table below describes how to remove a variable by converting it into a fixed
value:

Step	Action
1	In the Text pane of Text instructions , select the instruction with the variable you want to remove.
	<i>Result:</i> The parameters for the instruction are shown in the Instruction box .
2	Locate the required parameter in the Parameters field.
	Click the VAR button.
3	 Click the Clear button to delete the variable. Click OK.
	<i>Result</i> : The VAR button changes to Var to confirm that the variable is removed.

Note: Variables can also be deleted in the **Edit Variables** dialog box in the **Method Editor**. See **6.5.2 The Variables tab** on page 126 for more information.

6.5 Run Setup

Introduction Run Setup is a part of the Method Editor. It has several tabs for defining method properties. This section describes how to use the tabs and the information displayed on the tabs.

In this section This section contains the following sub-sections

Торіс	See
Overview of Run Setup	6.5.1
The Variables tab	6.5.2
The Questions tab	6.5.3
The Notes tab	6.5.4
The Evaluation Procedures tab	6.5.5
The Reference Curves tab	6.5.6
The Method Information tab	6.5.7
The Result Name tab	6.5.8
The Start Protocol tab	6.5.9
The Sequence tab	6.5.10
How to export the values in the Run Setup	6.5.11

6.5.1 Overview of Run Setup

Introduction

To access **Run Setup**, either

• Click the Run Setup icon on the Method Editor toolbar,



or

• Select View: Run Setup.

Illustration of RunThe illustration below shows an example of the Run Setup with the Variables tabSetupselected:

Block		Variable	Value	Range
Main		Column_Volume {m}	6.300	0.100 - 999999.000
START_parameters	Γ	Column_Volume {m}	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	Γ	Column_Number	Column_1 💌	
Amidite_Purge_volume		Amidite_Purge_volume {m}	1.00	0.00 - 999999.00
Solvent_Purge_volume		Solvent_Purge_valume (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				

The tabs

The table below contains brief descriptions of the tabs of **Run Setup**. If you want more detailed descriptions, see sections on the respective tabs:

Tab	This tab
Variables	lists all variables used in the method with their default values, organized by method block.
Questions	displays the questions used in the method. Questions provide a means for entering run-specific information at the start of a run. Use this tab when you want to define questions.

Tab	This tab
Notes	shows the descriptive comments that form a part of the method documentation.
Evaluation Procedures	shows the evaluation procedures that will run at the end of the current method.
Reference curves	displays the curves that will appear in the System Control curve dialog box during the run of the current method.
Method Information	displays information about the method, such as method name, target system, and last date of change.
Result name	specifies how the result files will be named for the res- ults of a run, and where the result file will be saved.
Start Protocol	determines which items of the Run Setup that are displayed at the start of the run.
Sequence	defines the sequence that will be used in the method and some optional method steps.

6.5.2 The Variables tab

Introduction The Variables tab lists all variables used in the method with their default values, organized by method block. You can change the default values to create a variant of the method.

Note: The variables of a block are only displayed once on the **Variables** tab, even if the block is called several times in a method. **Variables** are displayed only if the method contains variables.

Check boxes There are three check boxes on the **Variables** tab. The table below describes these boxes:

Check box	Select this box if you want
Show details	detail variables to be shown. Detail variables are indic- ated by a D in the column immediately to the left of the Variable column.
Show unused variables	unused variables to be shown. Unused variables are indicated by a U in the column immediately to the left of the Variable column.
Display tooltip for ex- tended variable cells	to display useful tips when you move the cursor to fields that can have several functions.

Note: The options to show detail and unused variables can be set up as default options in the **Administration:Change User Attributes** settings in the **UNICORN Manager**.

How to change the default values	Enter new values in the appropriate fields to change the default variable values. For some variables, pre-set values are available on drop-down menus. Save the method when you have made your changes.
	<i>Note:</i> The Variables box must be selected on the Start Protocol tab if you want to be able to change variable values at the start of a method.
Blue values	For variables with values shown in blue, the value input can be toggled between OFF , INFINITE or other single position values, and a variable range. To change the value, right-click the value cell.
Variables can also be changed in the Text Instructions Editor	Variables can be changed in the Text Instructions Editor as well as on the Variables tab of the Method Editor . Changed values will be displayed for the corresponding instructions in both windows.

How to delete or	The table below describes how to delete or rename a variable in the Run Setup .
rename variables	

Step	Action
1	• Click the Edit Variable button on the Run Setup Variables tab.
	or
	Choose the Edit:VariableMethod Editor menu option.
	<i>Result</i> : The Edit Variables dialog box opens. The variables are listed alphabetically.
2	Select the variable to edit.
3	Rename
	• Type a new variable name in the New name text box.
	Click the Rename button.
	<i>Result</i> : The variable is renamed.
	Delete
	Click the Delete button.
	Confirm that you want to delete the variable.
	<i>Result</i> : The variable is deleted.

How to change a	Detail variables are only shown if the Show details checkbox is selected on the
variable into a de-	Variables tab. The table below describes how to set up a detail variable.
tail variable	

Step	Action
1	• Click the Edit Variable button on the Run Setup Variables tab.
	or
	Choose the Edit:VariableMethod Editor menu option.
	<i>Result</i> : The Edit Variables dialog box opens. The variables are listed alphabetically.
2	Select the variable to be changed.
3	 Select the Set visible in details only checkbox. Click the Close button. <i>Result</i>: The variable is marked by the detail indicator D.

How to change a The detail variable into a regular variable able

How to change a The table below describes how to change a detail variable into a regular variable.

Step	Action
1	• Click the Edit Variable button on the Run Setup Variables tab.
	or
	Choose the Edit:VariableMethod Editor menu option.
	<i>Result</i> : The Edit Variables dialog box opens. The variables are listed alphabetically.
2	Select the variable to be changed.
3	 De-select the Set visible in details only checkbox. Click the Close button. <i>Result</i>: The detail variable indicator D is removed.

6.5.3 The Questions tab

Introduction The Questions tab of Run Setup is used for viewing and adding questions that the system asks a user at the start of a run. These questions provide a means for entering structured run-specific information. Templates supplied with UNICORN are defined with a set of questions for sample, column and eluent identification.

Note: For questions to be shown in the start protocol, the **Questions** option must be checked on the **Start Protocol** tab of **Run Setup**.

Question statusDifferent types of questions have different status. The illustration below shows the
Question field, an example of a question and the status alternatives that can be used:

Enter Loading and Lo	t number of the Support	
	chamber of the Support	

The table below explains the different alternatives:

Question status	Explanation
Mandatory	These questions must be answered before a method is started.
Authorized	These questions must be signed with the users signa- ture password to unlock and continue the method.
Chromatogram	These questions will be printed with the answers on the same page as the chromatogram, if a question is chosen in an evaluation report.

Answer type

A question has to be defined to accept one of four types of answers. The illustration below shows an example where the **Value** option has been selected. The appearance of the box to the right of the **Answer type** field depends on the answer type option selected:

Answer type: C Input field C Multiple choice C No Answer	-Value:	
● <u>V</u> alue		

Answer type	This option
Input field	accepts any alphanumerical input as the answer. Input field questions may have a default answer.
Multiple choice	allows the user to choose one of a defined set of an- swers. To allow a blank answer, enter a space in one of the predefined answers.
NoAnswer	 is used to display important information or to split a question over more than one line by setting all but the last line in a question to No answer. (Normally, each question consists of one line only.) It is impossible to give an answer to questions with this option selected.
Value	accepts only numerical answers. Value questions must have specified maximum and minimum limits, and may be defined to accept only integer values.

The table below describes the different answer types:

How to insert a question

The table below describes how to insert a question:

Step	Action
1	If there are questions on the list, select the question that should be followed by the new question.
2	Enter the question text, status, answer type and answer option as re- quired.

Step	Action	
3	The Answer type determines what is displayed in the question defini- tion field to the right of the Answer type field. For each answer type, do as follows:	
	Input field	
	Enter a default answer if required.	
	Multiple choice	
	Click in the text field under Alternatives .	
	Enter the answer.	
	Click the Add/Delete button.	
	<i>Result:</i> The new alternative is added at the end of the list.	
	• Repeat this procedure to add new alternatives. To remove an altern- ative, mark the alternative in the scroll list and click the Add/Delete button.	
	No answer	
	No action taken.	
	Value	
	Enter maximum and minimum limits. Select the Integer box if the question is to accept integers only as answers.	
4	Click the Insert button.	
	Result: The new question is added to the list.	

How to previewThe table below describes how to preview the questions as they will appear in thequestionsStart Protocol.

Step	Action
1	Select a question.
	Click the Preview button.
	<i>Result</i> : The question is displayed.
2	Click the Edit button to return to the question editing mode.

How to edit a question	The table below describes how to edit a question:	
	Step	Action
	1	Select the question you want to edit.
	2	Change the text, status, type and answer as required
	3	Click the Replace button.
How to delete a	Do one o	f the following to delete a question:
question	 Select 	a question and click the Delete button to remove the selected question.

• Click the **Delete all** button to delete all questions.

6.5.4	The No	tes tab	
Introduction	Notes are templates the metho	descriptive comments that form part of the method documentation. Method are supplied with notes describing the system requirements for running od. Read through these notes carefully before using a method.	
Sub-tabs	There are	four sub-tabs:	
	Metho	d Notes	
	• Start N	lotes	
	Run No	otes	
	• Evalua	ition Notes	
	Only the I accessible	Method Notes can be edited from the Method Editor ; the other notes are e at the respective stages in a run.	
Recommended usage	We recommend that you use Method Notes to describe the system setup required by the method (for example eluent and sample inlets, outlets and column connections).		
	Use the S	tart Notes or Run Notes for run-specific information.	
	<i>Note:</i> Met method.	hod Notes are saved with the method and apply to all runs made with the	
How to write method notes	To write n the Notes to edit the	nethod notes in your own methods, place the cursor in the white area of tab and type the relevant text. Use standard Windows editing functions e notes.	
How to search for text strings	You can s to perform	earch for text strings in the method notes. The table below describes how n a search.	
	Step	Action	
	1	Click the Find button.	
		<i>Result</i> : The Find dialog box opens.	
	2	Type the text string in the Find what text box.	
		Select search criteria and click OK .	
		Result: The located text string is highlighted in the text area	

6.5.5	The Evaluation Procedures	tab
-------	---------------------------	-----

Introduction	The Evaluation Procedures tab lists all evaluation procedures associated with the method. Evaluation procedures can be called automatically at the end of a method to evaluate and/or print the results. Many UNICORN strategies are supplied with method templates that include a number of evaluation procedures. User defined procedures are created in the evaluation module and can be saved in method files (see 11.3 Automated evaluations procedures on page 336).
Changes in the Evaluation mod- ule	A procedure in a method will not be updated when a procedure with the same name is changed in the Evaluation module. The same applies to report formats saved in a procedure.
References to curves	Evaluation procedures that process chromatogram data rely on consistent identification of curves in the result file for correct operation. If you include evaluation procedures with a method, make sure that references to curves in the procedure will be valid when the procedure is executed at the end of the run (see 11.3 Automated evaluation procedures on page 336 for more details).
How to print eval- uation results	If you use an evaluation procedure to print results automatically from a run controlled from a remote station in a network installation, the results will be printed on the printer currently set up on the local station, not on the remote station. If you execute the procedure interactively from the Evaluation module on the remote station, the results will be printed on the printer set up on the remote station where you are working.
How to define and view evaluation procedures	Evaluation procedures are defined in the Evaluation module. Procedures imported to a method can also be viewed and edited in the Method Editor . To do this, select the required procedure on the list and click the Edit button.
How to select pro- cedures to run	To select procedures to run, select the procedure(s) that are to be executed at the end of the run. The procedures will be executed in the order they appear on the list.

	Sten	Action
evaluation proced- ures	<i>Note:</i> Procedures saved with one method file can be imported to another.	
How to import	The table describes how to import global evaluation procedures:	

Step	Action
1	Select the Evaluation Procedures tab and click the Import button.
	<i>Result:</i> The Import dialog box is displayed.
2	Choose either option 1 or 2 below.
	Option 1: Select a global UNICORN procedure
	1. Select a procedure on the Select list.
	<i>Result:</i> The evaluation procedure name is displayed in the Import as field.
	Option 2: Select a procedure from another method
	1. Select a method, that contains a procedure, in the left part of the dialog box.
	<i>Result</i> : The procedures of the selected method will be displayed on the Select list.
	2. Select the desired procedure on the Select list.
	<i>Result</i> : The method name is displayed in the Import as field.
	<i>Note:</i> Click Procedure List to return to the list of UNICORN's global evaluation procedures.
3	If desired, change the procedure name in the Import as field.
	<i>Note:</i> The imported evaluation procedure cannot have the same name as an existing evaluation procedure in the method. If the default name is not allowed for this reason, the Import button will be gray and dis- abled. When you change the name in the Import as field, the button will become available again.
4	Click the Import button.
	<i>Result:</i> The evaluation procedure is imported into the method.
5	Repeat steps 2 - 4 until you have imported all procedures.
6	Click the Close button.

How to delete The table describes how to delete evaluation procedures from the method: evaluation proced-Т ures

Step	Action
1	Select the Evaluation Procedures tab.
2	Select the procedure(s) that you want to delete.
3	Click the Delete button and confirm the deletion when prompted. <i>Result:</i> The deleted procedures are immediately removed from the method file.

How to rename evaluation proced-

The table describes how to rename evaluation procedures in a method.

ures

Step	Action
1	Select the Evaluation Procedures tab and click the Rename button. <i>Result</i> : The Rename dialog box is displayed.
2	 Select a procedure from the list and change the name in the Rename item to field. Click Rename.
3	Repeat step 2 until you have renamed all procedures required.
4	Click the Close button.

How to edit an evaluation proced- ure	The table describes how to edit evaluation procedures in a specific method:	
	Step	Action
	1	Select a procedure on the Evaluation Procedures tab and click the Edit button.
		<i>Result:</i> The Procedure Editor dialog box is displayed, with information about the selected procedure.
	2	Enter the new parameter values in the appropriate place of the Para- meters field, and click the Replace button.

Result: The selected instruction in the evaluation procedure is updated in accordance with the new parameters assigned to it.

Step	Action
3	If needed, insert new instructions after the currently selected procedure instruction. Do the following:
	1. Select an instruction type and instruction in the Instructions field.
	2. Enter the appropriate parameter values in the Parameters field.
	3. Click the Insert button.
	<i>Result:</i> The new instruction is added to the evaluation procedure.
4	To remove an instruction from the evaluation procedure, select it and click the Delete button.
5	Select File:Save as to save the edited procedure with a new name. Click the Close button.
6	Select File:Close from the menu in the Procedure Editor dialog box.
	<i>Result:</i> The Procedure Editor dialog box is closed and the procedure is saved automatically.

6.5.6 The Reference Curves tab

IntroductionReference curves are curves from existing result files that you can display in the
Curves pane of System Control during a run.How to choose
and display refer-
ence curvesYou can include up to five reference curves in a method. You choose which curves
to display during the run with the View:Properties:Curves command in System
Control (see 8.2.3 The Curves pane on page 182). Reference curves are only displayed
during the run. Reference curves are not saved in the result file.

Note: Although this function can be used it is normally not useful for oligo applications.

How to add reference curves The table below describes how to add a reference curve from a result file:

Step	Action
1	Select the Reference Curves tab and click the Import button.
	Result: The Import Reference Curve dialog is displayed.
2	• In the left field, select the result file containing the curve to be added.
	<i>Result</i> : The Select list displays the available curves for the result file.
	• Select the curve you want to add from the Select list.
3	• If desired, change the curve name in the Import as field.
	<i>Note</i> : The curve name has to be changed if a reference curve with that name already exists.
	Click Import.
4	Repeat steps 2 and 3 if you want to add more curves.
5	Click the Close button to close the Import Reference Curve dialog box.

How to delete reference curves

Step	Action
1	Select the curves you want to delete.
2	Click the Delete button and confirm the action when prompted.

Note: Deleting curves from the method does not affect the curves in the result file from which they were imported.

How to rename reference curves

The table below describes how to rename a reference curve in a method:

Step	Action
1	Click the Rename button.
2	 Select a curve from the list. Change the name in the Rename item to field. Click the Rename button.
3	Repeat steps 2 and 3 if you want to rename more reference curves.
4	Click the Close button. <i>Result:</i> The reference curve name is changed.

0.3.7	me method m				
Introduction	The Method Information tab displays information about the method. This tab is for information only and cannot be edited.				
	There are three sub-	tabs on this tab: Information, Signatures, and Method duration.			
The Information	The Information sub-tab displays				
sub-tab	 method information such as method name, creation date, creator and date of last change, 				
	 target system, 				
	 strategy information such as strategy name, date and size. 				
The Signatures	The Strategy Notes strategy is designed The Signatures sub-	button displays what systems, programs and file versions the d for. -tab has five information fields for all signatures. The table below			
sub-tab	describes the content of each field:				
	Field	Description			
	Date	Date of the signature.			
	Meaning	Short description explaining the meaning behind the signature.			
	User Name	User name of the user who signed the method.			
	Full Name	Full name of the user who signed the method.			
	Position	Position of the user.			
The Method Dura-	The Method Durati	on sub-tab presents			
tion sub-tab	the estimated total time				
	• the estimated bu	Iffer volume required for the method.			

6.5.7 The Method Information tab

ntroduction The Result Name tab is used to specify: • how the result files will be named for the results of a run • where the result file will be saved Ilustration The illustration below shows an example of the Result Name tab: Variables Notes Reference Curves Evaluation Procedures Motion Start Protocol Sequence Questions Result directory Broggee	
 how the result files will be named for the results of a run where the result file will be saved Ilustration The illustration below shows an example of the Result Name tab: Variables Notes Reference Curves Evaluation Procedures Method Information Start Protocol Sequence Questions Result Name No result @ phangeable batch ID Result directory Home Brogse Brogse 	
where the result file will be saved Ilustration The illustration below shows an example of the Result Name tab: Variables Notes Reference Curves Evaluation Procedures Method Information Start Protocol Sequence Questions Result Name No result Phone Brogse Brogse	
Illustration The illustration below shows an example of the Result Name tab:	
Variables Notes Reference Curves Evaluation Procedures Method Information Start Protocol Sequence Questions Result Name No result Changeable batch ID Result directory Home Broggse	
Scouting subdirectory:	۶
<u>Нер</u>	

Construction of the result file name

The result file name is constructed by one of the base options listed below. The serial number is changed automatically each time the method is run.

Base options of the result file name are:

- The Method name plus a 3-digit serial number,
- The **Date** of the run (in an 8-digit format determined by the country setting in Windows 2000 or XP) plus a 3-digit serial number,
- A freely specified **Name** (within the file naming restrictions of the operating system) plus a 3-digit serial number.
- A selected **Variable** (from the droplist) plus a 3-digit serial number.

Note: If a result names includes decimal points (e.g. numeric variables) or underscore characters, these characters will automatically be replaced by spaces. Points and underscores are not allowed in the result names.

Serial numbers and unique identi- fiers	 If the result file folder already contains files with the same file name base, the serie number is changed automatically. A unique identifier can also be generated automatically, in addition to the serial number. The identifier is a string of numbers inserted between the result file name and the three-digit serial number. Select Add unique identifier to result name in the Result name field. 			
Batch ID for each		will automatically issue a Batch ID to each method run. This ID is displayed		
test run	illustration in 8.2.5 The Logbook pane on page 188. If Changeable batch ID is selected, another ID string can be typed in the Start Protocol .			
Specify result name as change- able	The result name can be specified as changeable in the Start Protocol (see 6.5.9 The Start Protocol tab on page 142). In that case, the information you supply on the Result Name tab will be the suggested result name, but you can change this at the start of the run.			
How to save the result files in a different folder	By defaul The table	t, result files are stored in the home folder of the user who starts the run. below describes how to change the folder where the result file will be stored:		
	Step	Action		
	1	If the run contains information that is not important, you can save disk space by selecting the No result check box, thereby storing the result in the Temporary folder (named Manual Runs , where only the latest 10 result files are saved). If not, go to step 2.		
	2	Click the Browse button.		

• Double-click the required folder icon.

• Click the **OK** button.

3

6.5.9 The Start Protocol tab

Introduction The Start Protocol tab determines which items of the Run Setup are displayed at the start of a method run. Click the Start Protocol tab and select the items that you want to be displayed.

Checkboxes

The table below describes the check boxes of the **Start Protocol** tab:

Checkbox	Displays
Variables	values for method variables that can be changed at the start of the run.
	These values will override the default values for the particular run and be saved in the result file. The default values stored in the method are not affected.
Text Method	method instructions. They cannot be changed from this display.
Notes	the Notes tab.
Reference curves	the reference curves associated with the method.
Evaluation procedures	the evaluation procedures set to be executed at the end of the method.
Method information	the method information.
Settings	the settings.
Sequence	the sequence. This is for information only and cannot be edited.
Questions	questions defined in the method.You are recommended to always use this option, since the answers to ques- tions can form an important part of the UNICORN run documentation.
Result name	the result name, which is changeable if this option has been selected. Click the Browse button to change the result folder.
	If the box is not selected, the result name will still be displayed, but you will not be able to change the name or folder.
6.5.10 The Sequence tab

Introduction The Sequence tab defines the sequence that will be used in the method. It is also referred to as the Sequence Editor. The Sequence Editor can be used to open saved sequences, to edit or create new sequences. The sequence can be saved and added to the Sequence List.

Illustration The illustration below shows the **Sequence** tab with a pre-defined 20 base sequence displayed.

Variables Notes Reference Curves Evaluation Procedures Method Information Start Protocol Sequence Questions Result Name		
Sequence name: TEST-20 from Standard Amidite Valve 1 pos, Trityl-OFF. (QZ)		
© DNA © -S © Modified Group © BNA © -Q © Standard		
5' ATA CO3 ATT AAG COA AGT IT		
Optional method steps Image puge amidite Image puge solvents Image colvents Image puge solvents Image puge puge solvents Image puge puge puge solvents Image puge puge puge puge puge puge puge pu		
Create Method Open Seq Save Seq Cross References		

How to open a se- The table describes how to open a saved sequence.

quence

StepAction1• Click the Open Seq... button.Result: The Open Sequence dialog box opens.2• Select a sequence from the Sequence list.• Click OK.Result: The sequence is displayed in the Sequence tab.

How to create or	A saved sequence can be edited or a new sequence can be created in the Sequence
edit a sequence	Editor. The table below describes how to do this.

Step	Action
1	Position the cursor where you want to insert the base.
2	 Use the radio buttons to select DNA or RNA Oxidated (-O) or thiolated (-S) from the Standard or Modified reagent position.
3	Type the letter for the base.
4	Repeat step 1 to 3 for all subsequent bases until the sequence is completed. A maximum of 200 bases can be included.
5	Click the Group button to display the bases in groups of three.

Note: The synthesis reaction proceeds from 3' to 5'. The 3' base position is always the first base on the solid support. This base should be taken from the standard position and should be oxidated.

How to save a se- The table below describes how to save a sequence.

quence

Step Action 1 • Click the **Save seq...** button. *Result*: The **Save Sequence** dialog box opens. 2 • Type a name in the **Sequence name** textbox. • Click OK. *Result*: The sequence is saved and available in the **Sequence list**.

Note: The saved sequence is only available to the current user. User logged in with other user names will not be able to display this sequence.

How to delete a The table below describes how to delete a sequence.

sequence

Step	Action
1	Click the Delete seq button.
	<i>Result</i> : The Delete Sequence dialog box opens.

Step	Action
2	• Select the sequence to be deleted in the Sequence list . If the sequence isn't saved proceed to step 3.
3	• Click OK .
	<i>Result</i> : The sequence is deleted and the sequence textbox in the Sequence Editor is empty.

How to edit the
sequence crossThe table below describes how to display and edit the cross references in the
Sequence Editor.referencesI

Step	Action		
1	Click the Cross References button.		
	Result: The Cross References List dialog box opens.		
	Cross Reference List X Coupling Purge Solvent Purge Amidite Column wash Final detritylation DEA Treatment Base Block X 1 A ddd_DNA_A X 2 A ddd_DNA_A X 3 A ddd_DNA_A X 4 A ddd_DNA_C X 5 C Add_DNA_C X 5 C Add_DNA_C X 6 C Add_DNA_C X 7 C Add_DNA_C X 8 C Add_DNA_C X 9 G Add_DNA_G X 11 G Add_DNA_G X 12 C Add_DNA_G X 13 T Add_DNA_G X X X X X		
2	 Edit the cross references as needed: Choose the block you want to edit. Click the down arrow beside the Block droplist and select a block name. 		
	Click the Insert button.		
	<i>Result</i> : The block is changed to the selected block name.		

Step	Action
3	 Repeat step 2 to change other cross references as needed. Click OK.
	Result: The Cross References List dialog box closes.

Optional method steps

The following optional method steps can be selected in the **Run Setup Sequence** tab:

- Purge amitide
- Purge solvents
- Column wash
- Final detritylation
- DEA treatment

Note: **DEA treatment** will add an extra method step where the oligonucleotides are treated with a solution of diethylamin to increase the yield of full-length oligonucleotide product. This treatment is described in detail in the ÄKTAoligopilot User Manual.

How to create a method

The table below describes how to create a method.

Step	Action
1	Click the Create Method button.
	<i>Result</i> : The Save As dialog box opens.
2	 Type a name for the method in the Method name text box. Click OK.
	<i>Result</i> : The method is saved.

Note: The **Create Method...** button also performs the following functions:

- Sequence check for invalid combinations.
- Update of method variables to default values.

6.5.11 How to export the values in the Run Setup

InstructionYou can easily export the values in the Run Setup to a file, and save it in ASCII format.This is useful when you want to enable others to read the methods without having
access to UNICORN on their computers.

The table below describes how to export the values in the **Run Setup** and save them to a file.

Step	Action
1	In the Text instructions Editor or the Run Setup, select File:Export:Run Setup. Result: The Export Run Setup dialog box is displayed. Export Run Setup Select parts to include in the export: Wethod Information Variables Questions Start Protocol Result Name Method Notes ExportCancel Help
2	 Select the boxes to select the parts of Run Setup that you want to export. Click the Export button. <i>Result</i>: The Export dialog box is displayed.
3	 Type a file name and select the target drive and folder. Click the Save button.

6.6 How to use selected method instructions

Introduction This section provides recommendations for how to use some common programming features in UNICORN methods. They are available from the Instruction box in the Method Editor.

In this section This section contains the following sub-sections

Торіс	See
Base instruction	6.6.1
Instructions at the same breakpoint	6.6.2
Block and method length	6.6.3
Messages and Set_Marks	6.6.4
How to delay a method	6.6.5
Linear flow rates	6.6.6

6.6.1	Base instruction
Bases	Every method block must start with a Base instruction, defining the base for calculating breakpoints.
	Different blocks can use different bases. The base can be one of the following:
	• volume (the unit depends on the scale defined in the system strategy)
	• time (minutes)
	• column volume , CV (defined as a numerical value or taken from the column definition)
	• SameAsMain (all blocks apart from the main block), which means that the block will inherit the base defined in the main block.
	Method blocks that use a volume or column volume base
	Make sure that the flow rate is not zero. Volume breakpoints are calculated from the flow rate of the pump, and the method will not progress if the flow rate is zero.
What base should I use?	Use the base that most closely suits the purpose of the block. Column volume is recommended as the base for most steps in a run. In some situations, however, it may be more suitable to use a time or volume base for individual blocks.
	To change the base for an existing method
	Be careful when changing the base for an existing method. Changing between time and volume bases can affect the relative duration of steps in the method if different steps use different flow rates.
Column paramet- er: named column	If a named column is selected for the Column parameter in the Other:Base instruction, the volume specified in the selected column definition will automatically be used for column volume in the method block. The column volume for base CV cannot then be changed in the instruction or defined as a variable. However, the Column parameter should be defined as a variable. Choosing a column definition also enables linear flow rate and column performance calculations.
Column paramet- er: Any	If the Column parameter in the Other:Base instruction is set to Any and the Base parameter is set to CV , the column volume is set numerically by the Volume parameter. The column volume may be defined as a variable, allowing the scale of the run to be decided when the method is actually run.

6.6.2 Instructions at the same breakpoint

Description

Instructions placed at the same breakpoint in a block are executed simultaneously.

Exceptions

Exceptions are successive **Block** instructions, which are executed in the sequence in which they are written. This can have important consequences in some situations.

The instruction sequence below shows an example of instructions with the same breakpoint, where the **AutoZero_UV** will start *after* the **Wash** block is completed.

Breakpoint	Instruction
0.00	Block Column_Wash
0.00	AutoZero_UV
0.00	Block Detritylation

6.6.3	Block and method length
General descrip- tion	The time or volume of a method run is determined by the sum of the block lengths. In turn, the length of a block is determined by the breakpoint of the last instruction in the block.
	<i>Note</i> : Depending on how conditional calls are used (see 6.7 Standard Watch conditions on page 156), the overall method time or volume may vary according to watch events during the run.
Block length	A block in which all breakpoints are set to 0 will take no time or volume during a method run. The illustration below shows an example of this:
	 0.00 Block DNA_parameters (DNA_parameters) 0.00 Base Time 0.00 Eq_Amidite (1.50)#Eq_Amidite_DNA {Eq} 0.00 %_Tetrazole (60)#Percent_Tet_DNA {%} 0.00 Amidite_Conc (0.1)#Conc_Amidite_DNA {M} 0.00 End_block
	To extend the length of a block without performing any other operation, set the breakpoint of the End_block instruction appropriately, for example, as in the illustration below:
	(Equilibration)

(Equilibration) 0.00 Base SameAsMain 4.00 End_Block 0.00 End_Block

6.6.4 Messages and Set_Marks

When to use aMessages are used to inform the operator of the progress of the run. It is a good ideamessageto issue messages at critical points in the method, for example, when Watch
instructions are used for conditional events.

How to add aThe Message instruction can be used to set up a message that will be displayed for
the user during the execution of the method run. The message can be for information
in a screen only, or it can require a signature before the user can control the system.
The messages are all added to the logbook text.

The table below describes how to add a **Message** instruction to the method.

Step	Action
1	• Select Other in the Instructions field of the Instructions box .
	Select Message in the instructions list.
2	Type a message in the Message text box in the Parameters field.
3	Select one of the display options on the Mode menu:
	• Screen, i.e. only a text message is displayed.
	• Noscreen , i.e. the message will not be displayed but only inserted into the logbook.
	• Authorize , i.e. the message will require a signature from the user before the user can interact with the system again.
4	• Select a sound on the Sound menu if desired.
	Click the Insert button.

Note: If the **Message** instruction is inserted in a conditional block it will only be displayed if the conditions of the block (for example a **Watch**) is fulfilled.

Note: All messages are erased when the system reaches the **End** status. This also includes **Authorize** messages.

When to use a Set_Mark

- Set_Mark instructions are useful text messages. They can be used
- to insert manual notes, for example, when a problem occurs in a run
- to highlight certain stages in a method.

Set_Marks differ from **Messages** in that they are inserted into the chromatogram at set points as well as into the logbook during a method run.

Example of aThe illustration below shows an example where Set_Marks are used to highlight the
start of the Detritylation and Detritylation Wash steps in a method:

0.00 Block AddDNA_T
(AddDNA_T)
0.00 Base Time
🛨 🗖 0.10 Block Detritylation
😑 📃 0.20 Block Detrit_wash
(Detrit_wash)
0.00 Base SameAsMain
0.00 Set_mark "Det_Wash"
0.00 Solvent_A ACN_Amidites_3.1
0.00 Flow_AB 20 {ml/min}, 20 {ml/min}
1.00 PFlow A 10.00 {Bar}

How to issue a Set_Mark **Set_Marks** are issued from the **Instructions box** of the **Text Instructions** editor. The table below describes how to do this:

Step	Action
1	Select Other:Set_Mark in the Instructions box.
2	Type the message in the Mark text field.
3	Click the Insert button. <i>Result</i> : A new line with the Set_Mark is added to the text instruction.

6.6.5	How to delay a method	
Introduction	A method can be programmed to be delayed at critical points. There are three instructions for this purpose: Hold , Pause and Hold_Until . These instructions are described below.	
Hold	The Hold instruction suspends the execution of the method, but the pump continues to function.	
	Resume the method	
	The method may be resumed if you click Continue on the System Control toolbar.	
Pause	The Pause instruction suspends execution of the method and stops the pumps so that the system comes to a standstill. In ÄKTAdesign systems valves remain in the position they were in before the pause. The pause may be defined as indefinite or for a given number of minutes. This instruction is most useful for stopping the system in the event of an unexpected condition.	
	Resume the method	
	The method may be resumed if you click Continue on the System Control toolbar.	
Hold_Until	The Hold_Until instruction is a special kind of Watch instruction. The method is put on hold until a specific condition is met (signal, test or value) or the time-out is reached. Thereafter the remaining instructions in the method are executed.	
	Instructions that share the same breakpoint as the Hold_Until instruction, but are placed after it in the method, will be executed after the Hold_Until conditions have been met.	

6.6.6 Linear flow rates

Introduction Linear flow rates (cm/h) can be specified for **Flow** instructions. The volume flow rate is calculated from a specified linear flow rate and the column diameter as given in the column instruction.

How to use linear The table describes how to use linear flow rates.

Step	Action
1	Select a specific column on the Variables tab of the Run Setup,
	ог
	Insert a column for the Base instruction of the block in the Text Instruc- tions Editor.
2	In the Instruction box of the Text Instructions editor, select Flow and select the Linear Flow option as shown in the illustration below:
	C Watch PPDox A8 Recycle C Dither Disorth V

Note: If the column is changed, you will be asked if the linear flow rate or the default flow rate should be used. If the linear flow rate cannot be used due to the max flow rate of the system or new column, you will be advised that the max flow rate will be used instead.

6.7 Standard Watch conditions

Introduction Watch instructions allow the progress of a method run to be determined by the events during the method run, for example wash the column until the conductivity has reached a given value. This is facilitated by the **Watch** instructions. The system strategy includes **Watch** instructions for each monitor defined in the system. These instructions are used to survey method runs, and instruct the system to call a specified block or an instruction when a particular monitor signal meets a given condition. As long as the condition is not met, the block is not activated. *Note:* Watch instructions are shown in the Instruction box of the Text Instructions editor, indicated in the **Block** pane by a green line that shows the start and duration of the watch. When is a Watch The breakpoint when the **Watch** instruction is issued determines when the watch active? begins, not when the block is activated. A watch is active from the point at which it is issued until • the **Watch** condition is met or a new watch is set for the same monitor or a **Watch_Off** instruction is issued for the monitor. •

How to insert aWatch instructions are inserted in the Instruction box of the Text Instructions Editor.Watch instructionThe table below describes how to do this.

Step	Action
1	In the Breakpoint field, select the appropriate breakpoint. This decides when the watch begins.
2	 Select Watch in the Instructions field. Select a Watch instruction from the list. Select appropriate values under Test, Value and Action in the Parameters field.
3	Click the Insert button. <i>Result:</i> The new Watch instruction is inserted on the list of actions in the Text window.

Parameters field

Test options in the The table below describes the **Watch** options that are available on the **Test** drop-down list of the **Parameters** field:

Option	Explanation
Greater_Than	The signal exceeds a certain value.
Less_Than	The signal falls below a specified value.
Slope_Greater_Than	The rate of change of the signal ex- ceeds a specified value, expressed in monitor units/minute (for example, mAU/min).
Slope_Less_Than	The rate of change of the signal falls below a specified value, expressed in monitor units/minute (for example, mAU/min).
Less_Than_Or_Valley	The signal falls below a specified value or a valley is detected. A valley is detec- ted only after a Peak_Max has been detected, and the valley is defined by a local minimum followed by an in- crease to 102% of the local minimum value plus the Delta_Peak value (see below).
Peak_Max	The signal falls to a specified fraction of the most recent peak maximum minus the Delta_Peak value. Factor=1 detects peak maximum.
Stable_Baseline	The signal is stable within the limits of the Delta_Base value for the period specified by the minutes parameter.

Note: For slope values, use the **Differentiate** function in the **Evaluation** module to measure the slope of the test chromatogram. The **Simulate Peak Fractionation** technique can also be used to find the slope values.

for air sensors and AuxIn

Watch conditions Two Watch conditions are available for systems with air sensors, although they may be handled differently depending on the system. The table below describes the conditions and their explanations:

Condition	Explanation
Equal 0	No air detected.
Equal 1	Air detected.

Note: To use the Watch_AirSensor instruction for air sensors, the Alarm_AirSensor setting must be disabled.

Actions when a Watch condition is met

The table below describes possible actions when a watch condition is met:

Instruction	Effect
Block name	Calls the named block.
Pause, Hold	Pauses or holds the method.
Continue	Continues the method if paused or held.
End_block	Ends the current block and return to the point from which the block was called.
End_method	Ends the method.
Ready	Indicates that the next step in a MethodQueue may start.

How to enter set-

tings for Delta_Peak and Delta_Base

Permanent settings

Permanent settings for Delta_Peak and Delta_Base are entered with the WatchPar instruction (for example WatchPar_UV, WatchPar_Cond) under System:Settings in the System Control module (see the Administration and Technical Manual).

Temporary settings

Temporary settings that apply only for the duration of a given run can be entered in the Instructions field of the Instruction box in the Text Instructions editor. Select Alarms&Mon and then WatchPar.

The Delta_PeakThe Delta_Peak setting helps the software to detect valleys, peaks and peaksettingmaximum, and to ignore noise in the chromatogram.

The **Delta_Peak** value should be set

- large enough so that signal noise does not activate the conditions *and*
- small enough so that the condition is activated close to the valley or peak.

As a general guideline, set the value to 2-3 times the noise level and 5-10% of the smallest expected peak height. If you set a too high value you can prevent a new peak from being detected after a local minimum.

Use of the Delta_Peak set- ting	 The Delta_Peak setting sets the threshold for signal increase after a local minimum that will be interpreted as a valley for the Less_Than_Or_Valley condition. A valley and a new peak are detected when the signal increases to 102% of the local minimum plus the Delta_Peak value.
	<i>Note:</i> A valley is detected only after a Peak_Max has been detected.
	Example:
	If there is a local minimum at 0.05 AU and a Delta_Peak of 0.01 AU, a valley will be detected at:

(1.02 x 0.05)+0.01=0.111 AU

• sets the threshold for signal decrease after a local maximum that will activate the **Peak_Max** condition. **Peak_Max** is detected when the signal falls to the specified fraction of the most recent peak maximum minus the **Delta_Peak** value.

The figure below illustrates the **Delta_Peak** setting where **Peak_Max** is detected when the signal falls by **Delta_Peak** from a local maximum if the **Peak_Max factor** is set to 1:



The Delta_Base setting

The **Delta_Base** setting helps the software to determine when the baseline is considered to be stable. In other words, it defines the permitted variation for the **Stable_Baseline** condition. For this condition to be activated, the signal may not vary by more than the **Delta_Base** value up or down over the time interval specified in the **Stable_Baseline** condition in the **Watch** instruction.

Note: The **Delta_Base** setting affects the **Stable_Baseline** condition only.

The condition Watch Stable_Baseline

The condition **Watch Stable_Baseline** is met if the signal does not deviate by more than **±Delta_Base** from the baseline during the time interval specified for the watch. The baseline value is determined by the signal at the start of the watch. If the condition is not met, a new interval is started with a new baseline value defined by the signal level at the start of the new interval.

The illustration below shows an example of this:



6.8 How to save or delete a method template

How to save aYou can save a method that you have created yourself as a template if you havemethod as a templateEdit global lists authorization (see the Administration and Technical Manual).plateRecommendation

The templates for each system are common for all users. Be restrictive in saving methods as templates. We recommend that only methods that are useful for all users be saved as templates.

Step	Action
1	Choose File:Save as Template in the Method Editor.
	<i>Result</i> : The Save as Template dialog box is displayed.
2	Enter a name for the template in the Name field,
	or
	choose an existing template name from the Templates list that shows the available templates within the chosen system.
3	• Select the system for which the template is intended in the For system field.
	Select Any on the Technique list.
	• Click OK .
	<i>Result:</i> The method is saved as a template.

The table below describes how to save a method as a template:

How to delete a The table below describes how to delete a template:

How to delete a template

Step	Action
1	Choose Edit:Delete template in the Method Editor.
2	 Select the system and the template that you want to delete. Click the OK button and the Yes button to confirm.

6.9 How to print a method

Instruction You can print a copy of the method, including items from the method documentation, in **Run Setup** and the **Text Instructions** editor.

Step Action In the Method Editor, select File:Print 1 or click the print icon. *Result:* The **Print** dialog box is displayed, showing the available items from the Method Editor. Print × Variables E 🔽 Text Method 🔲 Block List Current Expansion Exclude Unused Blocks Method Notes Questions Reference Curves Evaluation Procedures 🗄 🗹 Method Information Signatures Method Duration Sequence Result Name Instruction Set ΟK Cancel Help 2 • Select the options you want to print. Click **OK**. • Note: For comments on the different alternatives, see "The Print dialog box" below.

The table below describes how to print a method:

The Print dialog	The table below describes some of the check box options in the Print dialog box
box	

Check box	If you select this box
Text Method	all instructions will be printed, including those in unused blocks.
Text Method:Current Expansion	the method will be printed according to the current expansion in the Text pane.
	(Only available from the Text Instructions editor.)
Exclude Unused Blocks	only blocks that are used in the method will be printed.
Text Method: Block List	only the main method and a list of the blocks that are used in the method will be printed.

6.10 How to export a method

Instruction You can easily export a method to another file, and save it in another format, for instance .rtf. This is useful when you want to enable others to read the methods without having access to UNICORN on their computers.

Step	Action
1	In the Text Instructions editor or the Run Setup, select File:Export:Method. <i>Result</i> : The Export Method dialog box is displayed. Export Method Block list Defines Main gnly Current expansion Export Cancel Help
2	 Do the following: Select whether the current method should be exported as a Method or as a Block list. Select the appropriate boxes in the Options field to define the level of detail in the information. Click the Export button. Result: The Export Method to file dialog box is displayed.
3	 Enter a file name and select the target drive and folder. Click the Save button.

The table below describes how to export a method and save it to another file:

e:
See
7.1
7.2

7.1 How to create a new MethodQueue

Instruction The table below describes how to create a **MethodQueue** in the **UNICORN Manager** module.

Step	Action		
1	Select File:New:MethodQueue.		
	or		
	• Right-click in the Methods window and select New:MethodQueue on the shortcut menu.		
	or		
	Click the MethodQueue icon.		
	<i>Result</i> : The MethodQueue Editor dialog box is displayed.		
	MethadQueue Cas Soon As Possible At time Dag: Image: Condition Start MethodQueue Cas Soon As Possible At time Dag: Image: Condition I Condition System Add System Image: Condition Image: Condition I Condition System Image: Condition Image: Condition Image: Condition I Condition System Image: Condition Image: Condition Image: Condition I Condition System Image: Condition Image: Condition Image: Condition I Condition System Image: Condition Image: Condition Image: Condition I Condition System Image: Condition Image: Condition Image: Condition I Condition System Image: Condition Image: Condition Image: Condition I Condition System Image: Condition Image: Condition Image: Condition I Condition System Image: Condition Image: Condition Image: Condition I Condition System Image: Condition		
2	 The default selection for Start MethodQueue is As soon as possible. Click the At time radio button and select a time and weekday for the start of the MethodQueue, if desired. 		
3	• Double-click the cell in the first row of the System column.		
	Result: The Method for row number 1 System dialog box opens.		
	<i>Note</i> : See "How to set up MethodQueues on several systems" below if you have more than one system available.		
4	• Select a method and click OK .		
	<i>Result</i> : The method is displayed in the System column.		

Step	Action		
5	• Click the Insert Row After button and repeat steps 3 and 4 to add more methods to the MethodQueue .		
	<i>Note:</i> The timing of MethodQueue steps performed on different sys- tems can also be controlled by the Ready instruction in the method (see "Relative timing of steps" below).		
	By default, each method step will start as soon as possible (ASAP) after the completion of the previous method step. Use the Condition cell of the chosen method to set another time interval for starting a selected step.		
	• In the Conditions column, double-click the cell for the method to be delayed.		
	<i>Result</i> : The Condition for row number X dialog box opens.		
	Condition for row number 4 × • As soon as possible • Wait Hours: • Hour		
	<i>Note</i> : Use the Previous Row and Next Row buttons to select other methods for editing.		
	• Click the Wait radio button, select the number of hours and minutes that the method is to be delayed and click OK .		
	<i>Result</i> : The execution of the MethodQueue will be held for the selected number of hours and minutes and then resume.		
	Click the Save button to save the method.		
	Result: The Save MethodQueue dialog box opens.		
	• Type a file name and click the Save button.		

How to set upIf you have more than one system available, the System column will not be displayedMethodQueues onat first in the MethodQueue Editor. The table below describes how to set up aseveral systemsMethodQueue for several systems.

Step	Action	
1	Click the MethodQueue icon.	
	Click the Add System button and select a system for the first MethodQueue step from the Add System dialog box.	
2	• Repeat this for each system when you want to use a different system in the MethodQueue .	
	<i>Result</i> : Another system column will be added for each additional system.	
The Start Protocol for each method step in the MethodQueue is displayed when the corresponding method is run. If you want the MethodQueue to operate unattended you must ensure that the methods do not include a Start Protocol . See 5 How to create a method on page 78 for more information.		
The table new meth	below describes how you can create a MethodQueue if you try to start a nod run while the system is still busy with another method run.	
Step	Action	
1	Right-click on the method in the UNICORN Manager module and select Run:system name on the shortcut menu. Result: The System Busy dialog box opens.	
	Step 1 2 The Start correspon you must See 5 How The table new meth Step 1	

-

Step	Action
2	 Select the Add the method to a MethodQueue that will execute as soon as the system is free option. Click OK.
	<i>Result</i> : A MethodQueue will automatically be created in the default queue folder. The name of the MethodQueue will be the same as the method name, followed by a five-digit sequence number.
3	The method will be executed as soon as the system is free. <i>Note</i> : A warning note is displayed in the System Busy dialog box if the method includes a Start Protocol . The Start Protocol must be com- pleted at the start of the method run before it can be executed.

7.2 How to edit a MethodQueue

Method Queues are saved in a separate folder **MethodQueues** are saved in a separate folder within the folder that you specified when you saved the **MethodQueue**. The **MethodQueue** folder is represented by a special icon in the **Methods** window of the **UNICORN Manager**.

A **MethodQueue** folder contains the **MethodQueue** definition and copies of all included methods.

How to edit a MethodQueue file The **MethodQueue** files are *copies* of the original method files. If changes are made in the original method, these will not affect the method in the **MethodQueue**.

To avoid confusion between different versions of method files, make sure that **MethodQueue** definitions always contain updated methods. To implement changes in a **MethodQueue** method, do one of the following:

- Edit the method in the **MethodQueue** folder, *or*
- Edit the original method, then use the **MethodQueue** editor to update the **MethodQueue**, and replace the old method with the changed version.

Instruction

The table below describes how to edit an existing **MethodQueue**.

Step	Action
1	Right-click the selected MethodQueue folder icon in the UNICORN Manager, and select Edit from the displayed menu. Result: The MethodQueue Editor dialog box is displayed.
	Save Save As

Step	Action			
2	Select a table row to edit and do the following as required:			
	• Double-click the System cell and select a new method from the Method for row dialog box.			
	• Double-click the Condition cell and edit the delay time for the method.			
	• Click the Add System button to add a new system to the queue and use it for a MethodQueue step.			
	• Click the Delete System button to remove a system and all associated methods from the MethodQueue .			
	• Click the Insert Row Before or Insert Row After buttons to add new rows before or after the selected row.			
	• Click the Delete Row button to remove the selected row.			
	• Click the Move Row Up or Move Row Down to move the selected row one step up or down in the queue.			
3	 Click the Save button. Click the Run button to execute the MethodQueue immediately or the Close button to close the dialog box. 			

8 How to perform method runs

Introduction This chapter describes how to perform and monitor different kinds of method runs from the **System Control** module. It also describes how to control the system with manual commands and instructions.

In this chapter This chapter contains the following sections

Торіс	See
How to start a method run	
How to monitor a method run	
Manual system control	
How to perform a MethodQueue run	
If the network connection fails	8.5

8.1 How to start a method run

Before you start	Before you start a method, make sure thatthe correct system is connected in control mode
	<i>Note</i> : If the system is connected via a CU-950 Advanced unit, the Ethernet connection must not be broken during the start-up phase of the method run.
How to start from the UNICORN Manager	 You can start a method from the UNICORN Manager in two ways: Select a method in the Methods window and select File:Run. Select a method, right-click and select Run from the displayed menu.

How to start from System Control

How to start from The table below describes how to start a method run from System Control:

Step	Action
1	Select File:Run
	or
	click the Run button.
	<i>Result</i> : The Run dialog box is displayed.
	<i>Note</i> : The Run button will open the method that was used for the pre- vious run, if a run has been performed since you logged on.
2	Select a method and double-click the method icon.
	<i>Result</i> : The method run starts. If the method includes a Start Protocol this must be completed before the actual method run starts. Se further instructions below.

How to add meth-
ods to the FileFor methods that are used frequently (for example column cleaning methods or
routine synthesis), it may be convenient to define the methods as commands in the
File menu.MenuFile menu.

The table below describes how to define a method as a command:

Step	Action
1	Choose File:Menu in System Control and select the required method.
2	Click the Add button and click OK . <i>Result:</i> The method name will appear as a command in the File menu. If you choose the command, the method will start.

How to start an
instant runYou can start a method template directly if your system has defined templates.
To do this, either

• click the Instant Run icon in the UNICORN Manager toolbar



or

• select File:Instant Run in System Control.

How to use theIf the method is defined with a Start Protocol, this will be displayed before the methodStart Protocolactually starts.

The table below describes how to use the **Start Protocol**:

Step	Action
1	Start the method run.
	• Work through the start protocol, answering questions as required.
	The start protocol items that can be displayed are described in 6.5.9 The start protocol tab on page 142.
	• As each screen is completed, click the Next button to move to the next screen or the Back button to return to the previous screen.
2	Click the Start button in the last window to start the run.

Confirm/Sign authorization for the Start Protocol

If there are any questions in the **Start Protocol** that require authorized confirmation, you will be asked for a user name and password when you attempt to leave the screen containing the questions. Only users with **Confirm/Sign** authorization may authorize answers to such questions. Each question that requires an authorization must have a separate authorization.

How to start a method when the system is busy with a method run in progress, you can still start a new method.
 You will have the option to place the method in a MethodQueue, which can be executed as soon as the system becomes available again. The table below describes how to do this.

Step	Action
1	• While a method run is in progress, right-click on the next method you want to run and select Run:System .
	Result: The System Busy dialog box opens.

Step	Action
2	 Select the Add the method to a MethodQueue that will execute as soon as the system is free option. Click OK.
	<i>Result</i> : A MethodQueue will automatically be created in the default queue folder. The name of the MethodQueue will be the same as the method name, followed by a five-digit sequence number.
3	The method will be executed as soon as the system is free. <i>Note</i> : A warning note is displayed in the System Busy dialog box if the method includes a Start Protocol . The Start Protocol must be completed at the start of the method run before it can be executed.

Note: See **7.2 How to edit a MethodQueue** on page 171 for more information.

8.2 How to monitor a method run

Introduction This section describes how to monitor a method run by using the **System Control** module and how to customize the different panes.

In this section This section contains the following sub-sections

Торіс	
How to customize System Control panes	
The Run Data pane	
The Curves pane	
The Flow Scheme pane	
The Logbook pane	
The Synthesis Data pane	

8.2.1 How to customize System Control panes

Introduction The System Control module displays the status of the current system. On the Windows taskbar, there may be up to four System Control modules available that can be connected to different systems. Separate systems may be controlled and displayed independently of each other.

Illustration The illustration shows the System Control module with the Run Data, Curves, Flow scheme and Logbook panes displayed. The Synthesis Data pane is displayed on top of the other panes.



How to select what panes to display Each **System Control** module displays up to four panes for monitoring different aspects of the run. To select what panes to display, either

• click the Customize Panes icon,



or

• choose View:Panes.
How to display the Synthesis Data	 The Synthesis Data pane is displayed as a moveable dialog box on top of the other panes. Choose View:Synthesis Data.
How to customize System Control panes	 Change the size Select a split-bar and drag up and down to change the size of a specific pane. Maximize, restore or hide Right-click a pane and select the appropriate option to: maximize, restore or hide the pane.

8.2.2 The Run Data pane

Description

The **Run Data** pane displays the current values for selected run parameters. The update interval is defined in the system strategy.

The figure below displays an example of the **Run Data** pane:



How to change the appearance of the pane

The appearance of the pane can be changed so that it includes more or fewer data **f** displays. The table below describes how this is done:

Step	Action
1	In System Control, select View:Properties
	or
	right-click on the pane and select Properties on the menu.
	<i>Result</i> : The Properties dialog box is displayed.
2	Select the Run Data Groups tab and, if desirable, do one or more of the following:
	• Select an available group to be displayed in the list to the left.
	 Edit an available group: Select the group from the list on the left, and click the Edit Group button. Modify the included readings in the list to the right, and click OK.
	• <i>Create</i> a new group: Click the New group button and select the readings that you want to view from the list. Enter a name for the group, and click OK .
	• <i>Delete</i> a group: Click the Delete Group button and select a group in the Delete Layout dialog box, click OK and confirm the deletion.
3	Select the run data parameters that you want to display in the list to the right.
4	Click OK to view the selected items in the Run Data pane. The name of the selected layout replaces the default layout name Run Data .

How to change text color or text background The table describes how to change the text color or background in the displayed reading boxes.

Step	Action
1	Right-click on the pane and select Properties.
	<i>Result</i> : The Properties dialog box is displayed.
2	Select the Run Data Color tab.
3	Click the Text or Background buttons.
	Select a new color, and click OK .
	<i>Result:</i> The color change is displayed in the test field.
4	Make further adjustments to the colors as appropriate.
5	Click OK to apply the changes.

How to view and select manual instructions

Some strategies directly link specific manual instructions to the reading boxes in the **Run Data** pane. This is indicated by a double arrow (>>). A particular reading box can have one or more instructions attached to it. In cases where there is more than one instruction, one of the instructions is the main instruction.

There are two ways to view the manual instructions:

Option 1:

• Double-click the reading box.

Result: The dialog box for manual instructions is displayed, showing the instruction, or main instruction if there is more than one.

Option 2:

- Right-click the reading box. Select **Instructions** in the displayed menu. Another menu shows the specific manual instruction(s).
- Click an instruction to select it.

Result: The dialog box for manual instructions is displayed in which you can execute the appropriate command.

For more details on how to use manual instructions, please see **8.3.2 Manual instructions** on page 196.

8.2.3 The Curves pane

Introduction

The **Curves** pane of the **System Control** module displays monitor signal values graphically.

The figure below shows an example of the **Curves** pane:



How to select curves to be displayed

You can decide which curves you want to display in the **Curves** pane. Curves will only be shown for components present in the system.

The table describes how to select the curves to be displayed on the screen.

Step	Action
1	In System Control , select View:Properties . <i>Result:</i> The Properties dialog box is displayed.
2	Select the Curves tab. <i>Note:</i> The curves in the list are those for which Store is set to On in the system settings, together with any reference curves defined in the method.
3	In the Display curves list, select the curves you want to display. If you want all curves to be displayed, click the Select All button. If you do not want any curves to be displayed, click the Clear All button. Click OK .

How to display a vertical marker line

The table below describes how to display a vertical marker line:

Step	Action
1	Right-click the Curves pane and select Marker .
2	Drag the marker line with the mouse. <i>Result:</i> Where the line bisects the curve, the X-axis and Y-axis values are displayed at the top right corner of the pane.

Note: Right-click and select Snapshot to record the marker position values. See 2.2.7 Snapshots on page 39 for more information about the Snapshot function.

ence point

How to set a refer- When the vertical marker is displayed, you can set a reference point to display curve data. The table describes how to set a reference point:

Step	Action
1	 Display a Marker in the Curves pane. Right-click and select Set Marker Ref. Point to define a reference point for the marker position.
2	 When the marker is moved from the reference point, the X-axis and Y-axis values for the new position are displayed together with: the new position in relation to the position of the reference point, the minimum, maximum and average values for the curve interval between the reference point and the new position.

How to change The **Curves** pane displays graphs for the selected curves in different colors, with any the curve colors reference curves included with the method as dashed lines. and styles The table below describes how to change the curve colors and styles:

Step	Action
1	Select View:Properties.
	<i>Result:</i> The Properties dialog box is displayed.
2	Select the Curve Style and Color tab.
3	Select a curve from the Curve list.
	Select an appropriate color and style.

How to change the scale of the Yaxis

In most cases, the Y-axis is automatically scaled for each of the curves. Values on the Y-axis apply to the curve with the same color as the axis markings. To get the correct Y-axis, click the legend. The table below describes how to fix the scale of individual curves.

Step	Action
1	Select View:Properties.
	<i>Result</i> : The Properties dialog box is displayed.
	• Select the Y-axis tab.
2	Select the appropriate curve.
	• Select Fixed and type a minimum and maximum range in the fields within the specified limits.
3	Repeat step 2 for other curves if needed.
4	Click OK .

How to change the scale of the Xaxis

 Step
 Action

 1
 • Select View:Properties.

 Result: The Properties dialog box is displayed.
 • Select the Properties dialog box is displayed.

 • Select the X-axis tab.
 2

 2
 Select the appropriate base, Time or Volume.

 Note: Curves are collected in time and recalculated for display in volume. Thus, the resolution of the two bases may appear slightly different.

 3
 Select the appropriate Axis scale:

 • Total will show the curves as far as they have come in the run.

 • Window allows you to set the partian of the total page to be displayed.

The table below describes how to change the scale of the X-axis:

Window allows you to set the portion of the total pane to be displayed, either in minutes or ml depending on the selected base.
Click OK.

How to switch between time and volume units

• Click the legend of the X-axis

or

• right-click and select **Base Type**

to switch the display between time and volume units. The run is controlled according to the time/volume base defined in the current block, regardless of the base in the curves display.

How to zoom inThe table below describes how to zoom in on a selected region of the curve pane:the Curves paneI

Step	Action
1	 Press and hold the left mouse button and drag a rectangle out on the screen to encompass the area to be viewed. Release the mouse button. <i>Result</i>: The display is now zoomed in on the selected area.
2	Repeat the process for further magnification of selected areas.

How to zoom out

To reduce the scale of the zoom, right-click in the **Curves** pane, and select one of the following options:

- Undo Zoom: reverses each zoom-in action a step at a time.
- **Reset Zoom**: reverses all zoom-in actions to the default scale.

How to select curve pressure units If the **Pressure** curve is displayed in the **Curves** pane, you can set the displayed units. The table below describes how to do this:

Step	Action
1	Right-click in the Curves pane, and select Properties in the displayed menu. <i>Result</i> : The Properties dialog box is displayed.
2	Select the Y-Axis tab.
3	Select the Pressure curve and select the appropriate Pressure unit button. Click OK .

How to edit text inYou can select the way that text is aligned for the Logbook curves. You can also select to show only part of the Logbook information. The table below describes how to do this:

Step	Action
1	Right-click in the Curves pane, and select Properties in the displayed menu.
	<i>Result</i> : The Properties dialog box is displayed.

Step	Action
2	Select the Curve Style and Color tab.
3	 Select the following: Logbook curve in the Curve list as appropriate. Select the appropriate Logbook text alignment option: Horizontal Vertical Fly over (displays the text if you place the mouse pointer over the generated mark).
4	 To filter the type of Logbook information overlaid on the Curves pane, do the following: Click the Filter button. <i>Result</i>: The Filter Logbook dialog box is displayed. Select the appropriate check boxes and set the maximum block depth. Click OK to return to the Curve style and Color tab.
5	Click OK .

How to view the complete logbook information

At some breakpoints there can be more logbook information than what is possible to conveniently display in the **Curves** pane. The additional information that is not displayed is indicated by an arrow point symbol by the break point.

• Hold the mouse cursor over the break point to display the complete information in a flyover text box, as shown in the illustration below.



8.2.4 The Flow Scheme pane

Introduction The flow scheme is a graphical representation of the oligonucleotide synthesis system that shows the current status of the run. During a run, the flow scheme displays open flow path(s) in color and monitor signals with numerical displays.

Illustration The illustration below shows an example of a flow scheme for a run:



How to stretch aThe flow scheme can be stretched to fit the screen. To do this, right-click in the paneflow schemeand select Stretch in the shortcut menu.

How to view and select flow scheme manual instructions Some strategies link specific manual instructions directly to the components in the flow scheme pane. The components in the flow scheme that are associated with instructions are indicated with double arrows (>>). A particular component can have one or more instructions attached to it. In cases where there is more than one instruction, one of the instructions is the main instruction.

To display and select instructions:

- double-click a component
- or
- right-click a component, select **Instructions** and an instruction in the shortcut menu.

Result: The manual instructions dialog box for the selected instruction type opens.

8.2.5 The Logbook pane

Introduction All actions (including method start and end, base instruction, method instructions and manual interventions such as **Pause** or **Hold**) and unexpected conditions such as warnings and alarms are logged for every run, with date, time and current user name where appropriate. The logbook thus provides a complete history of any given run. The log is saved in the result file.

Illustration The illustration below shows an example of the **Logbook** pane:

0.00 ml Method Run 2002-10-29, 16:19:30, Method : 02no337, Result : c:\...\Default\AKOP10 0.00 ml Batch ID: 75885179-3670-4E46-A0E6-1864CC13BC96 0.00 ml Base_Id_dT 0.00 ml Bock START_parameters 0.00 ml Bock START_parameters 0.00 ml Bock Stolum_Number 0.00 ml Bock Column_5 0.00 ml Base Time {min} 0.00 ml End Block 0.00 ml End Block 0.00 ml Bock UV_Detrit 0.00 ml Bock UV_Detrit 0.00 ml Bock Tume {min} 0.00 ml UV_Wavelength 350 nm, 290 nm, 0 nm

Note: The second logbook line is the **BatchID** that is automatically generated.

Autoscroll

The **Logbook** pane can autoscroll to display the latest entries. Right-click in the pane, and select **Autoscroll**. You can also select the **Autoscroll** option in the **Properties** dialog box (**View: Properties** and select the **Logbook** tab).

How to filter theYou can choose to display only selected items in the logbook. The table belowlogbook contentsdescribes how to activate the filter.

Step	Action
1	Right-click in the Logbook pane and choose Properties.
	<i>Result</i> : The Properties dialog box opens.
2	Choose the Logbook tab.
	 Select the items you want to display in the logbook (all items are selected by default).
	Click the OK button.
	<i>Result</i> : Only the selected items will be displayed in the logbook. The Logbook title in the upper right corner will show the text (Filter on) to indicate that not all items are visible. All items will still be logged in the result file.

How to find log-
book text entriesThe logbook can be searched for specific text entries. The table below describes the
function:

Step	Action
1	Right-click in the Logbook pane and choose Find . <i>Result</i> : The Find dialog box opens.
2	 Type the text you want to locate. Select search criteria if necessary. Click OK. <i>Result</i>: The located logbook entry is highlighted.

8.2.6 The Synthesis Data pane

IntroductionThe Synthesis Data displays the online integrated trityl values, which shows the
coupling efficiency, in a spreadsheet format. Duration and Retention are displayed
as ml or min, depending on what has been selected for the X-axis in the Curves pane.
The highlighted row in the Synthesis Data pane shows the currently running cycle.

How to displayThe Synthesis Data pane is displayed as a moveable dialog box on top of the otherthe Synthesispanes.

Data

• Choose View:Synthesis Data.

Illustration

The illustration below shows an example of the **Synthesis Data** pane:

Synthe	sis Data							×
	Base	Retention (min)	Duration (min)	Detrit Area	Peak Height	Last Eff. (%)	Average Eff. (%) 革	
8	С	1,63	1,13	44340,50	3084,00	100,00	99,74	4
9	G	1,73	0,86	29505,20	3065,00	78,40	97,37	4
10	A	1,77	0,89	32736,10	3043,00	88,40	96,47	
11	A	1,99	0,87	32138,00	3135,00	98,20	96,63	
12	T	2,13	1,09	40076,50	3082,00	94,50	96,45	
13	T	2,07	1,12	40226,50	3045,00	100,40	96,75 🚽	
14	Å						—	1
15	G						±	
						Close	<u>H</u> elp]

8.3 Manual system control

Introduction This section describes how to control the system with manual commands and instructions.

In this section This section contains the following sub-sections

Торіс	See
The toolbar and status bar	8.3.1
Manual instructions	8.3.2
Alarms and warnings	8.3.3

8.3.1 The toolbar and status bar

Toolbar buttons

Ittons The toolbar at the top of the **System Control** module contains three sets of buttons:

- Manual Direct Commands buttons for starting and stopping the run
- **Windows** buttons to access dialog boxes for pane selection, documentation and layout properties
- System Access buttons to control the system connection.

Show and hide

The toolbars can be shown and hidden by choosing **View:Toolbars** and selecting the relevant boxes.

The figure below shows the toolbar:

	Run	Hold	Pause Continue	End	1
--	-----	------	----------------	-----	---

Manual DirectThe available Manual Direct commands buttons in System Control are dependentCommandson the control status of the connection. The table below shows when each button is
available:

Control Status	Available buttons
End	Run
Running	Hold, Pause, End
Manual	Run, Pause, End
Hold	Pause, Continue, End
Method pause	Hold, Continue, End
Manual pause	Run, Continue, End

Direct command The table below button functions

The table below describes the functions of the **Manual direct command** buttons.

Button	Function
Run	Opens the Run dialog box, which shows all available methods, as the first step in a method run. If a method is loaded, Run Setup opens. The run will start immedi- ately if a start protocol isn't part of the method.

Button	Function
Hold	Suspends execution of a method, but continues
	• to pump liquid at the current flow rate. All settings remain unchanged.
	to increase accumulated time and volume.
	Method instructions are not executed until the Contin- ue button is pressed.
Pause	Behavior of the Pause button is strategy-dependent. The Pause button suspends execution of a method and stops all pumps so that the system comes to a stand- still.
	For ÄKTAdesign systems, valves remain in the position they were in before the pause.
	Accumulated time and volume is not increased during a Pause .
	Method instructions are not executed until Continue is pressed.
Continue	Resumes execution of a paused or held method.
End	Terminates method execution
	• Puts the system into an End state.
	<i>Note</i> : You can choose to save the partial result or discard it.

Note: The commands can also be found on the **Manual** menu.

Windows buttons The table below describes the functions of the Windows buttons:

Button	Function
	Opens a dialog box where you can choose which win- dow panes to display. This button is equivalent to the menu command View:Panes .
	Opens the documentation pages. Run notes can be entered on the Notes tab and settings can be changed. Other tabs are displayed for information only. This button is equivalent to the menu command View:Doc- umentation .

8.3 Manual system control

8.3.1 The toolbar and status bar

Button	Function
	Opens the properties pages. This button is equivalent to the menu command View:Properties .

System Access buttons

There are two functions of the **System Access** buttons:

Disconnect/Connect system



The **Disconnect** button is used to disconnect the system and leave it in a locked or unlocked state.



The **Connect** button connects the system.

Leave/Take control of the system



The Leave control button leaves the system in a locked or unlocked state.



The **Take control** button takes control of the system.

Status bar, con-
nection statusThe status bar displays a message indicating the connection status of the window.The table below describes the different messages:

Message	Connection status
Controlled by: <user></user>	The indicated user has a control mode connection to the system. Other users can establish a view mode connection.

Message	Connection status
Locked by: <user></user>	The indicated user has left the system in a locked state. Users who can supply the required password can un- lock the system and establish a connection. The pass- word is case sensitive.
	<i>Note:</i> It is possible to unlock with the "lock" password or with the UNICORN logon password. Anyone who uses the UNICORN logon password must have Unlock systems access rights. The "lock" password is the password entered by the user who locked the system.
System is available	Any user can establish a connection.

status

- **Status bar, Watch** The status bar displays a message indicating if a **Watch** is active in the method.
 - Click the **Active watch** status message to open the **Watch** dialog box with information about the active **Watch** instruction.

8.3.2 Manual instructions

Introduction	The oligonucleotide synthesis system can be controlled with manual instructions issued from the Manual menu in the System Control module. The available instruction options are dependent on the strategy.
Manual instruc- tions during a	Manual instructions can be issued while a method is running. A manual setting applies until the next method instruction of the same type is executed
method run	<i>Example</i> : A manual Flow instruction will set the flow rate until the next Flow instruction in the method is executed. Manual instructions that you issue during a method are recorded in the logbook for the method run.
The manual in-	The Manual menu in Sustem Control opens a dialoa box similar to the Instruction

structions dialog

The **Manual** menu in **System Control** opens a dialog box similar to the **Instruction box** in the **Method Editor**. The name of the connected system is displayed on the title bar of the dialog box. See an example in the illustration below:

×
Inset Delete Execute Close Help

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

How to use manual instructions

Manual instructions are entered in the same way as method instructions from the dialog box in the **Method Editor**. The table below describes how to add a manual instruction:

Step	Action
1	• Select an instruction group and a component in the Instructions field.
	• Select instruction parameters in the Parameters field.
2	• Click the Insert or Execute buttons as needed. (See the descriptions of the different functions below)

The buttons of the manual instructions dialog box

The buttons of the The table below describes the functions of the manual instructions buttons:

Button	Function
Insert	This button places the current instruction in the list at the bottom left of the dialog box.
Delete	This button deletes the selected instruction from the current list only. One instruction can be deleted at a time.
Execute	This button
	• executes all instructions in the list at the same time
	or
	• executes the currently marked instruction if the list is empty.
	<i>Note</i> : Although all instructions are executed simultan- eously, some may take some time to complete in the liquid handling module.
Close	If you click the Close button without first clicking the Execute button, commands in the list
	will not be executed
	• will be deleted from the command list.

How to save When you choose to run the system manually - as opposed to a Method run - the results are automatically stored in a folder called Manual Runs. The Manual Runs folder stores the ten most recent results from your manual runs. To save a result file from the Manual Runs folder more permanently, you need to move or copy it to

another location.

An alternative way to save the results from a manual run is to record the results manually in a result file. The table below shows how to do this:

Step	Action
1	Choose Manual:Other.
	• Select the instruction Record On at the beginning of the run.
2	Click the Execute button.
	<i>Result</i> : UNICORN will prompt for a result file name.

8.3.3 Alarms and warnings

Introduction	Alarms and warnings are displayed regardless of the activity currently in progress in UNICORN. You will be notified of an exceeded limit in a running system even if you are developing a method, evaluating data or monitoring a method run on a different system. Warnings and alarms are also recorded in the logbook for the run.
Limits for monitor signals	The system settings determine the acceptable limits of monitor signals during a run. The limits can also be set for the current run by an instruction in the method. Limits set with a method instruction override the limits set in system settings. If these limits are exceeded in a run, a warning or alarm dialog box is displayed on the screen.
Effects of alarms and warnings	 Alarms and warnings have different effects on the system: <i>Warning</i>: The run continues. <i>Alarm</i>: The system is paused.
In a network sys- tem	In a network installation, alarms and warnings are displayed on the controlling station and all stations viewing the system. An alarm can be acknowledged only from the computer connected in control mode. Alarms are displayed but cannot be acknowledged on computers connected in view mode.

8.4 How to perform a MethodQueue run

Instruction The table below describes how to run a MethodQueue:

Step	Action
1	• Make sure that all systems used in the MethodQueue are connected with control mode connections.
2	Select a MethodQueue in the Methods pane in the UNICORN Manager and
	 right-click the MethodQueue icon in the Methods pane and select Run from the shortcut menu.
	or
	• double-click the MethodQueue icon in the Methods pane and click the Run button in the MethodQueue Editor dialog box.
	<i>Result:</i> The MethodQueue will start in accordance with the conditions defined in the MethodQueue setup.
See 7.1 How to create a new MethodQueue on page 167 for information about how	

Unattended Meth- odQueue opera- tion	The Start Protocol for the first and each subsequent method step in the MethodQueue is displayed when the corresponding method is run. If you require unattended MethodQueue operation after the start of the first method step, make sure that subsequent method steps do not include a Start Protocol .
	<i>Note</i> : If the Start Protocol for a method in the queue is cancelled, the MethodQueue is paused. Select MethodQueue:Display Running in the UNICORN Manager and Restart or End the run in the displayed dialog box.
MethodQueues when the system is busy	You can choose to place a method in a MethodQueue if the system is already busy with another method run (See 7.1 How to create a new MethodQueue on page 167). In a similar manner you can also start a new MethodQueue while another MethodQueue is in progress. It will be placed in queue and executed when the first queue is completed.

How to display and edit pending and running MethodQueues

Definition: A pending **MethodQueue** is one for which **Run** has been requested but which has not yet started, either because the system is not available or because the setup time has not been reached.

The table describes how to display running and pending **MethodQueues**.

Step	Action
1	Click the Running MethodQueue icon.
	Result: The Running MethodQueue dialog box is displayed.
	Running MethodQueues Image: Status: Stat Time Image: Status: Stat Time Image: Status: Stat Time Image: Status: Stat Time Image: Status: Stat Time Image: Status: Status: Stat Time Image: Status: Sta
2	Select a MethodQueue in the Active MethodQueues list box.
	<i>Result:</i> Information on the selected MethodQueue is displayed in the Details for field of the dialog box.
	Choose from the following:
	• The Restart button restarts the currently running MethodQueue if a Start Protocol has been terminated by Cancel .
	• The End button terminates a running MethodQueue after the cur- rent step. Any methods currently in operation will continue to run and must be terminated with the End button in the System Control window if they are not to run to completion. If you click the End button for a pending MethodQueue , it is deleted from the pending list.
	• The End All button terminates the running MethodQueue and de- letes all MethodQueues from the pending list.
	• The Close button closes the dialog box.

8.5 If the network connection fails

Results will be saved in the Failed folder If the results of a method run are stored on a server or other location, and there is a network communication failure during a method run that has been started from a remote station, the method run will continue and the results will be saved in the **Failed** folder on the local station. A control mode connection can be established on the local station to control the running system. See the Administration and Technical Manual for more details.

9 How to view results

Introduction A result file is automatically generated at the end of a method run and contains a complete record of the method run, including method, system settings, curve data and method run log. The **Evaluation** module offers extensive facilities for presentation and evaluation of curve data.

This chapter describes how to present the chromatograms and curves of your result file and how to create and print reports.

In this chapter

This chapter contains the following sections

Торіс	See
How to open a result file	9.1
How to use the File Navigator	9.2
Basic presentation of chromatograms	9.3
How to optimize the presentation of a chromatogram	
How to print active chromatograms	9.5
How to create and print reports	9.6
Run documentation	

9.1	How to open a result file
Introduction	All contents of the result files are opened in the Evaluation module. By default, the chromatograms in a run are shown as opened windows. The chromatogram window on top is the active window. There is also a minimized Temporary chromatogram window. See 9.3 Basic presentation of chromatograms on page 208 for further information about chromatograms.
	<i>Note</i> : It is not possible to open the same result file from two different locations simultaneously.
How to open a result from the UNICORN Man- ager	 To open a result file from the UNICORN Manager, do one of the following: Double-click a result file in the Results window of the UNICORN Manager, or
ugei	 Select a result file icon in the Results window of the UNICORN Manager and select File:Open,
	 or Click the Evaluation icon in the UNICORN Manager, open the Evaluation module and select a result file from the Open Result dialog box.
How to open a result in the Evalu- ation module	 To open a result file in the Evaluation module: Do the following: Select File:Open Select a result file from the Open Result dialog box. Or Do the following: Select View:File Navigator Locate and select a result file from the File Navigator.
	<i>Note</i> : See 9.2 How to use the File Navigator on page 204 for detailed instructions on how to locate files and set up File Navigator preferences.

9.2 How to use the File Navigator

IntroductionThe File Navigator can be used to locate and open result files in the Evaluation
module. Recent runs are also listed based on the user preferences.

How to open the File Navigator

To open the File Navigator:

- Click the **Evaluation** module icon in the Windows task bar.
- Select View:File Navigator

Result: The **File Navigator** opens in the **Evaluation** module. The **File Navigator** can be resized and dragged to other positions in the module.

 How to open files
 The table below describes how to use the Files list to locate and open a result file.

 from the Files list
 Step

 Action

Step	Action
1	 Click the Files tab Result: The Files list opens in the File Navigator. The list is identical to the Results window in the UNICORN Manager and shows all user available folders and files. Recent Runs Files Find Time File 20030924 20030925 20030925 20031001 20031002 20031007 20031016 20031017 Example files Manual runs (System M4) Manual runs (System M4)
2	Navigate to the desired folder
	Double-click the desired result file
	<i>Result</i> : The result file opens in the Evaluation module.

How to use Find toThe Find function in the File Navigator is used to locate result files in the availablesearch for filesfolders. The table below describes how to use the Find function to locate and open
a result file.

Step	Action	
1	Click the Find tab	
	Result: The Find list opens in the File Navigator.	
	Recent Runs Files Find	
	Result file name	
	Value of variable 'Sample_ID*'	
	Quick Find Find	
	Example Result001 (c:\ Example Result002 (c:\	
	Example Result003 (c:\	
2	• Type a file name or part of a file name in the Result file name text	
	or	
	• Type a Sample ID value in the Value of variable Sample_ID text	
	box.	
	<i>Note</i> : The defined variable name must begin with Sample_ID .	
3	Click the Quick Find button	
	<i>Result</i> : The located result files are listed in the File Navigator .	
4	Double-click the desired result file or chromatogram	
	<i>Result</i> : The file or chromatogram opens in the Evaluation module.	

Note: Click the **Find** button to open the **Find Files** dialog box where more search functions are available. See **4.3 How to arrange and locate your files** on page 73 for more information.

How to open a Re-
cent RunThe Recent Runs list shows all the available recorded recent runs based on the
selected user preferences. The table below describes how to use the Recent Runs
list to locate and open a result file.

Step	Action	
1	Click the Recent Runs tab	
	<i>Result</i> : The Recent Runs list opens in the File Navigator .	
	Recent Rure Fired Recent Results Fired Fired ID57001 (o:\\latta\\Wizardver\0p6\) Fired ID57001 (o:\\latta\\Wizardver\0p6\) Fired ID57001 (o:\\latta\\Wizardver\0p6\) Fired ID57001 (o:\\latta\\Wizardver\0p6\) Fired ID57001 (o:\\latta\\Instruction verification\P2\0p80pd Fired ID32001 (o:\\latta\\Instruction verification\P2\0p80pd B-ID33002 (o:\\latta\\Instruction verification\P2\0p80pd B-ID33002 (o:\\latta\\Instruction verification\P2\0p80pd B-ID33001 (o:\\latta\\Instruction verification\P2\0p80pd B-ID33001 (o:\\latta\\Instruction verification\P2\0p80pd B-ID35001 (o:\\latta\\Instruction verification\P2\0p80pd B-ID35002 (o:\\latta\\Instruction verification\P2\0p80pd B-ID35002 (o:\\latta\\Instruction verification\P2\0p80pd B-ID35002 (o:\\latta\\Instruction verification\P2\0	
	and saved they are noted in bold text. When they are opened and saved the text is changed to plain text.	
2	• If needed, click the Refresh button in the bottom of the File Navig- ator	
	<i>Result</i> : The Recent Runs list is updated with all runs that were per- formed since the File Navigator was opened the last time.	
3	Locate the desired run	
	Double-click the file	
	<i>Result</i> : The result file opens in the Evaluation module.	

Note: Click the **+** signs to view or select individual chromatograms from the result files. Individual result files can be selected and removed from the list by clicking the **Remove** button. The **Remove all** button clears the whole list.

Note: **Remove** only clears the list, the files are not deleted.

ences for Recent Runs

How to set prefer- The File Navigator will display Recent Runs based on the individual user preference settings. The table below describes how to adjust the preference settings:

Step	Action	
1	Click the Preferences button	
	Result: The Preferences dialog box opens.	
	Preferences	
	Maximum number of files to keep 10	
	Maximum no of days to keep files	
	Files created by the current user only Files created by the specified users Specify	
	Remove files when saved	
	OK Cancel Help	
2	 Type the maximum number of files to keep on the list 	
	• Type the maximum number of days to keep the files on the list	
3	Select which files to display on the list:	
	Only files created by the current user	
	All files created by specified users	
	<i>Note</i> : Click the Specify button to open a dialog box and select from a list with all accessible users.	
	All accessible files regardless of the creator	
4	• Choose Remove files when saved if the files are to be removed from the list when they have been saved.	
	Click the OK button.	
	<i>Result</i> : All new results will be displayed on the Recent Runs list based on the changed preferences.	

How to close the File Navigator

To close the **File Navigator**:

• Click the small cross in the top right-hand corner of the File Navigator.

Result: The **File Navigator** closes.

9.3 Basic presentation of chromatograms

Introduction This section describes how to access result files and optimize the presentation of a chromatogram and its curves via the **Chromatogram Layout** dialog box.

In this section This section contains the following sub-sections

Торіс	See
Introduction and temporary chromatograms	9.3.1
The chromatogram window	

9.3.1 Introduction and temporary chromatograms

Contents of a chromatogram	Chromatograms can be viewed in the Evaluation module. A chromatogram includes a number of curves that have been created during a method run, such as UV, conductivity, etc. A chromatogram also contains the curves created and saved during an evaluation session. The original raw data curves cannot be deleted or modified, but they can be used as the basis for evaluation procedures and subsequent creation of new curves.
Temporary chro- matograms	A Temporary chromatogram is essentially an empty chromatogram that is specific to the Evaluation module. It is also user-specific, so that all users have their own. Information contained within a Temporary chromatogram is automatically saved from one evaluation session to the next, but is not saved within the result files.
How to copy curves into Tem- porary	Curves can be copied into Temporary and comparisons or evaluations can be performed. This is particularly useful if you do not want to clutter up your original chromatograms with a large number of curves. It can also be used to keep blank run curves or curves to compare when you open different result files. The table below describes how to copy curves into Temporary :

Step	Action
1	Open a result file.
2	Select Edit:Copy:Curves. <i>Result</i> : The Copy Curve dialog box is displayed.
3	Select a source chromatogram and a curve to be copied in the Source Chromatogram fields.
4	Select Temporary as the target chromatogram and a position for the new curve in the Target Chromatogram fields.
5	Click the Copy button. <i>Result</i> : The curve is copied into the Temporary chromatogram. Click the Close button.

How to clear a temporary chro-	The table b	elow describes how to clear the contents of a temporary chromatogram:
matogram	Step	Action
	1	Open the relevant result file.
	2	 Select Edit:Clear Temporary Chromatogram. Click the Yes button to confirm.

9.3.2 The chromatogram window

Main views

The chromatogram window is divided into four main views:

- File Navigator
- header information
- curves
- synthesis data

The displayed areas for the views can be adjusted by dragging the borders with the mouse cursor between the views.

The picture below shows an example of the window with all views present:



How to view header information

You can display header information at the top of a chromatogram, with details on variables, scouting variables, questions and/or notes. Header information cannot be displayed for imported chromatograms.

The table below describes how to display header information:

Step	Action	
1	Open a result file.	
2	In the Evaluation module, select Edit:Chromatogram Layout <i>Result</i> : The Chromatogram Layout dialog box is displayed.	

Step	Action	
3	 Click the Header tab. Select the options you want in the header. Click OK. 	
4	 In the chromatogram window, place the cursor at the top of the curve window (just below the toolbar) until the window sizing tool appears. Drag the cursor down to display the header window. 	

How to view synthesis data

The table below describes how to display the integrated trityl values:

Step	Action	
1	Open a result file.	
2	 Choose View: Synthesis Data. Result: The Synthesis Data dialog box opens as a spread sheet on top of the Evaluation module. 	

Run curves, default appearance and information

The first time a result file is opened and viewed, a default layout is applied to display all the original curves. The default layout can be changed by the user (see 9.4.5 How to save and apply a layout on page 224).

Information for each curve

Each curve is automatically assigned a default color and style, with default information about each curve displayed in the key above the curves. This information includes

- result file name
- chromatogram name •
- curve name. •

Choose the Y-axis scale

Each curve has a correspondingly colored Y-axis. To choose the appropriate Y-axis scale

• click on the Y-axis until the desired scale is displayed

or

• click on the name of the curve.

Run curves, short-
cut menuWhen viewing curves in the Evaluation module, you can access a menu that provides
a quick alternative to menu commands. Right-click the run curves view to display
the menu shown in the picture below:

	<u>U</u> ndo Zoom
	Reset Zoom
	Add Text
	E <u>d</u> it Text Mode
ւր	Peak Integrate
	Shift <u>O</u> ffset
	<u>H</u> atch
~	<u>M</u> arker
	<u>S</u> et Marker Ref. Point
	R <u>e</u> set Marker Ref. Point
	S <u>n</u> apshot
	Copy to Clipboard
	Copy to Metafile
	Base Type
	Properties

Optimizing the workspace

The chromatogram window can be minimized and maximized using ordinary Windows commands. The table below describes extra features to optimize the workspace:

Use the command	if you want
Window:Arrange icons	to arrange icons of minimized windows.
Window:Tile	to view several chromatogram windows side by side.
Window:Cascade	to stack the open windows like a deck of cards.

How to display a vertical marker line

The table below describes how to display a vertical marker line:

Step	Action
1	Right-click the Curves pane and select Marker .
2	Drag the marker line with the mouse. <i>Result</i> : Where the line bisects the curve, the X-axis and Y-axis values are displayed at the top right corner of the pane.

Note: Right-click and select **Snapshot** to record the marker position values. See **2.2.7 Snapshots** on page 39 for more information about the **Snapshot** function.

ence point

Step	Action
1	 Display a Marker in the Curves pane. Right-click and select Set Marker Ref. Point to define a reference point for the marker position.
2	 When the marker is moved from the reference point, the X-axis and Y-axis values for the new position are displayed together with: the new position in relation to the reference point, the minimum, maximum and average values for the curve interval between the reference point and the new position.

How to set a refer- The table describes how to set a reference point:

How to displayThe table below describes how to display the logbook entries as an overlay in thethe logbook over-chromatogram.layImage: Comparison of the logbook entries as an overlay in the l

Step	Action
1	• Right-click in the chromatogram window and choose Properties on the shortcut menu.
	<i>Result</i> : The Chromatogram Layout dialog box opens.
2	 Choose the Curve tab. Select the Logbook curve.
3	 Choose the Curve Style and Color tab. Click the Filter button in the Logbook text alignment field. <i>Result</i>: The Filter Logbook dialog box opens.
4	 Select all the logbook items you want to display and click OK. Click OK in the Chromatogram Layout dialog box. <i>Result</i>: The selected logbook items are displayed in the chromatogram window.

How to view the complete logbook information

At some breakpoints there can be more logbook information than what is possible to conveniently display in the chromatogram window. The additional information that is not displayed is indicated by an arrow point symbol by the break point.

• Hold the mouse cursor over the break point to display the complete information in a flyover text box, as shown in the illustration below:


9.4 How to optimize the presentation of a chromatogram

Introduction This section describes some of the ways you can optimize the presentation of a chromatogram.

In this section This section contains the following sub-sections

Торіс	See
How to make changes in the Chromatogram Layout dialog box	9.4.1
The Curve tab and Curve Names tab	9.4.2
The Curve Style and Color tab	9.4.3
How to change and fix the axes	9.4.4
How to save and apply a layout	9.4.5
How to show part of a curve	9.4.6
How to change the size of the Logbook marks	9.4.7

9.4.1 How to make changes in the Chromatogram Layout dialog box

Instruction

The **Chromatogram Layout** dialog box is used to make changes regarding chromatogram presentation. The main features of the **Chromatogram Layout** dialog box regarding chromatograms are described in the subsequent sections in this chapter. Features regarding peak tables are described in **11.1.2 How to perform a peak integration** on page 291.

The table below describes how to make changes in the **Chromatogram Layout** dialog box:

Step	Action		
1	Open a result file.		
2	Right-click the chromatogram window and select Properties		
	or		
	Choose Edit:Chromatogram Layout.		
	<i>Result:</i> The Chromatogram Layout dialog box is displayed. The view from which you activate the Properties command determines the tab that is displayed in the Chromatogram Layout dialog box.		
3	Carry out the changes on the different tabs to get the desired layout for header, curves and peak table.		
	Select Apply to all chromatograms if you want to apply changes made in the Chromatogram Layout dialog box to all open chromatograms.		
	Click OK .		

9.4.2 The Curve tab and Curve Names tab

The Curve tab The **Curve** tab of the **Chromatogram Layout** dialog box contains a list of all the curves included in the chromatogram. Select the curves you want to display in the chromatogram, and click **OK**.

Curve name ap-
pearanceYou select options for the curve name appearance on the Curve Names tab. This is
an example of a default curve name:

Result:11_UV1_280

The table below describes the three components that make up the default curve name:

Component	Description	Example
Result name	Name of the result.	Result
Chromatogram name	Number given automatic- ally during a run or a name defined by the New_Chromatogram in- struction.	11
Curve name	Curve type. In this example, the sys- tem uses a variable wavelength detector, so the wavelength (280) for the UV curve is also giv- en.	UV1_280

How to choose curve name appearance You can choose to view only part of the curve name. The table below describes how to do this:

Step	Action
1	Open a result file.
2	Choose Edit:Chromatogram Layout.
	<i>Result</i> : The Chromatogram Layout dialog box is displayed.
3	Click the Curve Names tab.

Step	Action
4	 Select the appropriate boxes for Curve name appearance. Select the appropriate Curve legend position. Click OK.

Note: It is usually sufficient to select the **Curve Name** option if only one chromatogram is being evaluated. However, confusion can arise when more than one chromatogram is shown, so more complete names might be necessary.

9.4.3 The Curve Style and Color tab

Introduction	All curves within a chromatogram are represented by a default color and line style. Curves imported into the chromatogram or newly created curves are automatically assigned a color and line style.		
Peak label set- tings	Peaks car dialog bc • Reten	n be labeled on the Curve Style and Color tab of the Chromatogram Layout ix. Use a combination of the following labels: tion (the default label)	
	sequeuser-c	defined Peak name .	
Logbook text alignment set- tings	The Logb • Vertic • Horiza • Fly Ov is care	book text can be set to the following alignment options: al bontal ver , which sets text labels as hidden text that appears only when the cursor efully positioned over a fraction mark.	
the color and stule of a curve	Sten		
	1	Open a result file.	
	2	Choose Edit:Chromatogram Layout . <i>Result</i> : The Chromatogram Layout dialog box is displayed.	
	3	Click the Curve Style and Color tab.	
	4	 Select the curve you want to change from the list. Select the desired color and style. Click OK. 	

How to display and filter logbook information

The table below describes how to display and filter logbook curve information:

Step	Action
1	Open a result file.

Step	Action
2	Choose Edit:Chromatogram Layout.
	<i>Result</i> : The Chromatogram Layout dialog box is displayed.
3	Click the Curve tab.
	Select the logbook curve.
4	Click the Curve Style and Color tab.
	• Click the Filter button in the Logbook text alignment field.
	<i>Result</i> : The Filter Logbook dialog box is displayed.
5	Select the type of logbook information you want to show.
	Set the maximum block depth to show.
	Click OK.

 How to display a
 The table below describes how to display a hatched background in the chromatogram window:

 ground
 Stem

Step	Action
1	Open a result file.
2	Choose Edit:Chromatogram Layout.
	<i>Result</i> : The Chromatogram Layout dialog box is displayed.
3	Click the Curve Style and Color tab.
	• Select the Hatch box.
	 If desired, select the Apply to all chromatograms box and click OK.
	Result: Hatch marks are displayed as a background.

Note: You can also right-click in the **Chromatogram** window and select **Hatch**.

How to change and fix the axes 9.4.4

How to change	
and fix the Y-axis	

The table below describes how to change and fix the Y-axis:

Step	Action		
1	Open a result file.		
2	Choose Edit:Chromatogram Layout .		
	Result. The Chromatogram Layout alalog box is displayed.		
3	Click the Y-Axis tab.		
4	Select the appropriate curve from the list.Click the Fixed option.		
5	 Type the desired minimum and maximum values. Click the All with this unit button if you want other curves with the same Y-axis units as the current scaled curve to be similarly scaled. Note: The values will only be applied to existing curves. They will not be applied to new curves created after this function was last used. Click OK. 		

How to add a

The table below describes how to add a second Y-axis to the chromatogram.

•			aaa	~
S	seco	nd	Y-ax	kis

Step	Action
1	Choose Edit:Chromatogram Layout . <i>Result</i> : The Chromatogram Layout dialog box is displayed.
2	Click the Y-Axis tab.
3	 Select the appropriate curve from the Right Axis droplist. Click the OK button.

How to change and fix the X-axis

The table below describes how to change and fix the X-axis:

Step	Action
1	Open a result file.

Step	Action			
2	Choose Edit:Chromatogram Layout.			
	<i>Result</i> : The Chromatogram Layout dialog box is displayed.			
3	Click the X-Axis tab.			
4	Select the appropriate option in the Base field:			
	Time of retention			
	Volume			
	Column Volume			
	<i>Note:</i> Some calculated curves, for example baselines, exist in only one base and might seem to disappear when the base is changed. Curves are collected in time and recalculated for display in volume. Thus, switching the base between Time and Volume can slightly alter the resolution.			
5 • Click the Fixed option in the Axis scale field to set the ax manually.				
	Type the desired minimum and maximum values.			
	• Click OK .			

9.4.5 How to save and apply a layout

Introduction All configurations that you make in the Chromatogram Layout dialog box can be saved as a layout. It is possible to apply saved layouts to other chromatograms. All saved layouts are user-specific.

How to save a layout

The table below describes how to save a layout:

Step	Action
1	Open a result file.
2	Choose Edit:Chromatogram Layout . <i>Result</i> : The Chromatogram Layout dialog box is displayed.
3	Make the appropriate layout configuration within the various tabs. View your changes Click OK if you want to return to the chromatogram window to see the applied affects of a given configuration. Return to the Chromato- gram Layout dialog box to perform further changes.
4	 Select the Layout Library tab. Click the Save current layout as button. <i>Result</i>: The Save Layout dialog box is displayed.
5	 Type a name for the layout. If you want the current layout to be the new default layout, select the Save as default option. Click OK. <i>Result</i>: The new name is added to the Saved layouts list. Click OK.

How to apply a layout

The table below describes how to apply a layout:

Step	Action
1	Select the Layout Library tab on the Chromatogram Layout dialog box.

Step	Action		
2	• Select a layout from the Saved layouts list.		
	Click the Apply selected layout button.		
	<i>Result:</i> The layout is automatically applied to the active chromato- gram window.		
	• If the same layout is to be applied to all chromatograms on the Evaluation workspace, select the Apply to all chromatograms checkbox.		
	• Click OK .		

9.4.6 How to show part of a curve

Introduction

You can select a part of a curve in order to examine details more closely.

You can

• use the zoom to magnify

or

• cut the axes.

It is also possible fix the axes, see **9.4.4 How to change and fix the axes** on page 222.

How to use the zoom function

In the active chromatogram window, you can zoom in on a designated area of the chromatogram. This is the easiest and quickest way to enlarge different parts of a curve. The table below describes how to do this:

Step	Action	
1	Open a result file.	
2	 Place the mouse pointer in any corner of the area you want to magnify. Press and hold the left mouse button. A magnifying glass icon will be added to the mouse pointer arrow on the screen. Drag a box to cover the area to be magnified, and release the mouse button. <i>Result</i>: The selected region is now displayed in the entire chromato- 	
	gram window, together with appropriate scales for the Y and X axes.	
3	Use the arrow keys on the keyboard to move around in the chromato- gram at the current zoom scale.	
4	Undo zoom	
	Right-click in the window and select Undo zoom to undo the last zoom step.	
	Reset zoom	
	Right-click in the window and select Reset zoom to reset all zoom steps at once.	

How to cut a a new curve

The table below describes how to cut the curve between two values on the X-axis curve and store as and store this part of the curve as a new curve:

Step	Action			
1	Open a result file.			
2	Choose Operations:Cut curve .			
3	 Select the curves to be operated on. Click OK. 			
	<i>Result:</i> The selected curves are shown in the Cut dialog box which contains two vertical cursor lines.			
4	To select the region to be cut, either			
	• drag the two cursor lines to define the left and right limits of the cut area			
	or			
	• type the desired left and right limit values in the Left limit and Right limit boxes.			
	<i>Note:</i> The areas outside of the Left limit and Right limit will not be saved in the newly created cut curve. Thus, the X-axis of the new curve will not begin at zero unless this is designated as one of the limits. The original curve is not changed.			
5	Click OK .			
	<i>Result</i> : The Save Cut Curves dialog box opens.			

Step	Action			
6	Select whether to save the new cut curve in			
	- the Source chromatogram , that is the current active chromato- gram,			
	or			
	 a New chromatogram (if you select this option, you can change the name of the chromatogram. Note that it is a recommenda- tion not to use only numbers as names for chromatograms.). 			
	• Click OK .			
	Result:			
	- If the destination of the cut curve was the source chromatogram, the cut curve is automatically displayed in the source chromatogram.			
	- If the destination of the cut curve was a new chromatogram, this will be represented as a new, open chromatogram window.			

9.4.7 How to change the size of the Logbook marks

Introduction The sizes of the Logbook marks are all determined by your user settings. The settings are applied for all your chromatograms.

Instruction The table below describes how to change the size of the **Logbook** marks:

Step	Action			
1	Choose Administration:Change User Attributes in the UNICORN Manager module.			
	<i>Result</i> : The Change user attributes dialog box opens.			
2	Select the unit for the Logbook mark height :			
	Percent of window height			
	Character Heights			
	• Pixels			
	Type a new size value in the Logbook mark height box.			
3	• Click OK .			

9.5 How to print active chromatograms

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

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

Note: The selected print format is outlined in red.

Print Chromatograms			×
Printer			
Acrobat Distiller			
Print Format			
	<mark></mark>		.시.시 시.시
	Chromatograms	in each <u>c</u> olumr	1
	Chromatograms	in each <u>r</u> ow	1
Use thick lines			Preview
Landscape		_	
	ок	Cancel	<u>H</u> elp

Instruction

The table below describes how to print active chromatograms.

Step	Action
1	Open all chromatograms that you want to print in the Evaluation module.
2	Select File:Print.
	ог
	Click the Print toolbar icon.
	3
	<i>Result</i> : The Print Chromatograms dialog box opens.
3	Select print format and layout options.

Step	Action
4	Click OK to print.
	or
	• Proceed with step 5 to preview and edit the layout.
5	Click the Preview button.
	Result: The Customise Report window opens.
6	• Click the Edit Mode button to make changes, e.g. change the order of the chromatograms (see 9.6.1 How to create and print a cus-tomized report on page 233 for more information about how to edit).
	Click the Preview button to return to preview mode.
7	 Select File:Print. or Click the Print toolbar icon. Result: The Print dialog box opens.
8	Select the print range and number of copies.Click OK.

9.6 How to create and print reports

Introduction The Evaluation module provides extensive tools to create detailed reports. This section describes how to create and print reports that are based either on a standard or a customized layout.

In this section This section contains the following sub-sections

Торіс	See
How to create and print a customized report	9.6.1
How to create and print a standard report	
How to edit an existing report format	

9.6.1 How to create and print a customized report

IntroductionYou can choose from a variety of objects to include in a report, including
chromatograms, methods, documentation, free text and more in the customized
report interface. You can also place, align and size the objects as you please. This
section describes how to create a customized report format.

Should you need to store store your reports in an electronic format you can save them as PDF files. This section also describes how to do this..

How to open theThe table below describes how to open the Report Editor in Edit mode to create a
customized report format.

Report Editor in edit mode

Step	Action
1	Open a result file in the Evaluation module.
2	Select File:Report.
	or
	Click the Report icon.
	<i>Result</i> : The Generate Report dialog box opens.
3	Click the New button.
	Result: The Create New Report Format dialog box opens.
4	• Select the Customised format and click OK .
	Result: The Report Editor opens in Edit mode.

The Edit modeThe illustration below shows the Report Editor window in Edit mode with a blankwindowreport open:

Customise Report	X
ile Edit View Draet Laγout Help	
Preview NextFace PrevPage GrePage Zoomin ZoomOo: AddPage DeletePage E+1	
🗋 🚘 😹 🍠 🖇 🖻 🖕 T 💷 🕢 🖾 🗊 🗊 🕼 🖧 77 🖾 🗒 🤅	리밍 🕀 🗉
Normal and the state of the sta	
age Lof L Edit Mode	

Toolbar button functions in the Report Editor

The table below describes the different functions of the Edit mode toolbar buttons in the **Report Editor**:

Toolbar button	Function
Preview/Edit	This button toggles between a print preview of the report and the Edit mode .
Next Page	This button displays the next page or pair of pages (where there are more than one page).
Prev Page	This button displays the previous page or pair of pages (where there are more than one page).
One Page/Two Pages	This button toggles between single page view and pairs of pages view, when there is more than one page.
Zoom In	This button increases the magnification of the view.
Zoom Out	This button decreases the magnification of the view.
Add Page	This button adds a blank page to the report.
Delete Page	This button deletes the current page from the report.

Toolbar button	Function
Exit	This button closes the Customize Report window.

How to add and delete report pages

The table below describes how to add or delete report pages in the **Report Editor**:

If you want	then
to add new pages,	click the Add Page toolbar button.
	<i>Result</i> : A new page is added after the last page.
to delete a page while in One Page mode,	 select the page with Next Page or Prev Page, click the Delete Page toolbar button and confirm the deletion.
to delete a page in Two Page mode,	 select the page with Next Page or Prev Page, click an object on the page, click the Delete Page toolbar button and confirm the deletion.

How to change the page layout

The page layout is changed in the **Page Setup** dialog box. The table below describes how to set up the page layout:

Step	Action
1	Double-click anywhere on the report page in the Report Editor (not on an object). <i>Result</i> : The Page Setup dialog box opens.
2	 Type new values for the Margins if necessary. Select the appropriate Settings and Unit. Note: An extra Header tab will appear if you de-select the option to have the same header on all pages. The First Header tab is used for the first page header only, and the Header tab is used for all subsequent pages. Click the First Header tab.
3	 Select all the items you want to include in the header from the Select Items list. Click the Font button to change the font for all items if necessary.

9.6.1	How to create and print a customized report	
-------	---	--

Step	Action
4	• Type header text in the Free text box and click the Font button to alter the default font if necessary.
	• Type the report title in the Report title box and click the Font button to alter the default font if necessary.
5	• Select the Logo check box and click the Browse button if you want to locate and select a logo image file.
	 Select the Alignment for the logo, if necessary.
	<i>Note</i> : The logo file must be in bitmap format (.bmp) and smaller than 64 kB. Larger logo files or files in other formats must be inserted as Picture objects.
6	If you want to have a line under or over the header, select the appro- priate option in the Layout field.
7	 Repeat steps 3 to 6 on the Footer tab and the subsequent pages Header tab.
	<i>Note</i> : All Header and Footer tabs contain the same options. You can have all information in either the header or footer or split information between the header and footer as required.
	• Click OK .

How to add ob-
jects to the reportThe table below describes how to add objects to the report. The various objects are
described below this table.

Action
Click the appropriate icon in the Report items toolbar.
or
Choose an object from the Insert menu.
T Free text
i Text Method □ _chromatogram
Documentation Image: Evaluation log Image: Sequence

Step	Action
2	• Press and hold the left mouse button on the report page, and drag out a box to the size of the item you want to insert.
	<i>Note</i> : The mouse pointer shows a symbol for the type of item you have selected.
	Release the mouse button.
	<i>Result</i> : A Setup dialog box opens. The dialog is specific to the type of item that you want to insert.
3	• Select the desired options and click OK .
	<i>Result</i> : The object is inserted onto the page.

Note: If you want to edit an object later, double-click the object box.

How to add free The table below describes how to add free text to the report:

text

Step	Action
1	Click the Free Text icon.
	T
	• Press and hold the left mouse button on the report page and drag out a box to the size of the text. Release the button.
	<i>Result</i> : The Setup Free Text dialog box opens.
2	• Type text in the edit field.
	 Select if the text is to start on a new page.
	 Select if the text box should be automatically sized.
	• Select if the text should appear in the same position on all pages, for example as header and footer text.
3	Click the Font button to change the default font.
	<i>Result</i> : The Font dialog box opens.
	 Make the necessary changes and click OK to return.
	• Click OK .
	<i>Result</i> : The text object is inserted onto the page.

How to add a pic-	The Picture dialog box is useful to insert logos, pictures or other figures in the report.
ture	The table below describes how to add a picture object to the report:

Step	Action
1	• Press and hold the left mouse button on the report page and drag out a box to the size of the picture item. Release the mouse button.
	Click the Picture icon.
	<i>Result</i> : The Picture dialog box opens.
2	• Click the Browse button to locate the desired picture file.
	• Select the picture file and click the Open button.
	<i>Note</i> : The file formats .bmp , .emf , .jpg and .tif can be used.
	<i>Result</i> : A preview of the selected picture is displayed.
3	• Select the desired Settings and click OK .
	<i>Result</i> : The picture is inserted onto the page.

How to add a peak table

The table below describes how to add a chromatogram to the report. The layout can **chromatogram or** also be defined to include a peak or pool table if desired.

Step	Action
1	Click the Chromatogram icon.
	 Press and hold the left mouse button on the report page and drag out a box to the size of the chromatogram. Release the mouse button.
	<i>Result</i> : The Setup Chromatogram dialog box opens.
	Setup Chromatogram Selected chromatogram(s) Active chromatogram Settings Inick lines Landscape Start on new page Full page Qriginal file name Layout OK Cancel
2	Select which chromatogram(s) to insert from the Selected chromato-gram(s) droplist.
	• Active chromatogram inserts the chromatogram that currently is active in the Evaluation module.
	• All chromatograms inserts all chromatograms that are open in the Evaluation module.
	• 1, 2etc. inserts the corresponding chromatogram.
3	Select the desired Settings.If desired, change the Fonts.
	<i>Note</i> : Separate fonts can be selected for the Chromatogram , the Peak table and the Header text .

Step	Action
4	• Click the Define button in the Layout field if you want to re-define the layout of the chromatogram.
	Result: The Report Chromatogram Layout dialog box opens.
	• Make the appropriate changes and click OK to return to the Setup Chromatogram dialog box.
	<i>Note</i> : The changes that you make will only affect the report and not the view of the chromatograms in the Evaluation module.
5	Click OK .
	<i>Result</i> : The chromatogram is inserted onto the page.

Note: All curves can be de-selected in the **Report Chromatogram Layout** dialog box leaving only the selected peak table(s) in the report.

How to include a method

The table below describes how to include a method in the report:

Step	Action
1	Click the Method icon.
	• Press and hold the left mouse button on the report page and drag out a box to the size of the item. Release the button.
	Result: The Setup Method dialog box opens.
2	Select the items to be included in the report:
	• Main Method is the method on which the run was based.
	• Blocks are the blocks that were used in the method.
3	Select the appropriate Settings .
	Note: Expand main displays the expanded method view.
	• If desired, change the Fonts .
	• Click OK .
	Result: The method object is inserted onto the page.

How to add docu- The table below describes how to add documentation to the report: mentation

Step	Action
1	Click the Documentation icon.
	• Press and hold the left mouse button on the report page and drag out a box to the size of the item. Release the button.
	Result: The Setup Documentation dialog box opens.
2	Select the items to be included in the report:
	Select All includes all items in the report.
	Clear All removes all selections.
3	If desired, change the Fonts .
	• Select if the documentation should start on a new page.
	 If Select All, Logbook or Run summarySelect All or Logbook was selected, make the necessary changes to the Base and Logbook filter settings.
	Click OK.
	<i>Result</i> : The selected documentation items are inserted into the report.

How to add the Evaluation Loa	The table	below describes how to add the Evaluation Log to the report:
5	Step	Action
	1	Click the Evaluation Log icon.
		• Press and hold the left mouse button on the report page and drag out a box to the size of the item. Release the mouse button.
		Result: The Setup Evaluation Log dialog box opens.
	2	 If desired, change the Fonts. Select if the Evaluation Log should start on a new page. Click OK.
		<i>Result</i> : The Evaluation Log is inserted into the report.

quence Data		
	Step	Action
	1	Click the Sequence icon.
		 Press and hold the left mouse button on the report page and drag
		out a box to the size of the item. Release the mouse button.
		<i>Result</i> : The Setup Sequence dialog box opens.
		Setup Sequence ▼ Selected items will be included Select <u>A</u> II ♥ Detrivulation table □ □Cross reference list □ □Eonts □ □ Title □ □ Start on new page □ □ OK Cancel
	2	Select the items you want to include:
		Sequence
		Detritylation table
		Cross reference list
	3	• If desired, change the Fonts .
		• Select if the Sequence Data should start on a new page.
		• Click OK .
		<i>Result</i> : The Sequence Data is inserted into the report.

How to add Se- The table below describes how to add the Sequence Data to the report:

How to move and The table below describes how to select, move and resize objects freely: resize objects freely

lf you want	then
to select a single object,	click the Select icon,
	$\Box_{\mathcal{S}}$
	click the object of interest.
to select several ob-	click the Select icon,
jects,	 press and hold the <ctrl> key while you click the objects.</ctrl>
to move the selected object(s),	click on the objects, hold down the left mouse button and drag the object(s) to the new position.
to resize the selected object(s),	click one of the object border anchors, either in the corners or in the middle of a border, and drag the box to the new size.
	<i>Note</i> : Some Text objects cannot be resized.

icon functions

Alignment toolbar Objects can be placed in exact positions and sized in relation to other objects. The table below describes the function of the **Alignment** toolbar icons in the **Report Editor**:

Toolbar icon	Function
	Align left Matches the left alignment of all selected objects to that of the high- lighted object.
⇒	Align right Matches the right alignment of all selected objects to that of the highlighted object.
	Align top Matches the top alignment of all selected objects to that of the high- lighted object.
<u>8</u>	Align bottom Matches the bottom alignment of all selected objects to that of the highlighted object.

9.6.1 How to create and print a customized report

Toolbar icon	Function
	Adjust to margins
D	Stretches the selected object(s) to the left and right margins.
	Adjust to left margin
þ	Adjusts the selected object(s) to the left margin.
	Adjust to right margin
<u> </u>	Adjusts the selected object(s) to the right margin.
	Adjust to centre
0	Adjusts the selected object(s) to the center of the page.
	Make same size
	Adjusts the selected objects to the same size as the highlighted reference object.
	Make same width
	Adjusts the selected objects to the same width as the highlighted reference object.
	Make same height
	Adjusts the selected objects to the same height as the highlighted reference object.

Note: The Make same size and Make same width functions can only be used to resize the width of chromatograms, free text and picture objects.

How to print the

The table below describes how to print the report:

10.00		P	me	une	
еро	rt				

Step	Action
1	Choose File:Print.
	or
	Click the Print icon.
	3
	<i>Result</i> : The Print dialog box opens.
	<i>Note</i> : Printers are set up in the File menu of the UNICORN Manager .

Step	Action
2	Select the printing range.
	Select the number of copies.Click OK.

Note: You can also print the report from the **Generate Report** dialog box.

How to save the report in PDF	The table below describes how to save the finished report as a PDF file:		
format	Step	Action	
	1	Click the UNICORN Manager icon on the Windows taskbar.	
		Result: The UNICORN Manager opens.	
		Choose File:Printer Setup.	
		<i>Result</i> : The Print Setup dialog box opens.	
	2	 Select an Adobe Acrobat printer from the Printer Name list (e.g. Acrobat Distiller). 	
		 Click the Properties button and edit the document properties if needed. 	
		Select the appropriate paper size and orientation.	
		• Click OK .	
	3	Click the Evaluation icon on the Windows taskbar.	
		<i>Result</i> : The Evaluation module opens	
	4	• Print the report as described in "How to print the report".	
		<i>Result</i> : The report is created as a PDF file and saved in the location specified in your Acrobat settings.	

Note: You must have a full installation of Adobe Acrobat or a suitable printer driver to be able to do this.

Step	Action
1	Choose File:Save.
	or • Click the Save icon.
	<i>Result</i> : The Save Report Format dialog box opens.
2	• Type a name for the format.
	• Select if you want to save the format for global use.
	Select if you want to save the format as default.
	<i>Note</i> : The name for the default format will automatically be changed to DEFAULT.
	Click OK.

How to save the
report formatThe table below describes how to save the finished report format:

9.6.2 How to create and print a standard report

How to create a Standard report

You can only select a number of pre-formatted items when you create a **Standard** report format. If you want to edit the layout in detail you must create a **Customized** report format. See **9.6.1 How to create and print a customized report** on page 233.

Step	Action
1	Open a result file.
2	Select File:Report.
	or
	Click the Report icon.
	<i>Result</i> : The Generate Report dialog box opens.
3	Click the New button.
	<i>Result</i> : The Create New Report Format dialog box opens.
4	Select Standard format and click OK.
	<i>Result</i> : The Create Standard Report Format dialog box opens.
	The illustration below shows the Create Standard Report Format dialog box with the Header tab selected:
	Create Standard Report Format Evaluation log Sequence Header Method Documentation Chromatogram The selected items will be included in the report Select Items Current user Select All Qurrent date & time Clear All QRun date & time Clear All Page number Frames Beport title Save As. Cancel Save As.
5	Click the appropriate tabs and select the check boxes for each item that you want to include in the report.

The table below describes how to create and save a **Standard** report format:

Step	Action
6	Click the Chromatogram tab and select the chromatogram(s) you want to include.
	• Select the Current option in the Layout field to apply the current layout in the Evaluation module.
	or
	• Click the Define button in the Layout field to open the Curve tab in the Report Chromatogram Layout .
	- Select the curves that you want to include in the report and click OK .
7	• Click the Contents tab to see a list of all the selected items.
	Click the Preview button to see the entire report layout.
	Click the Close button to return.
	Click the Print button to print a test report.
8	• Click the Save As button.
	Result: The Save Report Format dialog box opens.
	• Type a name in the Report format name text box.
	- Select the Save as global format check box to make the format available to other users.
	- Select the Save as default report format check box if desired (The format is saved as DEFAULT).
	• Click OK .
	<i>Result</i> : The Generate Report dialog box opens again. The new report is saved and available in the Format list.
9	Click the Close button
	or
	• Click the New button to create another Standard report.

How to print aThe table below describes how to print a Standard report format in the Evaluationstandard reportmodule.

Step	Action
1	Open a result file.

Step	Action
2	Select File:Report.
	or
	Click the Report icon.
	<i>Result</i> : The Generate Report dialog box opens.
	Generate Report
	Format Contents
	Print_Detrit_AKTA B: Documentation Print_Inst_Test_AKTA B: Chromatogram Print_SutData AKTA B: Synthesis Data
	<u>Editor</u>
	Print Preview Close Help
3	Select a Standard report format.
	<i>Note</i> : The contents of a Standard report format is displayed in the
	Contents field.
	• Verify in the Contents field that the report format contains all the
	the report format if needed.
4	Click the Print button.
	<i>Result</i> : The Print dialog box opens.
	Choose what pages and how many copies to print.
	• Click OK .
	<i>Note</i> : Printers are set up in the File menu of the UNICORN Manager .

9.6.3 How to edit an existing report format

Introduction

This section describes how to edit an existing report format.

How to edit a standard report

The table below describes how to edit a standard report format in the **Evaluation** module.

Step	Action
1	Open a result file.
2	Select File:Report.
	or
	Click the Report icon.
	<i>Result</i> : The Generate Report dialog box opens.
3	Select a Standard report format to edit.
	Click the Edit button.
	Result: The Edit Report Format dialog box opens.
	Select Standard format and click OK.
	Result: The Edit Standard Report Format dialog box opens.
4	Click the appropriate tabs and select the check boxes for each item that you want to include in the report format.
	<i>Note</i> : See 9.6.2 How to create and print a standard report on page 247 for more information.
Step	Action
------	---
5	Click the Contents tab to see a list of all the selected items.
	Preview Save As.
6	 Click the Save As button. <i>Result</i>: The Save Report Format dialog box opens. Type a name in the Report format name text box. Select the Save as global format check box to make the format available to other users. Select the Save as default report format check box if desired (The format is saved as DEFAULT).
	• Click OK . <i>Result</i> : The Generate Report dialog box opens again. The new report format is saved and available in the Format list.
7	 Click the Close button. or Click the Edit button to edit another report format.

How to edit a cus-
tomized reportThe table below describes how to edit a customized report format in the Evaluation
module.

Step	Action
1	Open a result file.

Г

т

Step	Action
2	Select File:Report.
	or
	Click the Report icon.
	<i>Result</i> : The Generate Report dialog box opens.
3	• Select a Customized Report Format to edit.
	Click the Edit button.
	<i>Result</i> : The report format opens in the Report Editor .
4	Double-click the report item you want to edit.
	 Make the desired changes in the dialog box.
	Continue to edit all items until the format is complete.
	<i>Note</i> : See 9.6.1 How to create and print a customized report on page 233 for more information.
5	• Select File:Save As.
	Result: The Save Report Format dialog box opens.
	• Type a name in the Report format name text box.
	- Select the Save as global format check box to make the format available to other users.
	 Select the Save as default report format check box if desired (The format is saved as DEFAULT).
	• Click OK .
	<i>Result</i> : The new report format is saved and available in the Format list.

5.1					
Introduction	The full doo describes:	cumentation for a method run is stored in the result file. This section			
	 some of 	f the contents of the run documentation,			
	• how to	view and print the run documentation,			
	• how to :	save the method from the run as a new method.			
How to view and print the run docu-	The table b	pelow describes how to view and print the run documentation.			
mentation	Step	Action			
	1	Open a result file.			
	2	Choose View: Documentation in the Evaluation module.			
		or			
		Click the view Documentation icon.			
		<i>Result</i> : The Documentation dialog box opens.			
		See further information about some of the tabs below.			
3 • Click the Print button.		Click the Print button.			
		<i>Result</i> : The Print dialog box opens.			
		• Select the documentation items you want to print and click OK .			

The tabs of the Documentation dialog box

The table below describes the contents of some of the **Run Documentation** tabs.

Documentation tab	Contents
Variables	The Variables tab lists the parameters that were used during the method run.
Notes	The Notes tab displays the notes that you have made at various times during the method run. You are also able to type new comments on the Evaluation Notes sub-tab.
	<i>Note</i> : Click the Find button to search for a specific text string in the Notes .

Documentation tab	Contents
Logbook	The Logbook tab displays what happened during a method run. You can view information concerning alarms, the method, manual changes during the run, errors, etc.
	<i>Note</i> : Click the Find button to search for a specific text string in the Logbook .
Evaluation Log	The Evaluation Log lists all of the evaluation operations that you have performed for the result file during all sessions, including at the end of the method.
Method Information	The Method Information tab displays information about the method, such as the method name, the tar- get system and the date of the last change. Information about the strategy includes name, date and size. There is also a sub-tab for Signatures .
Result Information	See "The Result Information tab" in this section.

The Result Inform- The **Result Information** tab displays information about the result file, such as **ation tab**

- the result file name
- the system that was used
- the last date it was changed.

Information about the strategy includes name, date and size. The **Run Summary** sub-tab is a summary of the run expressed in volume or time per block. There is also a sub-tab for **Signatures** and a sub-tab where all **Snapshots** that have been taken during the run are displayed.

formation Signatures Run Summary Snapsh Base Unit © Lime © Volume min	lots				
Block	Start	End	Length	_	
Main	0.00	405.24	405.24		
START_parameters	0.05	2.30	2.25		
Column_Number	0.05	0.10	0.05		
UV_Detrit	0.10	0.20	0.10		
Purge_Detrit_pumpA	0.20	2.30	2.10		
Purge_G	2.30	3.10	0.80		
Amidite_Purge_volume	2.35	2.45	0.10		
Amid_ACN_wash_C_G	2.45	3.05	0.60		
Purge_C	3.10	3.90	0.80		
Amidite_Purge_volume	3.15	3.25	0.10		
Amid_ACN_wash_C_G	3.25	3.85	0.60		
Purge_T_U	3.90	4.70	0.80		
Amidite_Purge_volume	3.95	4.05	0.10		
Amid_ACN_wash_T_U	4.05	4.65	0.60		
Purge_A	4.70	5.50	0.80		
Amidite_Purge_volume	4.75	4.85	0.10		
Amid_ACN_wash_A_X	4.85	5.45	0.60	-	
				Help	

Save the method used for the run as a new method You can save the method and the variables that were used for the run as a new method:

Step	Action	
1	• Select the Text Method tab in the Documentation dialog box.	
	Click the Save as button.	
	<i>Result</i> : The Save As dialog box opens.	

Step	Action
2	Select the appropriate destination folder.
	• Type a name in the Method name text box.
	Select Any in the Technique field.
	Select a technique in the Technique field.
	Click OK.
	<i>Result</i> : The method is saved.

10	now to east results		
Introduction	 This chapter describes how to edit the results that are presented in the Evaluation module how to import and compare runs how to import and export results. For more information about how to view results, see chapter 9 How to view results 		
In this chapter	on page 202. This chapter contains the following sections Topic	See	
	How to add curves	10.1	
	How to enter and edit text in the chromatogram	10.2	
	How to rename chromatograms, curves and peak tables	10.3	
	How to import and compare different runs	10.4	
	How to import and export results	10.5	
	How to sign results electronically	10.6	
	How to save results and exit the Evaluation module	10.7	

10 How to edit results

10.1 How to add curves

IntroductionIn some method runs, several sequential chromatograms might have been created.This can occur, for example, when the instruction New chromatogram has been
used in the method, thus creating different chromatograms during the run.

In order to view and evaluate the resultant curve of all the chromatogram parts, the curves must be added together. Usually, you have a number of chromatograms within the same result file and you want to add the curves. In some circumstances, curves might need to be imported from other result files.

Instruction

The table below describes how to add curves:

Step	Action		
1	Select and view the first chromatogram in the sequence.		
2	Choose Operations:Add .		
	<i>Result</i> : The Add dialog box is displayed.		
3	• Select the first curve in the desired sequence in the left field.		
	• Select the second curve in the sequence in the middle field.		
	Click the OK button to add the two curves together in a new result		
	curve.		
4	• Open the Add dialog box again.		
	• Select the result curve (.ADD) from the previous addition in the left field.		
	• Select the next curve in the sequence in the middle field.		
	• Click OK to add the two curves together in a new result curve.		
5	Repeat steps 3 and 4 until all curves have been added together. The final curve should be the cumulative curve for the whole run.		

Note: All curves created using the **Add** operation receive the **ADD** suffix by default. The default curve name can be changed as needed. The original curves are distinguished in the chromatogram by underlined curve names.

How to enter and edit text in the chromatogram 10.2

How to enter text Text can be added to the chromatogram. The table below describes how to do this:

Step	Action		
1	• Right-click the curves view of the chromatogram window and select Add text from the menu.		
	or		
	Choose Edit:Text:Add.		
2	Click where you want to insert text in the chromatogram.		
	<i>Result</i> : A text box opens.		
	Type the text.		
	Click outside the text box to set the text.		

How to edit the

text

The table below describes how to edit inserted text:
--

Step	Action
1	Choose Edit:Text:Edit . <i>Result</i> : The Edit Texts tab of the Chromatogram Layout dialog box is displayed.
2	 Select the text that you want to edit and make the appropriate changes in the Selected text field.
	Click the Change text button or the Delete text button.
	• Use the Font and Set Orientation buttons if needed, and make the desired changes in the resulting dialog boxes.
	Click OK to apply the changes.

Shortcut option

You can also right-click outside the text box and select Edit Text Mode from the shortcut menu. This activates all the text boxes in the chromatogram. The list below describes how to edit the text:

- Click the text and type the new text.
- Click outside the text box to set the text.

10.3 How to rename chromatograms, curves and peak tables

Instruction

The table below describes how to rename chromatograms, curves or peak tables in the **Evaluation** module:

Step	Action
1	Choose Edit:Rename and the relevant option Chromatogram , Curve or Peak Table .
	<i>Result</i> : The Rename dialog box opens.
2	Select the appropriate object.
	Type a new name in the Name field.
	• Click OK .

Note: The original raw data curves cannot be renamed. They will not be listed as options in the dialog box.

10.4 How to import and compare different runs

Introduction

This section describes

- how to present curves or chromatograms from different runs.
- how to compare curve parameters among curves from different runs
- how to view several chromatograms at the same time
- how to overlay curves from different runs in one chromatogram
- how to stack curves from different runs in one chromatogram
- how to stretch curves to make comparisons easier
- how to create mirror images

In this section

This section contains the following sub-sections

Торіс	See
How to import and compare chromatograms	10.4.1
How to import and compare curves	10.4.2
How to stack and stretch curves	10.4.3
How to produce a mirror image	10.4.4

10.4.1 How to import and compare chromatograms

Introduction	This sectionhow tohow to	n describes import chromatograms from other result files, compare with chromatograms in an already opened result file.
Commands to use	Two comm from result • File:Ope This is th folder b with the • File:Ope This is th files in c File:Ope	ands in the Evaluation module can be used to import chromatograms files into an already opened result file: an to compare The preferred option when you search for many chromatograms in a <i>specific</i> ased on defined selection criteria. See "How to import chromatograms e command File:Open to compare " below. En The preferred option to import any individual chromatograms from result <i>different</i> folders. See "How to import chromatograms with the command en " below.
How to import chromatograms with the com- mand File:Open to	The table b compare of search crit	elow describes how to import chromatograms with the File:Open to command. The search is performed at specific locations or with specific eria.
compare	Step 1	Action Choose File:Open to compare:Chromatograms in the Evaluation module. Result: The Open Chromatogram to Compare dialog box is displayed.

Step	Action
2	• Click the Search button in the Found chromatograms field and a list of chromatograms will be displayed based on the designated search criteria.
	• A new search can be performed with new search criteria without erasing the first found chromatograms from the list.
	• Select the chromatograms that you want to import. If you click the Select All button, all the displayed chromatograms will be imported.
	 If you want to clear the list of displayed chromatograms, click the Clear button.
	• Click OK .
	<i>Result</i> : All the selected chromatograms are shown in the Evaluation workspace.
	<i>Note</i> : If the names of the imported chromatograms already are used they will be sequentially numbered for identification purposes. Up to 10 chromatograms can be made available at the same time in the Evaluation workspace.

How to import chromatograms with the command File:Open

The table below describes how to import chromatograms one by one, using the command **File:Open**:

Step	Action
1	Choose File:Open:Chromatogram in the Evaluation module.
	Result. The Open Chromotograms dialog box is displayed.
2	Double-click a result file to select it. <i>Result</i> : All the chromatograms contained in the result file will be dis- played in the Available field.
3	 Select the chromatogram(s) of interest and click the Select button. <i>Result</i>: Selected chromatograms are added to the Selected chromatograms list. <i>Note</i>: Chromatograms can be deselected with the Remove button.

chromatograms:

Step	Action
4	 Repeat steps 2-3 if you want to import chromatograms from other result files. Click OK.
	<i>Note</i> : If the names of the imported chromatograms already are used they will be sequentially numbered for identification purposes. Up to 10 chromatograms can be made available at the same time in the Evaluation workspace.

The table below describes how to simultaneously display and compare the imported

How to display and compare the imported chromatograms

Step	Action	
1	In the Evaluation module, select	
	• Window:Tile to display the chromatograms side by side.	
	or	
	• Window:Cascade to display the chromatograms in layers.	
	<i>Note</i> : Chromatogram windows can be individually sized and the presentation of the curves changed.	
2	Display all chromatograms on the same scale	
	Open the Chromatogram Layout dialog box for any chromatogram	
	Make the changes to the chromatogram axes.	
	Select the Apply to all chromatograms option.	

Note: Imported chromatograms cannot be shown with column volume as the X-axis base.

10.4.2 How to import and compare curves

Introduction This section describes how to import or copy curves from different runs into one chromatogram for comparison.

Commands to use Two commands can be used to import curves from result files into one chromatogram:

• File:Open to compare

This is the preferred option if you want to automatically search result files that are stored in the same folder to locate all curves of a specified type, for example, all UV curves. This is especially useful for comparison of curves from scouting runs. Moreover, the imported curves can be automatically overlaid, stacked or presented as mirror images. See "How to use File:Open to compare" below.

• File:Open:Curves

This is the preferred option to import individual curves. See " How to use File:Open:Curves" below.

Note: Original curves are underlined in the chromatogram, imported and created curves are not underlined.

How to use	The table below describes how to import curves to a chromatogram with the
File:Open to com-	command File:Open to compare:
pare	

Step	Action
1	In the Evaluation module,
	choose File:Open to compare:Curves
	or
	• click the Open curves to compare toolbar button.
	Result: The Open Curves to Compare dialog box opens.
	Open Curves to Compare
	Folder c:\\Default\AKTAoligopilot\ Browse
	Result: 01 No 157 001 Browse All
	Chromatogram: 1 Browse All
	Curve name: UV1_313nm;UV2_290nm;FlowA Browse All
	Search []01 No 157 001 01 No 157 001:1_UV1_313nm
	Curve options
	Store in new chromatogram Compare
2	• Select the desired search criteria in the Folder , Result , Chromato- gram and Curve name droplists of the Chromatogram selection section.
	• Click Search and a list of found curves will be displayed based on the selected search criteria.
	<i>Note</i> : A new search can be performed with new search criteria without erasing curves located in the previous search.
	• Select the check boxes for the curves that you want to import. Click the Select All button if you want to import all the curves.
	• If you select the Store in new chromatogram option, the curves will be imported into a new chromatogram. This is recommended to keep the source chromatogram free of too many additional curves.



Step	Action
4	If you selected the Stack option in step 3, the Shift Curves by Offset dialog box is displayed:
	Shift Curves by Offset X Offset Unit: ImAU Selected curves will be shifted Image: Selected curves will be shifted Select All Image: Select 200 Select 200 Image: Select 200 Select 200
	 You can set the Offset value to increase or decrease the offset distance between the curves. Click OK.
	<i>Result</i> : Depending on your previous choices, the imported curves are now displayed in the source chromatogram or in a newly created chromatogram.
	<i>Note</i> : If curves with several different units have been selected, the curves with each different unit will be grouped together with separate offset from the other groups.
5	 Change some comparison settings Choose Edit:Chromatogram Layout to open the Chromatogram Layout dialog box.
	 Select or de-select the check boxes on the Curve tab to compare a different set of curves.
	On the Y-Axis tab, the curves can be scaled
	- individually
	- all with the same scale (click the All with this unit button).
	Click OK to display the curves.

Step	Action
6	If you stacked the curves and want to change the stack offset
	choose Operations:Shift offset
	• type a new Offset value and click OK .
	<i>Note</i> : The individual curves can also be moved (see 10.4.3 How to stack and stretch curves on page 272).

How to use File:Open:Curves

The table below describes how to import individual curves into an active chromatogram with the File:Open:Curves command:

Step	Action
1	Make sure that the destination chromatogram for the imported curve(s) is active on the screen.
	 Select File:Open:Curves in the Evaluation module.
	<i>Result</i> : The Open Curves dialog box is displayed.
2	Select curves in the Open curves dialog box
	• Select the folder and the result file in the upper part of the dialog box.
	• Select a chromatogram on the Chromatogram drop-down list. Usually there is just one chromatogram.
	<i>Result</i> : The available curves are listed on the Available list.
	• Click the check boxes on the Available list for the curves that you want to import and click the Select button.
	<i>Result</i> : The selected curve(s) is displayed in the Selected curves list. To remove a curve from the Selected curves list, click the check box and then click the Remove button.
3	• Repeat step 2 if you want to import curves from other chromato- grams.
	Click OK when you have selected the curves you want.

Step	Action	
4	Change some comparison settings	
	• Choose Edit:Chromatogram Layout to open the Chromatogram Layout dialog box.	
	• Select or de-select the check boxes on the Curve tab to compare a different set of curves.	
	On the Y-Axis tab, the curves can be scaled	
	- individually	
	- all with the same scale (click the All with this unit button).	
	Click OK to display the curves.	

How to copy curves into one chromatogram

A practical way to compare curves is to create a chromatogram and copy curves from different chromatograms into the new chromatogram. The comparisons are then performed in the new chromatogram.

The table below describes how to copy curves into a chromatogram:

Step	Action	
1	Perform <i>either</i> A or B below:	
	A. Create a new chromatogram	
	• Choose File:New:Chromatogram to create a new chromatogram.	
	B. Use the Temporary chromatogram	
	Choose Window:Temporary.	
2	Open the source chromatogram(s)	
	Choose File:Open:Chromatogram to open the chromatogram(s) that contains the curves you want to copy.	
	Result: The Open Chromatogram dialog box opens.	
3	Select the result file.	
	• Click the check box for the source chromatogram in the Available list.	
	Click the Select button.	
	• Click OK .	
	<i>Result</i> : The source chromatogram opens.	

Step	Action	
4	Copy the curves	
	Choose Edit:Copy:Curves.	
	<i>Result</i> : The Copy Curve dialog box is displayed.	
5	 Select the source chromatogram and a curve of interest in the Source Chromatogram field. 	
	• Select the target chromatogram (the one you created, or Tempor - ary) in the Target Chromatogram field.	
	Click the Copy button.	
	• Repeat this step for as many curves as you want, from the same or other chromatograms.	
	<i>Note</i> : You can open more source chromatograms with the File:Open:Chromatogram command.	
	Click the Close button when you have copied all curves.	
6	Change some comparison settings	
	• Make sure the target chromatogram is open and that its window is active.	
	• Choose Edit:Chromatogram Layout to display the Chromatogram Layout dialog box.	
	 Select the curves that you want to view on the Curve tab and click OK. 	
	• The curves can be scaled individually or all with the same Y-axis scale. Use the All with this unit button on the Y-Axis tab to scale all curves with the same scale.	
7	If you used the Temporary chromatogram	
	• If you used the Temporary chromatogram you can perform eval- uations in the Temporary chromatogram and transfer the final curves to other destination chromatograms.	
	• All of the contents in the Temporary chromatogram can be re- moved with Edit:Clear Temporary Chromatogram .	

Alternative way to copy curves

An alternative way to copy curves into one chromatogram is to

- create a new chromatogram by copying an existing chromatogram and saving it under a new name
- import more curves into the new chromatogram according to the instructions described above in this section.

10.4.3 How to stack and stretch curves

Functions

You can stack and stretch curves from different runs to better visualize the differences. To achieve this you can use the following functions:

- Normalise
- Shift
- Multiply.

Note: All the functions require the curves to be present in one chromatogram.

How to use the Normalise function The **Normalise** function provides the simplest method to align curves with respect to the X-axis or the Y-axis for easier visualization.

The table below describes how to use the **Normalise** function:

Step	Action	
1	• Make sure that a chromation the Evaluation module.	ogram with the relevant curves is open
	Choose Operations:Norm	alise.
	Result: The Normalise dialog	box is displayed.
	Normalise	×
	Select curve to normalize	Select help ourve (to normalise against)
	02: 01 No 157 001:1_UV2_290mn 03: 01 No 157 001:1_UV2_0mm 04: 01 No 157 001:1_UV_Quot 05: 01 No 157 001:1_Cond	02: 01 No 157 001:1_UV2_230hm 03: 01 No 157 001:1_UV3_0rm 04: 01 No 157 001:1_UV_Quot 05: 01 No 157 001:1_UV_Quot
	06:01 No 157 001:1_FlowA 07:01 No 157 001:1_FlowB 08:01 No 157 001:1_FlowB 09:01 No 157 001:1_Freesure	06: 01 No 157 001:1_FlowA 07: 01 No 157 001:1_FlowB 08: 01 No 157 001:1_Temp 09: 01 No 157 001:1_Temp 09: 01 No 157 001:1_Pressure
		OK Cancel Help

Step	Action
2	• Select the curve you want to normalise in the left (Select curve to normalise) field.
	 Select the reference curve you want to normalise <i>against</i> in the right (Select help curve) field.<i>Example</i>: If you want to <i>stack</i> the curves, select the curve at the bottom of the stack as the reference curve. Click OK.
	<i>Result</i> : The Normalise window is displayed, where a box surrounds the curve selected to be normalised.
	Konnaise Sources Sources
	150 -
	ob s/s volo ref OK Bomatice OK Cancel

Step	Action	
3	In the Normalise window, you can use the following command buttons:	
	Size Allows the arrow keys to be used to stretch the selected curve along its Y-axis or X-axis. This is useful for comparison of curves with, for example, different gradient lengths.	
	• Click the Size button and use the arrow keys to stretch the the curve either along its Y-axis or X-axis.	
	Move Allows the arrow keys to be used to move the selected curve to any position on the chromatogram. Axes are automatically re-scaled to accommodate the new positioning. This function is useful for stacking curves.	
	• Click the Move button and use the arrow keys to move the curve into position. The curve can also be moved with the mouse pointer. Click the mouse button when the curve is in the correct position.	
	<i>Note</i> : The curve can also be moved and sized with the mouse pointer.	
	Normalise The curve to be normalised will be adjusted to the help curve. Thus, the height of the highest peak on both curves will be the same and will occur at the same retention point.	
	• Click the Normalise button. The curve to be normalised is automat- ically moved along the X-axis and stretched along the Y-axis.	
	Click OK to save the new normalised curve.	
	<i>Result</i> : The Save Curve dialog box opens.	
4	Choose a curve position to save the curve in and click OK .	
5	Choose Edit:Chromatogram Layout to open the Chromatogram Layout dialog box.	
	 Select the normalised curve for viewing on the Curve tab. Click OK. 	
6	Repeat steps 1-5 for all curves you want to stack or stretch.	

How to move a curve with the Shift function

If you want to position a curve more precisely, the **Shift** function should be used. The function is similar to **Normalise:Move** but each curve is repositioned by a precise value instead of by eye and the instruction is logged in the evaluation log. The table below describes how to use the **Shift** function:

Step	Action
1	• Make sure that a chromatogram with the relevant curves is open in the Evaluation module.
	Choose Operations:Shift.
	<i>Result</i> : The Shift dialog box is displayed.
2	• Select the curve to be shifted in the Source chromatogram list.
	• Select a curve position in the Target chromatogram list.
	Type a new Curve name or accept the default.
	• Select the axis/axes along which the shift is to be made:
	- along the X-axis (Shift retention)
	- along the Y-axis (Shift amplitude).
	Type the shift value(s).
	Click OK.

How to stretch and shrink a curve with the Multiply function

Curves can be stretched or shrunk on the x or y plane with the **Multiply** function. This function is similar to **Normalise:Size**, but each curve is repositioned with precise numbers instead of by eye and the instruction logged in the evaluation log. The table below describes how to use the **Multiply** function:

Step	Action
1	• Make sure that a chromatogram with the relevant curves is open in the Evaluation module.
	Choose Operations:Multiply.
	<i>Result</i> : The Multiply dialog box is displayed.

Step	Action	
2	• Select the curve to be multiplied in the Source chromatogram list.	
	• Select a curve position in the Target chromatogram list.	
	• Type a new Curve name or accept the default.	
	• Select the axis/axes along which the multiplication is to be made:	
	- along the X-axis (Multiply retention)	
	- along the Y-axis (Multiply amplitude).	
	Type the multiply value(s).	
	• Click OK .	

10.4.4 How to produce a mirror image

Instruction

A very useful way to compare the features of two curves is to produce a mirror image of one curve. The table below describes how to do this:

Step	Action
1	• Make sure that a chromatogram with the relevant curves is open in the Evaluation module.
	Choose Operations:Multiply.
	<i>Result</i> : The Multiply dialog box is displayed.
2	• Select the curve to be multiplied in the Source chromatogram list.
	• Select a curve position in the Target chromatogram list.
	• Type a new Curve name or accept the default.
	Select the Multiply amplitude check box.
	Type the multiply value -1.
	• Click OK .
	<i>Result</i> : The mirror image of the original curve is displayed in the active chromatogram window.

Step	Action	
3	 Shift the mirror image curve downwards Shift the mirror image curve downwards for an improved presentation: Choose Operations:Shift. Result: The Shift dialog box is displayed. Select the curve to be shifted in the Source chromatogram list. Select the same curve number in the Target chromatogram list box as in step 2. Select the Shift amplitude check box since the shift is to be made 	
	 along the Y-axis. Type a shift value. Click OK. The illustration below shows the original curve and the mirror image displayed. 	
4	 If you want to display other curves in the active chromatogram window, choose Edit:Chromatogram Layout to open the Chromatogram Layout dialog box select the curves that you want to display click OK. 	

10.5 How to import and export results

IntroductionCurves and data can be imported and exported in different formats. This section
describes how to import and export results.

In this section This section contains the following sub-sections

Торіс	See
How to import results	10.5.1
How to export results	10.5.2

10.5.1 How to import results

IntroductionThis section describes how to import curves in different formats and how to import
result data from SMART Manager or FPLCdirector™.

Curve formats

You can import curve files in the following formats:

- AIA (.cdf)
- ASCII (text)
- Lotus 1-2-3 spreadsheet (.wks)

How to import curves

The table below describes how to import curves.

Step	Action
1	Choose File:Import:Curve .
	Result: A menu with the available curve formats opens.
2	Choose the correct curve format.
	<i>Result</i> : The Choose File to Import From dialog box opens.
3	Locate the file that contains the curve and double-click the file.
	Result: The Import Curves dialog box opens.
4	• Select the curve(s) to import and click the OK button.
	<i>Result</i> : The curves are opened in the Evaluation module.

How to import data from SMART Manager and FPLCdirector The table below describes how to import data from **SMART Manager** and **FPLCdirector**:

Step	Action
1	Choose File:Import:Result.
	<i>Result</i> : A menu box with the available data sources opens. This box opens immediately after Import if no result file is open in the Evaluation module.
2	Choose FPLCdirector or SMART.
	<i>Result</i> : The Import FPLCdirector Result dialog box or the Import SMART Result dialog box opens.

Step	Action
3	Locate and double-click the result file.
	<i>Result</i> : The result file is opened in the Evaluation module.

Copy from a floppy disk

When you import **SMART** or **FPLCdirector** files from a floppy disk it is best to first copy the files to the hard disk and then import the files.

10.5.2 How to export results

IntroductionThis section describes how to export curves in different formats and how to copy
data and curves to the clipboard.

Data formats

You can export data in the following formats:

- AIA (.cdf)
- ASCII (.asc)
- Lotus 1-2-3 (.wks)
- Excel (.xls)
- XML (.xml)

Export options Select **File:Export** in the **Evaluation** module to export data from an open result file. The following export options are available:

- Curves
- Export curve to AIA
- Peak table
- Method
- Documentation
- Evaluation log

	Step	Action
	1	Choose File:Export:Curves.
		Result: The Export Curves dialog box opens.
		Export Curves
		Source chromatogram Curves to export 1 💌 ©01: 01 No 157 001:1_UV1_313nm
		□01: 01 No 157 001: 1_UV1_313rm □02: 01 No 157 001: 1_UV2_290rm □03: 01 No 157 001: 1_UV2_00m □05: 01 No 157 001: 1_UV2_00m □05: 01 No 157 001: 1_UV2_00m □05: 01 No 157 001: 1_EvQuot □05: 01 No 157 001: 1_EonA □06: 01 No 157 001: 1_FowB □09: 01 No 157 001: 1_FowBook
		Séjetov <u>B</u> emove
		Cut curves France Imile Imile
	2	Select the curve(s) you want to export.
		• Enter parameters to limit the curve(s) if necessary.
		Click the Select button.
		• Repeat Step 2 to select more curves.
	3	Click the Export button.
		Result: The Export Curves to File dialog box opens.
	4	Select the export file format from the Save as type droplist.
		• ASCII files (*.asc)
		• Lotus 1-2-3 files (*.wks)
		• Excel files (*.xls)
		• AIA files (*.cdf)
	5	Select a destination folder.
		• Type a file name and click OK .

Note: Curves are exported as series of numerical coordinates that refers to the time/volume and signal respectively.

How to limit the exported curves

You can optimize the exported curves to only the parts that you want to focus on, in the **Export Curves** dialog box. The table below describes how to use these editing options.

Dialog box option	Instruction
Cut curves	Enter retention values in the text boxes to limit the curve to only a portion of the original curve.
Cut graphically	This button opens the Export Cut dialog box. Move the vertical markers to the correct cutoff points.
Reduce number of samples	Adjust the factor value or the maximum number of samples. To reduce the number of samples by a factor of five means that only every fifth point will be sampled for export.
Normalise retention	Select the Normalise retention check- box to have all exported curves normal- ized to a common X-axis.

How to export curves in AIA format The table below describes how to export curves in AIA format.

Step	Action
1	Select File:Export:Export curve to AIA. <i>Result</i> : The Export curve in AIA format dialog box opens.
2	 Select the source chromatogram and the curve you want to export. Click the Export button. <i>Result</i>: The Export Curves to File dialog box opens.
3	 Select a destination folder. Type a file name. Click OK.

How to export	The table below
peak tables	

v describes how to export peak tables.

Step	Action	
1	Choose File:Export:Peak Table.	
	<i>Result</i> : The Export Peak Table dialog box opens.	
2	• Select the source chromatogram and the peak table you want to export.	
	Click the Export button.	
	<i>Result</i> : The Export Peak Table to File dialog box opens.	
3	Select the export file format from the Save as type drop-list.	
	• ASCII files (*.asc)	
	Lotus 1-2-3 files (*.wks)	
	• Excel files (*.xls)	
	• XML files (*.xml)	
4	Select a destination folder.	
	• Type a file name.	
	• Click OK .	

Note: Peak tables are exported as text strings in ASCII format and numerical values in the Lotus 1-2-3 formats. All possible columns in the peak table are exported.

The table below shows how to export methods, documentation and evaluation logs:

methods, docu- mentation and	Step	Action
evaluation logs	1	Select the data you want to export.
	2	Select options in the dialog box.Click the Export button.
	3	 Select a destination folder and type a file name. Click OK.

Copy to the clipboard

How to export

> You can also use the Windows clipboard to copy the contents of the active window and paste it into other programs, e.g. Microsoft Word. Curves and documentation are copied as Windows enhanced metafiles (.emf) and peak tables are copied as text. Only the peak table columns that are selected in the spreadsheet will be copied.

How to sign results electronically 10.6

Instruction Result files can be signed electronically to enhance data file security. The table below describes how to sign a result file electronically in the **Evaluation** module:

Step	Action
1	Choose File:Sign Result. <i>Result</i> : The Sign the Result dialog box opens. Sign the Result: c:\\Default\125200101
	Signing View Signatures Sign as user User: User: default Password:
2	• The Sign as user field shows the properties for the current user. You can also choose another user from the droplist. If you choose a new user, the corresponding password must be typed in the Password text box.
	 Type a short text description for the signed operation in the Meaning field (e.g. Result file reviewed).
	• The Lock check box is selected as default, to lock the result file from further changes.
	• Type your signature password in the Password field and click OK .
	<i>Note</i> : You should only lock the result when you are sure that the result file will not be modified anymore.

ated with the result

Signatures associ- The View Signatures tab of the Sign the Result dialog box provides a list of all signatures associated with the current result. The information on this tab is for viewing purposes only and cannot be changed.
10.7 How to save results and exit the Evaluation module

IntroductionAfter you have finished the evaluation process, you can save all the changes you
have made to the chromatograms, including newly created curves and
chromatograms that you have imported and created.How to delete un-
wanted curvesAll the curves that you created during your manipulations will be saved in the
chromatogram. If some of these curves are not be needed anymore, select
Edit:Delete:Curves in the Evaluation module to remove the curves.

Note: The original curves that were created during the run can never be deleted.

How to save the results

You can either save your edited results in the original file or in a new result file. The table below describes how to save the results in the **Evaluation** module.

If you want to save the edited results	then
in the original result file	• select File:Save.
	or • click the Save toolbar icon.
in a new result file	• select File:Save as.

Note: The previous version of the result file will be overwritten if you save the changes. This cannot be reversed. However, the raw data curves remain unchanged.

How to exit the The table below describes how to exit the **Evaluation** module:

Evaluation module

Step	Action	
1	Choose File:Exit.	
	<i>Result</i> : If there are unsaved changes, a dialog box opens with an option to save the changes before exit.	
2	Select Yes if you want to save the changes.	
	<i>Result</i> : The result file is closed in the Evaluation module and the UNICORN Manager module is displayed.	

11	Evaluation	
Introduction	This chapter describes:How to evaluate results with the focus on how to integrate peaks.How to automate evaluation operations.	
	How to export data and curves.	
In this chapter	This chapter contains the following sections	
	Торіс	See
	Peak integration	11.1
	Other evaluations	11.2
	Automated evaluation procedures	11.3
		•

11.1 Peak integration

Introduction

Peak integration is used to identify and measure a number of curve characteristics including peak areas, retention time and peak widths. This section describes:

- How to perform peak integrations.
- How to optimize peak integrations.

In this section This section contains the following sub-sections

Торіс	See
Baseline calculation	
How to perform a peak integration	
How to optimize the baseline with a morphological algorithm	
How to optimize the baseline with a classic algorithm	
How to edit the baseline manually	
How to edit the peaks	
How to integrate part of a curve and how to exclude or skim peaks	
Measurements	

11.1.1	Baseline calculation				
Introduction	The first step when you integrate peaks is to calculate a baseline. A correct baseline is crucial for accurate calculation of the peak areas. This section describes the options for how to calculate baselines in the Integrate dialog box.				
Baseline options	 UNICORN[™] offers several options for how to create an accurate baseline: To use the automatic Calculate baseline function. To create a baseline based on a blank curve. To use a Zero baseline. To reuse an existing baseline. 				
The Calculate baseline function	The Calculate baseline instruction provides automatic calculation of the baseline. In most cases the measurement is very accurate. The calculation can be performed using the Morphological algorithm or the Classical algorithm.				
Baselines based on a blank curve	 A blank curve can be used as the baseline for peak integration. You can use a blank curve with the same chromatographic conditions as the corresponding sample. or You can subtract the blank run from the source curve and then perform peak integration on the resulting curve with the Calculate baseline instruction. Note: In addition to blank run curves, it is also possible to select any curve from the current chromatogram as the baseline, e.g. an edited baseline. 				
Zero baseline	To use a Zero baseline means that there is no baseline subtraction at all.				
Reuse an existing baseline	To reuse an existing baseline for the selected curve is the default alternative whenever there is an existing baseline available. The option Correlated baseline is selected if this is the case.				

11.1.2 How to perform a peak integration

J. T. T. J.	Step	Action	
	1	Open a result file in the Evaluation module.	
	2	Choose Integrate:Peak Integrate.	
		or	
		Click the Peak Integrate toolbar icon.	
		fir	
		<i>Result</i> : The Integrate dialog box opens.	
	3	Select a source curve.	
		• Select a baseline or a calculation method from the Baseline list.	
		• Click OK to integrate with the default selections.	
		or	
		• Proceed with steps 4 to 6 to change the default selections.	
		<i>Note</i> : See also 11.1.3 How to optimize the baseline with a morpholo- gical algorithm on page 297 and 11.1.4 How to optimize the baseline with a classic algorithm on page 301.	
	4	• Click the Baseline settings button to change the calculation al- gorithm in the Settings dialog box. The default algorithm is Morpho- logical .	
		Change the selections or values.	
		Click OK	
	5	• Click the Peak window button to edit the peak window limits if ne-cessary.	
		• Click the Reject peaks button to set the parameters for peak rejection if necessary.	
		• Edit the Column height or Column V values if necessary.	

Step	Action
6	Click OK to integrate and close the dialog box.
	or
	• Click Save and Edit Peak Table to save the integration and open the integrated curve for editing.
	- See 11.1.5 How to edit the baseline manually on page 309
	- See 11.1.6 How to edit the peaks on page 312
	- See 11.1.7 How to integrate part of a curve and how to exclude or skim peaks on page 320

Illustration

This is an illustration of the **Integrate** dialog box:

enionalogram.		Target peak table:	
1 ▼ 01: 01 No 157 001:1 UV1_313nm. 02: 01 No 157 001:1_UV2_290nm 03 03: 01 No 157 001:1_UV2_0uot 05: 01 No 157 05: 01 No 157 001:1_UV_Quot 05: 01 No 157 05: 01 No 157 001:1_Cond 00:01:1_ElowA		Peaktable-A: Peaktable-B: Peaktable-D: Peaktable-D: Peaktable-F: Peaktable-F: Peaktable-G: Peaktable-H:	
07:01 No 157 001:1_FlowB 08:01 No 157 001:1_Temp		Peak table <u>n</u> ame:	
09: 01 No 157 001:1_Pressure		UV1_313nm@01,P8	AK
aseline:	<u> </u>	<u>P</u> eak window <u>B</u> eject peaks	<u>Accept negative peaks</u> <u>Peak</u> skim 10 ratio
Baseline settings			
Baseline gettings	Colu <u>m</u> n he	ight 0 cm	Column⊻t 0 m

Peak integration The peak table is displayed underneath the active chromatogram. The start point results and end point of each peak are marked by vertical marks, **drop-lines**, in the chromatogram. The peaks are automatically labelled according to what is selected

in the Curve Style and Color tab of the Chromatogram Layout dialog box.



Note: Peak tables can be copied from one chromatogram to another with the Edit:Copy command. However, to display the table you must right-click in the chromatogram, choose **Properties** and then select the new peak table on the **Peak** Table tab of the Chromatogram Layout dialog box.

How to display The peak retention times and several other peak characteristics are calculated peak characteristautomatically. The table below describes how to display other peak characteristics. ics

Step	Action		
1	 Right-click in the active chromatogram. Select Properties from the shortcut manual 		
	Result: The Chromatogram Layout alalog box opens.		
2	Click the Peak Table tab.		
3	 Select options from the Select peak table columns list. Click OK. <i>Result</i>: The selected items will be displayed in the peak table. 		

This is an illustration of the results after a peak integration:

How to filterPeaks can be removed from display in a peak table. The table below describes howpeaks from viewto filter the peaks:

Step	Action			
1	 Right-click in the active chromatogram or peak table. Select Properties from the shortcut menu 			
	Result: The Chromatogram Layout dialog box opens.			
2	Click the Peak Table tab.			
3	 Click the check boxes in the Filter Peaks field to select the filter criteria. Specify filter values. Click OK. 			

To filter peaks vs.The table below describes the major differences in the effect of filtering peaksto reject peakscompared to excluding the peaks by rejection.

Filter peaks	Reject peaks
excludes the peaks from display,	permanently excludes peaks from the integration,
does not exclude the peaks from the calculation of the total peak area,	excludes the peaks from the calculation of the total peak area,
can be reversed.	cannot be reversed.

Peak labels

Peaks can be labelled with their retention, sequentially numbered, or be marked with specific identification names. See table below for an instruction on how to display peak labels.

The label type can be selected on the **Curve Style and Colour** tab in the **Chromatogram Layout** dialog box. De-select all label options to hide the labels, e.g. for presentations.

The illustration below shows the **Chromatogram Layout** dialog box with the **Curve Style and Colour** tab opened:

Chromatogram Layout: 1		×
Header Curve Names Y-Axis Curve Style and Colour	Edit Texts	Curve Peak Table Layout Library
Select curve to modify colour and linestyle for 01: id148Quantitate001:1_UV1_280 02: id148Quantitate001:1_UV2_0nn 03: id148Quantitate001:1_UV3_0nn 04: id148Quantitate001:1_Cond 05: id148Quantitate001:1_Cond% 06: id148Quantitate001:1_Conc 07: 08: id148Quantitate001:1_Pressure 08: id148Quantitate001:1_Pressure 09: id140Quantitate001:1_Pressure		ur Line style
Peak label Text alignment Number ○ Vertical Peak Name ○ Horizontal Betention □ Horizontal	Fraction text alignment – C ⊻ertical C Horjzontal C Fly <u>D</u> ver	Logbook text alignment Vertical Horizontal Fly Over <u>Filter</u>
Apply to all chromatograms	OK	Cancel <u>H</u> elp

How to display peak labels

The table below describes how to display peak labels:

Step	Action
1	Choose Edit:Chromatogram Layout.
	or
	Click the Chromatogram Layout icon.
	Result: The Chromatogram Layout dialog box opens.
2	Click the Curve Style and Colour tab.

Step	Action
3	Select one or more of the following labelling options in the Peak label field:
	• Number
	Result: The peaks will be numbered sequentially.
	Peak Name
	<i>Result</i> : Peak names will be displayed. See 11.1.6 How to edit the peaks on page 312 for information about how to name the peaks.
	Retention
	<i>Result</i> : The retention volume or time will be displayed.
	• Click OK .

11.1.3	How to optimize the baseline with a morphological algorithm		
Introduction	The first of baseline morpholo	choice when you want to optimize the peak integration is to change the parameters. This section describes how to optimize the baseline with a ogical algorithm.	
The Morphologic- al algorithm	The Morp chromate wheneve a baselin	chological algorithm can be described as a line that follows the ogram parallel to the X-axis. Data points for the baseline are created r the line touches the curve, and the points are joined at the end to create e.	
	The Morp and peak curve wit morphole	chological algorithm gives the best result in curves with drifting baseline clusters. The morphological baseline follows the curve faithfully, and a h a baseline at a more even level can be created by subtracting the ogical baseline.	
	The Morp quantitat	bhological algorithm does <i>not</i> work well if there are negative peaks or if ive data from negative peaks are important in the run.	
	Note: The	Morphological algorithm is the default baseline setting.	
How to set a Mor- phological	The table baseline	below describes how to choose a Morphological algorithm and define settings.	
busenne	Step	Action	
	1	Select Integrate:Peak Integrate.	
		<i>Result</i> : The Integrate dialog box opens.	
	2	Click the Baseline settings button in the Integrate dialog box.	
		Result: The Settings dialog box opens.	
	3	Select the Morphological algorithm.	
		Change the Baseline parameters if necessary.	

• Click **OK**.

Note: The same settings can be edited in the **Calculate Baseline** dialog box when a new baseline is created. Choose **Integrate:Calculate Baseline** to open the dialog box.

See more information about the parameters below this table.

11.1 Peak integration

11.1.3 How to optimize the baseline with a morphological algorithm

Morphological al-	The parameters for the Morphological algorithm are:
gorithm paramet-	Structure width
ers	Noise window
	Minimum distance between points

Structure width Structure width determines the length of the straight line that follows the chromatogram. The default value is set at the widest peak in the chromatogram multiplied by 1.5.

The illustration below is an example of how a morphological baseline follows the peaks at the different levels in the curve:



The correct struc-
ture width set-
tingsToo low settingsToo low Structure width settings can re
the peaks of the surve Semetime quide

Too low **Structure width** settings can result in a baseline that reaches too high up in the peaks of the curve. Sometime a wider peak is not recognized because it contains a cluster of smaller peaks. The **Structure width** is then set to a value according to the largest width of the identified narrower peaks, and must be increased.

Too high settings

Too high **Structure width** settings mean that narrower peaks, especially in fluctuating curves, are not properly followed. This happens when an artifact in a curve is identified as the widest peak by the morphological algorithm, and then is used to set the default **Structure width** value.

The illustration below is an example of baselines using the default morphological algorithm settings (A) and a morphological algorithm with an increased **Structure** width value (B).



Noise window

Sometimes you get too many peaks after the peak integration, usually because noise on the baseline is erroneously detected as peaks.

The solution to this is to increase the **Noise window** parameter. However, this can result in peak limits too high up on the peak slopes.

Note: You can also use the **Reject peaks** function in the **Integrate** dialog box to reduce the number of peaks based on the total number of accepted peaks or the minimum peak height.

Minimum distance The Minimum distance between points is a measure of the distance between the data points used to generate a baseline. The largest number of data points is produced at the slopes of the curves. If you increase the Minimum distance between points value, fewer points will be collected on the slopes.

The illustration below is an example of a baseline (A) that is created with the **Minimum distance between points** parameter set at a low value. The number of data points is reduced when the **Minimum distance between points** parameter is set to a higher value (B).



11.1.4	How to optimize the baseline with a classic algorithm
--------	---

IntroductionThe first choice when you want to optimize the peak integration is to change the
baseline parameters. This section describes how to optimize the baseline with a
classical algorithm.

What is the Classic algorithm? The Classic algorithm searches for all parts of the source curve that are longer than a defined minimum baseline segment and fall within limiting parameters. Together, the parameter values define the limits for a rectangular box. A part of the source curve must fit entirely inside this rectangular box to be identified as a baseline segment.

The **Classic algorithm** is particularly useful when you need to integrate curves with negative peaks and when quantitative data from negative peaks are important.

Classic algorithmThe parameters for the Classic algorithm are:parametersShortest baseline segment

- Noise window
- Max baseline level
- Slope limit

See more information about the parameters below.

How to set a Clas- The table below describes how to set a Classic algorithm and define a baseline.

sic	base	ine

Step	Action
1	Click the Baseline settings button in the Integrate dialog box.
	Result: The Settings dialog box opens.
2	• Select the Classic algorithm.
	Change the Baseline parameters.
	See more information about the parameters below this table.
	• Click OK .

Note: The same settings can be edited in the **Calculate Baseline** dialog box when a new baseline is created. Choose **Integrate:Calculate Baseline** to open the dialog box.

Test your para-
meter changesThe best way to optimize the baseline is to change the baseline parameters step by
step and then check the resulting baseline after each change. When the desired effect
is accomplished it is best to go back and try a parameter value in between the two
last settings to avoid an unnecessarily low or high value.

How much the values should be changed depends on the cause of the peak integration problem. The table below is a general guideline.

Baseline parameter	Recommended initial change
Shortest baseline segment	20-50%
Noise window	10-30%
Max baseline level	Usually not necessary to adjust
Slope limit	25-50%

Note: If necessary, click the **Default** button to restore the default values.

Shortest baseline segment

If a too high **Shortest baseline segment** value is set, short curve segments between peaks in the middle of the chromatogram are not identified as baseline segments. The calculated baseline does not follow the source curve, see below:





The **Shortest baseline segment** value is decreased by 50% in this example:

Slope limit

A changed **Slope limit** will often improve the baseline calculation. The **Slope limit** sets the maximum slope of the curve to define when a peak is recognized. A too high **Slope limit** will cause the up-slopes of the peaks to be recognized as baseline segments.

The example above was improved by the shorter baseline segments but the high slope of the short segments in the region between the second and the fourth peak still makes the baseline unacceptable. In the example below the **Slope limit** is increased by a factor of 2.5, which produces a correct baseline:



Too high slope limit

A too high **Slope limit** value can cause peak limits too high up on the peaks. This can be the case when the chromatogram includes a very large flow-through or solvent peak. The large peak affects the calculation of the default parameters and leads to too high values for the **Slope limit**.

Note: A too high value for the **Noise window** can have the same effect and be caused by the same situation, often also in combination with a high **Slope limit**.

Peak limits are defined on peaks in the example below due to the high **Slope limit**:



The example below has a much lower **Slope limit**, and a lower **Noise window**:



Noise window

Sometimes you get too many peaks after the peak integration, usually because noise on the baseline is erroneously detected as peaks.

The solution to this is to increase the **Noise window** parameter. However, this can result in peak limits too high up on the peak slopes.

The illustration below is an example of noise detected as peaks (A) and the result of a second peak integration with an increased **Noise window** (B).



Note: You can also use the **Reject peaks** function in the **Integrate** dialog box to reduce the number of peaks based on the total number of accepted peaks or the minimum peak height.

11.1.4 How to optimize the baseline with a classic algorithm

Missing peaks Sometimes obvious peaks are not detected in the peak integration. The probable cause is that the **Noise window** is set too high. See the illustration below:



All peaks are detected if the **Noise window** is decreased, see example below:



Note: Missing peaks can also be caused by improper settings for **Reject peaks** in the **Integrate** dialog box, or **Filter peaks** in the **Chromatogram layout** dialog box.

When to change the Max baseline level

In rare cases the top of a broad, flat peak can be incorporated as a baseline segment. This is one of the very few situations where it is useful to change the **Max baseline level**. The illustration below is an example:



How to set the Max baseline level

The table below describes how to set the **Max baseline level**.

Step	Action
1	Right-click in the chromatogram and select Marker.
	<i>Result</i> : A vertical line is set in the chromatogram. A text box in the top left corner of the chromatogram displays the X-axis and Y-axis values of the curve at the point where the vertical Marker line crosses the curve.
2	Move the Marker with your mouse.
	 Measure the height of the peak you want to exclude from the baseline.
3	Choose Integrate:Calculate baseline.
4	Select the Classic checkbox as the Chosen algorithm.
	• Type a new value for Max baseline level . Set the level slightly lower than the value that you measured in step 2.
	• Click OK .

Example of a cor-
rect baselineThe illustration below is an example of a correct baseline after the Max baseline level
has been changed:



11.1.5 How to edit the baseline manually

The Edit BaselineYou can edit the baseline manually in the Edit Baseline dialog box in the Evaluationdialog boxmodule:

• Select Integrate:Edit Baseline to display the dialog box.

The **Edit Baseline** dialog box displays the baseline and the curve it was calculated from. The baseline points are marked with green squares. Hold the cursor above the baseline point to display its coordinates. See the illustration below:



How to use theThe table below describes how to use the zoom function in the Edit Baseline dialogzoom functionbox.

Step	Action
1	Click the Zoom icon.
	<i>Result</i> : The cursor is changed into a magnifying glass.
2	Press and hold the left mouse button.
	• Drag the cursor over the area you want to zoom in on.
	Release the mouse button.
	<i>Result</i> : The area is enlarged. Right-click and select Reset zoom to restore the full view.

How to edit and	The table below describes how to edit and insert baseline data points:
insert data points	

Step	Action
1	Select Integrate:Edit Baseline.
	<i>Result</i> : If there are more than one baseline available, the Select Baseline to Edit dialog box opens. If not, proceed to step 2.
	• Select the baseline you want to edit from the list.
	• Click OK .
	<i>Result</i> : The Edit Baseline dialog box opens
2	Click the Set Curve Points icon.
	<i>Result</i> : The cursor is changed into a cross.
3	Add a data point
	• Click the left mouse button to place a new baseline point in the chromatogram.
	<i>Result</i> : A new point is created, marked by a green square. The baseline curve is redrawn as a spline function based on the old and the new points. The baseline is guided by the points, but does not necessarily pass through them.
4	Delete a data point
	Double-click the data point.
	or
	• Click the data point to select it and click the Delete button.
	or
	• Right-click the data point and select Delete Point from the shortcut menu.
	<i>Result</i> : The data point is deleted and the curve is redrawn.
5	Move a data point
	• Select the data point and drag it to a new position.
	<i>Result</i> : The baseline curve is redrawn.
6	Click OK .
	<i>Result</i> : The Save Edited Baseline dialog box opens.

Step	Action
7	Confirm the location and type a new name if necessary.Click OK.
	<i>Result</i> : The new baseline is saved.

Edited baseline

The illustration below is an example of a baseline before and after editing:



How to draw a straight line

The table below describes how to force a straight baseline between two points.

Step	Action
1	Select the first of the two points in the point list.
2	Click the Draw straight to next point button. <i>Result</i> : The baseline is drawn through the points as a straight line.

11.1.6 How to edit the peaks

Introduction Once a peak table has been generated based on an appropriate baseline, it is possible to split or join peaks and to manually adjust the peak start and end points. The peaks will then be renumbered and the peak values will all be recalculated.

How to open the peak table for editing

e The table below describes how open the peak table for editing. The editing options are described below this table:

Step	Action
1	Select Integrate:Edit Peak Table.
	<i>Result</i> : If there are more than one peak table available, the Select Peak Table to Edit dialog box opens. The name of the baseline on which the peak table was based is displayed at the bottom of the panel.
2	• Select the peak table from the list and click OK .
	 Select one or more Help Curves to be displayed for reference if necessary.
	Result: The Edit Peak Table dialog box opens.
	<i>Note</i> : The Edit Peak Table dialog box will be opened immediately if you select Save and Edit Peak Table as the last step of the peak integration.
3	Perform the changes (described in the instructions below).
4	Click OK .
	<i>Result</i> : The Save Edited Peak Table dialog box opens. The dialog box displays a suggested name and location for the peak table.
5	Confirm the name and location and click OK .

How to adjust the
baselineThe baseline can be adjusted graphically (see also 11.1.5 How to edit the baseline
manually on page 309) in the Edit Peak Table dialog box. The table below describes
this:

Step	Action
1	Click the Set Curve Points icon.
	<i>Result</i> : The cursor is changed into a cross.

Step	Action
2	Perform the operations below as desired:
	Click to insert a new data point.
	 Double-click on a data point or right-click the point and select De- lete Point from the short-cut menu to delete the point.
	• Click a data point and drag the point to a new position to move the baseline.
	<i>Note</i> : Accept negative peaks must be selected before the peak integ- ration if you want to be able to drag a data point to move the baseline above the curve.

How to calculate a new baseline

The baseline can be recalculated in the **Edit Peak Table** dialog box. The table below describes how to do this:

Step	Action
1	Select Baseline:New:Calculate.
	or
	• Right-click and select New Calculate from the shortcut menu.
	<i>Result</i> : The Settings dialog box opens.
2	Select an algorithm (Morphological is default).
3	• Adjust the Baseline parameters as desired.
	or
	Click the Default Values button for the default values.
4	• Click OK .
	<i>Result</i> : The baseline is recalculated.

Note: Select **Baseline:New:Zero Baseline** to replace the calculated baseline with a zero baseline.



How to delete a The table below describes how to delete a peak in the Edit Peak Table dialog box: peak

Step	Action
1	• Click the Edit peaks icon.
	<u>₽</u>
	• Click the peak in the curve or in the peak table to select the peak.
2	• Right-click and select Delete Peaks from the shortcut menu.
	or
	Select Edit:Delete Peaks.
	<i>Result</i> : The peak is deleted and the remaining peaks are renumbered.

The illustration below shows the Edit Peak Table dialog box.

How to add colorThe table below describes how to add a fill color and a pattern to a peak in the Editto a peakPeak Table dialog box:

Step	Action
1	Click the Edit peaks icon.
	<u>v</u>
	• Move the cursor over the peak you want to edit.
	Result: The cursor is changed into a larger arrow.
	Click to select the peak.
2	Right-click and select Fill Peak from the shortcut menu.
	or
	Select Edit:Fill Peak.
	Result: The Color and Pattern dialog box opens.
	Color and Pattern Color Color Pattern Pattern OK Cancel OK Cancel
	• Click OK .
	<i>Result</i> : The peak is filled according to the selections.

Note: The color and pattern selections will override the general **Fill settings** that can be selected for all peaks on the **Peak Table** tab in the **Chromatogram Layout** dialog box.

Peak start and end points

The beginning of each peak is marked with a drop-line above the curve, and the end of each peak is marked with a drop-line below the curve. The illustration below shows an example of start and end point drop-lines:



Where there are two peaks beside one another, the end of the first peak will be at the same point as the beginning of the next peak. Thus, there will be a drop-line below and above the curve at the same point. See the illustration below:



How to split a peak

It is possible to split the peak into two new peaks by inserting a drop-line. The table below describes how to split a peak in the **Edit Peak Table** dialog box:

Step	Action
1	Click the Edit peaks icon.
	<u>4</u>
	• Click the peak in the curve or in the peak table to select the peak.
2	Right-click and select Split Peak from the shortcut menu.
	or
	Select Edit:Split Peaks.
	<i>Result</i> : A new drop-line is inserted at the middle point between the two existing drop-lines and the peak is split.

Note: The area under each new peak will not be the same if the symmetry of the original peak was not perfect.

How to join peaks It is possible to join the areas of adjacent peaks if they are separated by a drop-line. The table below describes how to join adjacent peaks in the Edit Peak Table dialog box:

Step	Action
1	Click the Edit peaks icon.
	<u>4</u>
	• Click the peak in the curve or in the peak table to select the peak.
2	Right-click and select Join Left or Join Right from the shortcut menu.
	or
	Select Edit:Join Left or Edit:Join Right.
	<i>Result</i> : The original intervening drop-line is removed and all peaks are renumbered.

How to add peakThe table below describes how to add names in the Edit Peak Table dialog box tonamesidentify the peaks:

Step	Action
1	Click the Edit peaks icon.
	1 L
	• Click the peak in the curve or in the peak table to select the peak.
2	Right-click and select Peak Name from the shortcut menu.
	or
	Choose Edit:Peak name.
	or
	• Double-click the peak in the peak table or the curve.
	<i>Result</i> : The Edit Peak Name dialog box opens. The number and reten- tion of the selected peak is displayed.
3	Type a name in the Peak name textbox and click OK .

 How to adjust
 The table below describes how to move the drop-lines to adjust the peak area in the

 peak areas with
 Edit Peak Table dialog box.

 Step
 Action

Step	
1	• Click the Edit peaks icon.
	<u>v</u>
	• Click the peak in the curve or in the peak table to select the peak.
	<i>Result</i> : Two vertical bars become superimposed over the drop-lines that delimit the selected peak. The area between the bars is filled with a yellow fill pattern.
2	Drag the bars to define the new limits for the selected peak.
	<i>Result</i> : The drop-lines are moved and the peak areas are automatically recalculated.

Note: A drop-line can never be moved beyond another drop-line or beyond a point where the peak meets the baseline.

How to use theThe table below describes how to use the zoom function in the Edit Peak Table dialogzoom functionbox.

Step	Action
1	Click the Zoom icon.
	<i>Result</i> : The cursor is changed into a magnifying glass.
2	Press and hold the left mouse button.
	• Drag the cursor over the area you want to zoom in on.
	Release the mouse button.
	<i>Result</i> : The area is enlarged. Right-click and select Reset zoom to restore the full view.

The IntegrateIf needed you can use the selections on the Integrate menu to perform a peakmenuintegration in the Edit Peak Table dialog box. This is useful for example if you want
to re-integrate the curve using different settings or integrate only part of a curve with
different settings.

See **11.1.7** How to integrate part of a curve and how to exclude or skim peaks on page 320 for more information.

11.1.7 How to integrate part of a curve and how to exclude or skim peaks

Introduction

There are several possibilities to improve the results if the peak integration is unsatisfactory. This section describes:

- How to select only part of a curve for integration.
- How to exclude peaks.
- How to skim peaks.

These operations can be performed both in the **Integrate** dialog box in preparation for the peak integration, or in the **Edit Peak Table** dialog box to adjust an unsatisfactory peak integration. This section describes both alternatives.

How to select partThe table below describes how to select only a part of a curve for peak integrationof a curvein the Integrate dialog box:



Step	Action
3	Click OK .
	<i>Result</i> : The baseline will be calculated from the whole curve, but the calculation of the peak areas is only performed on the selected section.

How to excludeYou can define criteria to exclude peaks from integration. The table below describespeakshow to define peaks to be excluded in the Integrate dialog box.

Action
Click the Reject peaks button. <i>Result:</i> The Reject Peaks dialog box opens
• Select the appropriate checkboxes and type values for height, width and area.
• Define how many of the largest peaks you want to include.
• Click OK .

How to includeSelect the Accept negative peaks checkbox of the Integrate dialog box to includenegative peaksnegative peaks in the integration.

Result: The negative peaks will be reported as negative areas in the peak table. By default, negative peaks are not included in the integration.

Peak skimming vs. The area under a peak can be calculated either using separating drop-lines or peak drop-lines skimming:

- Drop-lines are vertical marks that split two peaks at the valley. Drop-lines are used mostly for peaks of relatively similar size. When a peak has a shoulder, splitting with drop-lines will cause the first peak to lose too much of its area to the peak that forms its shoulder.
- The **Peak skim** option can be used to skim off the smaller peak with a straight line that starts in the valley between the peaks and ends at the other side of the smaller peak, at the point where the skim line and the curve slope are equal.

The illustration below is an example of how a drop-line (A) and a skimmed peak (B) affects the area under the main peak and the peak shoulder. The peak shoulder area is marked in gray:



How to skim The table below describes how to select a ratio to skim peaks in the Integrate dialog peaks box:

Step	Action
1	Select the Peak skim checkbox.


How to integrate
part of a curvePart of a curve can be selected in the Edit Peak Table dialog box and integrated with
settings that differ from the rest of the curve. The table below describes how to do
this.

Step	Action
1	Choose Integrate:Edit Peak Table.
	Result: The Select Peak Table to Edit dialog box opens.
	• Select the peak table to edit and click OK .
	Result: The Edit Peak Table dialog box opens.

11 Evaluation

11.1 Peak integration11.1.7 How to integrate part of a curve and how to exclude or skim peaks

Step	Action
2	• Click the Peak Window icon.
	Result: Two vertical cursor lines are displayed.
	• Drag the cursor lines to the beginning and the end of the selected part of the curve.
	CitAk Peak Table File Dir Second Interview Pile Second Interview Interview Pile Second Interview Interview <
	Ob 2.b 4.b e.b 100 120 140 160 min NO Peak name Retention (min) Peak start (min) Peak end (min) Area (mAU*min) A 1 Internal str S.63 S.53 6.28 61.1651 A 1 Rest 0.05 C.55 C.50 6.48 64.0627 A
	a Peak 8 (0.5 7.04 6.04 7.36 60.5619 4 Peak C (0.5 7.74 7.36 8.68 115.5646 ▼
	OK Cercel Perb
	<i>Note</i> : All operations described below will only affect the selected part of the curve.
3	If desired, change the integration parameters:
	Reject peaks
	Choose Integrate:Settings.
	<i>Result</i> : The Reject Peaks dialog box opens.
	Change the settings as desired and click OK .
	Skim peaks
	Choose Integrate:Peak Skim.
	<i>Result</i> : The Peak Skim dialog box opens.
	Select the Skim Peaks checkbox and type a ratio.
4	Choose Integrate:Peak Integrate.
	<i>Result</i> : The selected part of the curve is peak integrated based on the changed parameters.

11.1.8 Measurements

4

tions

Introduction It is possible to determine the coordinates of any point on a curve and to obtain values for retention and peak height. This is a useful tool for many other functions, such as for measuring the parameters used in baseline calculations.

Measurement op-	Coordinates can be obtained in two ways:

- Through direct measurement.
- From peak table data.

 How to make direct measurements
 The table below describes how to make direct measurements in a chromatogram:

 Step
 Action

 1
 Right-click in the chromatogram and select Marker. Result: A vertical line is set in the chromatogram. A text box in the top



Result: The Y-axis is changed to the one corresponding to the new curve.

ence point

How to set a refer- The table describes how to set a reference point:

Step	Action
1	Right-click in the chromatogram and select Set Marker Ref. Point to define a reference point for the marker position.
2	 When the marker is moved from the reference point, the X-axis and Y-axis values for the new position are displayed together with: the new position in relation to the position of the reference point, the minimum, maximum and average values for the curve interval between the reference point and the new position.

How to record a

The table below describes how to record a **Snapshot** of the current curve values:

Snapshot

Step	Action
1	Right-click in the chromatogram and select Snapshot from the shortcut menu.
	<i>Result</i> : The Snapshot dialog box opens.
2	The dialog box displays all the curve data that was current at the moment the snapshot was taken.
	• Click the Save to file button to save the snapshot as an Excel file.
	Click the Print button to print the snapshot.

How to select peak table data

The retention time and amplitude of any peak can be viewed directly in a peak table after an integration. This data and more is selected in the **Chromatogram Layout** dialog box. The table below describes how to select peak table data.

Step	Action
1	Click the Chromatogram Layout icon.
	<i>Result</i> : The Chromatogram Layout dialog box opens.
2	Click the Peak Table tab.

Step	Action
3	 Select the checkboxes on the Select peak table columns list for all items that you want to display in the table. Click OK.

11.2 Other evaluations

Introduction

This section describes how the results can be used for other types of evaluations.

In this section

This section contains the following sub-sections

Торіс	See
How to find slope values	11.2.1
How to create curves	11.2.2

11.2.1 How to find slope values

Where to useThe slope values can be used in the Method Editor as parameters for the Watchslope valuesinstruction.

Conditional **Watch** instructions can be set up to let the progress of a run be determined by the events during the run, e.g. start to collect fractions when the first peak emerges.

The slope of the curve can be set as a condition to satisfy a **Watch** condition in the method during the run. It is important to use accurate slope values for the specific **Watch** instruction parameter.

A sample run You must first make a separation run with the sample you intend to purify. The result from this separation run is then used to find the slope values.



Retention scale

Time should be used as the X-axis scale for retention.

Step	Action
1	Click the Chromatogram Layout icon.
2	 Click the X-axis tab. Select Time. Click OK.

How to differenti-
ate the curveThe slope values are measured on a differentiated curve. The table below describes
how to create a differentiated curve.

Step	Action
1	Select Operations:Differentiate.
	Result: The Differentiate dialog box opens.

Step	Action
2	• Select the UV curve you want in the Source chromatogram list.
	Click the First order radio button.
	• Click OK .
	<i>Result</i> : The differentiated curve opens in the chromatogram.

How to measureSometimes the differentiated curve must be filtered to reduce noise and ghost peaksthe slope valuesbefore the measurements.

The table below describes how to measure the slope values on the differentiated curve.

Step	Action
1	Click the name of the differentiated curve (above the chromatogram window) to select the curve.
2	Use the zoom function to magnify the curve over an appropriate area.
3	Right-click and select Marker from the short-cut menu. <i>Result</i> : A vertical cursor bar opens in the chromatogram.
4	Place the Marker at the beginning of a peak where you want the Watch conditions to be fulfilled, i.e. where the slope becomes higher.
5	Read the actual slope value in the active Marker text box in the top left corner of the chromatogram window.

Note: The unit for the differentiated curve is mAU/min or AU/min. Any Y-axis value for the differentiated curve is the UV curve slope at the selected retention point.

 Illustration: Slope
 The illustration below shows a measurement of the slope limit after differentiation:

 walue measurement
 Image: state sta



11.2.2 How to create curves

Introduction You can draw a curve of your own in the **Evaluation** module. This section describes how this is done.

Note: The right to create and rename curves is defined in the user access rights and may be restricted.

How to createThe table below describes how to set up a chromatogram window to create a curvecurves - step 1in the Evaluation module.

Step	Action
1	Open a result file.
2	Select Operations:Create Curve. Result: The Create Curve dialog box opens. Select help gurve(s) VI: 01 No 157 001:1_UV1_313nm 02: 01 No 157 001:1_UV2_290nm 03: 01 No 157 001:1_UV2_290nm 03: 01 No 157 001:1_UV2_290nm 04: 01 No 157 001:1_UV2_290nm 05: 01 No 157 001:1_UV2_290nm 05: 01 No 157 001:1_UV4_Quot 05: 01 No 157 001:1_Cond 06: 01 No 157 001:1_FlowA 07: 01 No 157 001:1_FlowA 08: 01 No 157 001:1_FlowB 08: 01 No 157 001:1_Pressure 10: 01 No 157 001:1_CreatedCurve 04 05: 01 No 157 001:1_CreatedCurve
3	Select one or more Help curves .
4	 Select minimum and maximum values for the Y-axis. appropriate units from the Unit list. <i>Note</i>: The help curve determines the minimum and maximum values for the X-axis.
5	Click OK . <i>Result</i> : The Create Curve chromatogram window opens.

How to createIn the Create Curve dialog box you can also create new units for the curve. The tablenew unitsbelow describes how this is done.

Step	Action
1	Click the New unit button.
	<i>Result</i> : The Create New Unit dialog box opens.
2	Type a new unit name and a number of decimal places.
3	Click OK .
	<i>Result</i> : The Create New Unit dialog box is closed. The new unit is now available in the Create Curve dialog box.

How to createThe new curve is created in the Create Curve window. The table below describescurves - step 2how to work in this window.

Step	Action	
1	Click the Set Curve Points icon.	
2	• Click to insert curve points in the chromatogram.	
	Add more points to draw the curve.	
	<i>Result</i> : A green square marks the new curve point. The curve is drawn from the previous point. Hold the cursor over the inserted point to see the coordinates displayed.	
	Curve mode	
	• The regular spline mode draws the curve as a smooth line near but not through every point.	
	• Click the Spline through checkbox to draw the curve through all of the curve points.	
3	Move a point	
	• Select the point and drag it to the new position.	
	<i>Result</i> : The curve is redrawn.	

Step	Action		
4	Delete a curve point		
	Double-click the curve point.		
	or		
	• Select the point and click the Delete button.		
	or		
	 Select the point, right-click and choose Delete Point from the shortcut menu. 		
5	• Click the Zoom icon to focus on details in the curve.		
	<i>Note</i> : Right-click and select Reset zoom to return to the full view.		
	• Right-click in the chromatogram window and select Marker .		
	• Position the Marker bar over peaks in the help curve to measure the coordinates.		
	<i>Result</i> : The coordinates are displayed in the Marker text box in the top left corner of the chromatogram.		
	<i>Note</i> : Click the Marker text box to display the coordinates for the cre- ated curve. Click again to return to the help curve coordinates.		
6	Click OK .		
	<i>Result</i> : The Save Curve dialog box opens.		
7	Type a new name if desired and click OK .		

Curve example The illustration below is an example of a curve created by using the **Draw Spline** command in the **Create Curve** chromatogram window.



How to force the curve through points

In cases where you have created a curve and not selected the **Spline through** option, you may want the curve to pass through some of the points that are outside the created curve. The table below describes how to force the curve through these points:

Step	Action
1	• Select the curve point immediately before the curve point you want to connect to.
2	Click the Draw straight to next point button.
	<i>Result</i> : The curve is adjusted so that it is drawn as a straight line between the two points.

11.3 Automated evaluation procedures

Introduction

An evaluation procedure is a recorded sequence of interactive operations in the **Evaluation** module, which can be executed for automated data evaluation and report generation. The concept is similar to the "macro" facilities in other programs. This section describes how to work with automated evaluation procedures.

In this section

This section contains the following sub-sections

Торіс	See
How to create a new procedure	11.3.1
How to edit a procedure	11.3.2
How to run a procedure	11.3.3
How to rename and remove procedures	11.3.4

11.3.1 How to create a new procedure

IntroductionYou can use the Procedure Editor to record or create a new procedure. The ProcedureEditorCan also be used to view and edit the instructions within a procedure. This
section describes how to use the Procedure Editor to record new procedures.

 The Procedure Ed The illustration below shows the Procedure Editor in Record mode.

 itor dialog box
 Record mode.

Procedure Editor	Untitled			
	Mode: Record			-
BASE(TIME)				
Instruction	ADD		Parameter	Insert
C Integration C File operation	AMP_MUL AMP_SHIFT CLEAB			Beplace
C Export C Chrom C Other C Lest	COPY CUT DERIVATE DIV	▼		Delete
				 Close

How to record a procedure

The table below describes how to record a new procedure.

Step	Action
1	Open the result file in the Evaluation module.
2	Choose Procedures:Record On.
	<i>Result</i> : The Procedure Editor dialog box opens in record mode.
3	Minimize the Procedure Editor dialog box.
4	Perform the evaluation steps that the procedure is to contain.
	<i>Result</i> : The steps are recorded in the order that they are performed.

11 Evaluation

11.3 Automated evaluation procedures

11.3.1 How to create a new procedure

Step	Action
5	Stop the recordingChoose Procedures:Record Off.
	or • Restore the minimized Procedure Editor dialog box and click the Stop button.
	 Restore the minimized Procedure Editor dialog box and select Control:End Record.
6	Choose File:Save or File:Save As in the dialog box. <i>Result</i> : The Save As dialog box opens.
7	 Type a name for the new procedure in the Procedure name text box. Select the Global procedure checkbox if desired (see further information below). Click OK. Result: The procedure is saved and available for future use.
8	Click the Close button to close the dialog box.

How to create a You can choose to save the new procedure as a **Global procedure**. This makes the Global procedure procedure available to all users. The procedure will have (Global) before the name to designate that it is available to all users.

You must have Edit global list(s) authorization to be able to save Global procedures.

How to build a procedure with instructions

You can select instructions in the **Procedure Editor** dialog box to build a complete procedure step by step. The procedure instructions are described in **B.4 Procedure** instructions on page 389. The table below describes how to create a new procedure with instructions.

Step	Action
1	Choose Procedures:Edit:New.
	Result: The Procedure Editor opens in Edit mode.

Step	Action
2	 Select an instruction from the Instruction list. Type the appropriate parameters in the Parameter field. Click Insert.
3	Repeat step 2 until the procedure is complete.
4	Choose File:Save .
5	Type a procedure name and click OK .
6	Click the Close button in the Procedure Editor .

11.3.2 How to edit a procedure

Introduction Evaluation operations are represented by instructions in the **Procedure Editor** dialog box. The instructions can be modified to suit other specific evaluation needs and be saved for later use. This section describes how to use the **Procedure Editor** to edit a procedure.

How to edit a procedure

How to edit a pro- The table below describes how to edit an existing procedure:

Step	Action
1	Select Procedures:Edit:Open.
	<i>Result</i> : The Open Procedure dialog box opens.
2	Select the procedure from the list and click OK .
	Result: The Procedure Editor opens in Edit Mode.
3	Select an instruction in the procedure window.
	<i>Result</i> : The instruction parameters are displayed in the Instruction and Parameter fields. A short definition of the selected instruction is displayed at the bottom left corner.
4	Type new values in the Parameter text boxes and click the Replace button.
	<i>Result</i> : The old parameters are replaced by the new parameters.
5	Add a new instruction
	• Select the instruction in the procedure immediately before where you want the new instruction.
	• Select a type and an instruction in the Instruction field.
	• Type parameter values in the Parameter field.
	Click the Insert button.
	<i>Result</i> : The new instruction is inserted after the selected instruction.
6	Remove an instruction
	Select an instruction in the procedure and click the Delete button to remove the instruction from the procedure.
7	Choose File:Save and click the Close button to close the dialog box.

Descriptions of the procedure in- structions	Appendix B.4 Procedure instructions on page 389 contains a list of procedure instructions with descriptions.		
How to add in- structions to a	If you start recording again you can add more instructions to a procedure that is already open in the Procedure Editor :		
procedure when recording	• The new instructions will be added to the end of the present procedure.		
	• The new instructions will be inserted after the selected instruction if an instruction has been selected.		
Invalid instruc- tions	The procedure will stop and display an error message if an instruction calls for an invalid operation when the procedure is run. Any subsequent instructions in the procedure will not be executed.		
Address the right curves	Curves are identified only by their storage position. An instruction can become invalid if it addresses the wrong curve:		
	Example		
	• The instruction ADD (01,02,03) will try to add curve 01 to curve 02 and store the result in position 03.		
	• A curve in position 03 that is not a raw data curve will be overwritten.		
	• A raw data curve in position 03 cannot be overwritten and the procedure will be stopped at that point.		
Default values for classic baseline instructions	When a classic or morphological algorithm is used to calculate a baseline, UNICORN will suggest default values for the four control parameters based on the appearance of the curve. To instruct UNICORN to use default values appropriate for the curve every time the procedure is run, choose the default setting in the appropriate fields for the parameters.		
	Example		
	• CALCULATE_BASELINE (01, 06, XXX, XXX, XXX, XXX)		
	Can be changed to:		
	• CALCULATE_BASELINE (01, 06, DEFAULT, DEFAULT, DEFAULT, DEFAULT)		
Global procedures	It is not advisable to edit existing global procedures. Open the global procedure instead and save a copy under a new name. Use this copy for editing purposes.		

11.3.3 How to run a procedure

Introduction You can run the saved procedures either for a specific chromatogram or as batch runs.

How to run a single procedure

The table below describes how to run a procedure for a specific chromatogram.

Step	Action
1	Open a result file.
2	Select Procedures:Run . <i>Result</i> : The Run Procedure dialog box opens.
3	Select the procedure from the list and click OK . <i>Result</i> : The procedure is executed.

Note: You can also open the procedure in the **Procedure Editor** dialog box and choose **Control:Run** or click the **Play** button.

Batch runsIt is possible to apply an evaluation procedure to a designated batch of result files if
they are not open in the Evaluation module. An open file will not run and an error
message will be displayed.

The batch run is performed in the background of the **Evaluation** module and the results of the run are not seen, with the exception of prints and documentation that are defined as steps in the procedure. For example, batch runs are useful

- to perform integration with the same parameter settings on many results,
- to print a number of results with the same settings.

How to perform a The table below describes how to perform a batch run:

batch run

Step	Action
1	Choose Procedures: Batch run .
	Result: The Open Procedure dialog box opens.
2	Select the procedure from the list and click OK .
	<i>Result</i> : The Batch Run dialog box opens.

Step	Action
3	Use the Browse button to find and select the folder to search for result files and chromatograms.
	<i>Note</i> : The search will only be performed in the selected folder. You can use standard wildcard characters and define restricting search criteria for the Result and Chromatogram fields. Up to 10 user-defined search filters can be saved in the drop-menus.
4	Click the Search button.
	<i>Result</i> : A list of found chromatograms is displayed.
5	Select the chromatograms you want to perform the run on.
	The Select All button selects all chromatograms.
	• The Clear button removes all chromatograms from the list.
6	Click the Run button.
	<i>Result</i> : The batch run is performed and any created curve or peak table will automatically be saved in each result file.

The Batch Run The illustration below is an example of search results in the Batch Run dialog box: dialog box The illustration below is an example of search results in the Batch Run dialog box:

E Daton nan (roport_omonotogram j				
Chromatogram s	election				
<u>F</u> older	c:\\Default\			Browse	
<u>R</u> esult	Baseline*			Browse	All
Chro <u>m</u> atogram	×			Browse	All
Found chromato	grams Second Baseline example 1 Baseline example 2 Baseline example 3	1 1 1			
		Run	₅∟∟	Cancel	<u>H</u> elp

How to batch-runEvaluation procedures combined with batch runs can be a useful tool to produce
printed documentation simultaneously for many result files, e.g. for a number of
scouting runs. The table below describes how to create a procedure to batch-run
reports.

Step	Action	
1	Choose Procedures:Record On to record a procedure.	
2	Choose File:Report.	
	Result: The Generate Report dialog box opens.	
3	Choose a report format.	
4	Click the Print button as the final instruction.	
5	Choose Procedures:Record Off.	
6	Save the procedure.	
	<i>Note</i> : A printing procedure can also be saved with a method to produce automatic prints at the end of a run.	

Note: When for example a batch run is performed, the latest version of the procedure will be used. However, procedures that are saved with a method are not affected if the original procedure is edited at a later time.

How to add procedures to the menu

You can add up to 15 created evaluation procedures to the **Procedures** menu in the **Evaluation** module. The table below describes how to add procedures to the menu:

Step	Action
1	Select Procedures:Menu . <i>Result</i> : The Edit Procedures Menu dialog box opens.
2	 Select the checkboxes of the procedures you want to display on the menu. Click OK. Result: The selected procedures are included on the Procedures menu.

Remove a procedure

Open the **Edit Procedures Menu** dialog box and select the checkbox again to de-select and remove a procedure from the menu.

How to rename and remove procedures 11.3.4

Introduction The procedures that you have created can be renamed or removed from the list of available procedures. This section describes how this is done.

How to rename a procedure

The table below describes how to rename a procedure.		
Step	Action	
1	Choose Procedures:Edit:Rename.	
	<i>Result</i> : The Rename Procedure dialog box opens.	
2	Select a procedure.	
	<i>Result</i> : The procedure name is displayed in the New name text box.	
3	Type the new name.	
4	Click OK.	
	<i>Result</i> : The procedure name is changed.	

How to delete a procedure

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The table below describes how to delete a procedure.		
Step	Action	
1	Choose Procedures:Edit:Delete.	
	Result: The Delete Procedure(s) dialog box opens.	
2	Select a procedure.	
3	• Click OK .	
	Click the Yes button to confirm.	

Global procedures It is not advisable to edit existing global procedures. Open the global procedure instead and save a copy under a new name. Use this copy for editing purposes.

Result: The procedure is deleted.

12 System settings

Introduction This chapter describes some of the general system settings.

In this chapter

This chapter contains the following sections

Торіс	See
General information about system settings	12.1
Alarms	12.2
Curves	12.3

System settings	The system settings				
	• define settings for alarms and warning	gs			
	• select the data that will be stored in re	esult files			
When to change	Each system has a set of default settings				
the system set-	Changes to the default settings should	d be made when the system is installed.			
tings	Certain system settings may need to be adjusted in the following cases:				
	• If system components are changed: e	.g. the alarm and warning limits			
	• For specific separation runs: e.g. the m	nonitor and curve settings.			
	<i>Note</i> : Only the settings for the selected components will be shown for strategies where you select the system components.				
How to change the default set- tinas	The table below describes the two different ways to change the default system settings.				
	Change	Effect			
	To assign a new value to a parameter within a method.	The specific change is valid only until End in the method. After End the para- meter returns to its default setting.			
		<i>Note</i> : Only some parameters can be changed in the method.			

12.1 General information about system settings

Note: You must have **System settings** authorization to assign a new value to an actual system setting.

How to assign a new value to a system setting

The table below describes how to assign a new value to a system setting in the System Control module.

Step	Action	
1	Select System:Settings . <i>Result</i> : The Instructions dialog box for the connected system opens The illustration below shows the dialog box opened with the Alarms group of settings selected.	
	AVTA oligopilot Alermes Instructions: X Instructions Made Instructions Made Specials High-Jamm 30030 G/cm Alam, UV1 Made Alam, UV1 Mode Mode High-Jamm 20000 Bg LowAlam 0.0 Bes High-Jamm 50000 mAU Alam, UV1 Mode Mode High-Jamm 50000 mAU C Durves LowAlam 0.0 Bes LowAlam 0.0 Set LowAlam 0.0 Bes LowAlam 0.0 Set LowAlam 0.0 MU LowAlam 0.0 Set LowAlam 0.0 Des LowAlam 0.0 Set Set Selected Perometer To Strategy Delaul/Volue OK OK Caroel	
2	 Click the radio button to select one of the following instruction groups: Alarms Specials Monitors Curves Result: The instructions for the group are displayed. The parameters are listed below each instruction. The title bar of the dialog box shows the selected instruction group. 	
3	 Select a parameter from the list. Change the setting value in the Parameters field. <i>Result</i>: The parameter is updated with the new value in the list. 	
4	Click the Set Selected Parameter To Strategy Default Value button to return to the default value (if necessary). <i>Result</i> : The default setting that was defined in the system strategy is restored. Only the selected parameters will be restored.	
5	Click OK .	

signals in methods

Limits for monitor If the system strategy allows, limits for certain monitor signals can be set in the method. These limits will only work locally in the method and override the global settings as long as the method is in operation.

12.2	Alarms		
Introduction	ction This section is a description of the Alarms system settings.		
Alarms and Warn- ings	The Alarms settings define the upper and lower Alarm and Warning limits for process monitor signals. The table below describes the difference between Alarms and Warnings .		
	If the signal exceeds	then	
	the Alarm limits	 an alarm sounds an alarm message is displayed the process is paused (i.e. the method execution is suspended and all pumps are stopped) the alarm is noted in the logbook. The situation must be acknowledged and corrected before the process can be continued. a warning message is displayed the process continues the warning is noted in the logbook. 	
Alarms in a net- work	 Note: The message text in an Alarm dialog box and the corresponding text in the logbook are both color-coded in red. Warning texts are color-coded in orange both in the dialog box and in the logbook. The text in the logbook is changed into black when the Alarm or Warning is acknowledged. Note: The Alarms are not active unless the mode is set to Enabled. Alarms and warning messages are displayed on all stations with a connection to the concerned system. This is regardless of the activity that is currently performed in UNICORN and regardless of the identity and access rights of the current user. Alarms and warnings can only be acknowledged from the station that is connected in control mode. 		

The hysteresisThe hysteresis setting (not available for ÄKTAdesign systems) for a warning determinessettingto which extent the signal can oscillate up or down from the warning limit threshold
without re-activating a warning.

After the signal has activated a warning, the warning will not be repeated as long as the signal remains within a window defined by the hysteresis setting above and below the warning limit. This prevents repeated warnings from noisy or oscillating signals close to the warning boundary.



Note: Hysteresis is only relevant for warnings, since an alarm puts the system into **Pause** mode at the first alarm.

12.3	Curves	
Introduction	This section is a short description of the Curves system settings.	
The Instructions dialog box	The illustration below shows the Instruction selected.	ons dialog box with the Curves instructions
	AKTA oligopilot Curves Instructions Instructions Alams Store ON Time between samples 0.100 s UV2 Store ON Time between samples 0.100 s Store ON Time between samples 0.100 s Store ON Store ON Time between samples 0.100 s Set Selected Parameter To Strategy Default Val	VV1 Parameters Store OFF ON Time between samples 0.100 S S Cancel Help
Curve settings	The curve settings determine which moni- the result file. Verify that Store:ON is set in that are to be stored. <i>Warning</i> : If a curve is set to Store:OFF , do displayed in the curves window during a in any way.	itor signals that will be stored as curves in In the Instructions dialog box for all signals Ita from the specific monitor cannot be process run. The data will not be recorded
Store and Time The table below describes the function of the two curve settings. between samples		the two curve settings.
·	Setting	Function
	Store (OFF/ON)	This setting determines whether the curve data is stored or not.
	Time between samples	This setting determines with which fre- quency curve data is recorded. It does not affect the reading frequency of the actual monitor. Default value is the shortest possible time between samples.

13 System maintenance and error reporting

Introduction This chapter describes the system maintenance and error reporting functions.

In this chapter

This chapter contains the following section

Торіс	See
How to generate problem reports	13.1

13.1 How to generate problem reports

Introduction UNICORN contains a Generate Report Wizard for registration of errors or problems that you have detected or that occur during a run. The Generate Report Wizard takes you through the steps to generate your report.

There are two ways of accessing the Generate Report Wizard:

- From the UNICORN Manager
- From the **System Control**.

In this section This section contains the following sub-sections

Торіс	See
How to generate a report from the UNICORN Manager	13.1.1
How to generate a report from the System Control	13.1.2

13.1 How to generate problem reports

13.1.1 How to generate a report from the UNICORN Manager

13.1.1 How to generate a report from the UNICORN Manager

Introduction The Generate Report Wizard is used to generate problem reports. This section describes how to generate a problem report from the UNICORN Manager.

Step 1: How to create the report

Step	Action
1	Select Administration:Create System Report in the UNICORN Man-ager module.
2	 The first step is a Welcome screen. Click the Next button. Result: The Systems dialog box opens with a list of the available sys-
	 tems for the logged-on user. Select a system for which the report is to be generated and click the Next button.
	Result: The Description dialog box opens.
3	 Add the following information in the dialog box: a short description of the problem the circumstances under which the problem occurs the consequences of the problem. Click the Next button.
	Result: The Reproducibility dialog box opens.
4	Specify whether the problem is reproducible or not. Select one of these alternatives: • Yes
	(Provide a short description in the text box of how the problem can be reproduced.)
	• No
	Unknown.
	Click the Next button to proceed to attach example files (see table below).

The table below describes how to create a report with the Generate Report Wizard.

Step 2: How to at-
tach a fileYou can attach result files, method files and/or log files to the problem report.tach a fileThe table below describes how to attach a file:

Step	Action
1	The Attachments dialog box is displayed:
	Attachments X Files Add Baseline example 1.res Add Baseline example 2.res Delete System information Quelete System information Aggraphic provides the provid
2	• Depending on the character of the file to be attached, select the appropriate tab: Result , Method , System log or Global log .
	Attach the file:
	- Click the Add button.
	- Select a file in the dialog box and click the Attach or OK button.
	<i>Result</i> : The selected file is added to the tab in the Attachments dialog box.
	<i>Note</i> : To remove a file, select the check box and click the Delete button.

13 System maintenance and error reporting13.1 How to generate problem reports13.1.1 How to generate a report from the UNICORN Manager

Step	Action
3	To include more information in the report, select the appropriate check boxes in the System information field. By default, all options are checked.
	Computer & operating system information
	A summary of the computer and operating system information, for example type of processor, processor speed, RAM, hard disk capacity and printer.
	ÄKTA hardware information
	A summary of the specific ÄKTAdesign hardware, for example the in- strument and PROM version for every instrument that is connected.
	Integrity check
	When UNICORN is installed a checksum calculation is performed on the stationary files (*.dll and *.exe) for the system. An integrity check means that a new checksum calculation is performed for the same files in their folders. This new calculated value is compared with the checksum value obtained during installation. The results of the com- parison are presented in the report and any deviations are included.
	Click the Next button.
	<i>Result</i> : The Generate report dialog box is displayed.
4	Proceed to Step 3: How to generate and save the report below.

Step 3: How to
generate and
save the report

The table below describes how to generate and save the report:

Step	Action
1	By default, the report is saved in the folder Unicorn\Reports. If you want to save the report at another location, select a folder in the tree structure.
2	 You also have these options: Click the Preview button to open the report in Notepad. Click the Print button to print the report without any preview.
3	Click the Finish button to generate and save the report.

13.1.2 How to generate a report from the System Control

Introduction The Generate Report Wizard is used to generate problem reports. When an error message appears in System Control, you can activate the report wizard from the error message dialog box. The Generate Report Wizard can also be activated anytime if you choose System:Report.

Step 1: How toWhen an error message appears in System Control, follow the instructions in thiscreate the reporttable to activate the Generate Report Wizard and create a report:

Step	Action
1	Click the Report button in the error message dialog box.
	or
	Choose System:Report.
2	The first step is a Welcome screen.
	Click the Next button.
	<i>Result</i> : The Description dialog box is displayed and shows a list of the problems/errors that have occurred. All the problems/errors that have occurred, together with help texts, are automatically recorded and included in the report.
	• If you select a specific error in the Description dialog box, the appropriate help text is shown in the error message box.
3	Add the following information in the Description dialog box:
	A short description of the problem.
	The circumstances under which the problem occurs.
	The consequences of the problem.
	Click the Next button.
	Result: The Reproducibility dialog box opens.

13 System maintenance and error reporting

13.1 How to generate problem reports

13.1.2 How to generate a report from the System Control

Step	Action	
4	Specify whether the problem is reproducible or not. Select one of these alternatives:	
	• Yes	
	(Provide a short description in the text box of how the problem can be reproduced.)	
	• No	
	Unknown.	
	Click the Next button to proceed to attach example files (see table below).	

Step 2: How to at-
tach a fileYou can attach method files and/or log files to the problem report.tach a fileThe table below describes how to attach a file:

Step	Action	
Step 1	Action The Attachments dialog box is displayed:	
	Bint Pregiew K Back Next > Cancel Help	
Step	Action	
------	---	--
2	• Depending on the character of the file to be attached, select the appropriate tab: Result , Method , System log or Global log .	
	Attach a file:	
	- Click the Add button.	
	- Select a file in the dialog box and click the Attach or OK button.	
	<i>Result</i> : The selected file is added to the tab in the Attachments dialog box.	
	<i>Note</i> : To remove a file, select the checkbox and click the Delete button.	
3	To include more information in the report, select the appropriate check boxes in the System information field. By default, all options are checked.	
	Computer & operating system information	
	A summary of the computer and operating system information, for example type of processor, processor speed, RAM, hard disk capacity and printer.	
	ÄKTA hardware information	
	A summary of the specific ÄKTAdesign hardware, for example the in- strument and PROM version for every instrument that is connected.	
	Integrity check	
	 When UNICORN is installed a checksum calculation is performed on the stationary files (*.dll and *.exe) for the system. An integrity check means that a new checksum calculation is performed for the same files in their folders. This new calculated value is compared with the checksum value obtained during installation. The results of the comparison are presented in the report and any deviations are included. Click the Next button. 	
	<i>Result</i> : The Generate report dialog box is displaued.	
4	Go to stan 3 helow	
4		

13 System maintenance and error reporting

13.1 How to generate problem reports

13.1.2 How to generate a report from the System Control

Step 3: How to generate and	The table below describes how to generate and save the report.		
save the report	Step	Action	
	1	By default, the report is saved in the folder: Unicorn\Reports.	
		If you want to save the report in another location, select a folder in the tree structure.	
	2	 You also have these options: Click the Preview button to open the report in Notepad. Click the Print button to print the report without any preview. 	
	3	Click the Finish button to generate and save the report.	

Α	Troubleshooting
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 Introduction
 This appendix describes different problems which may arise in UNICORN and how to solve the problems.

 In this chapter
 This chapter contains the following sections

 In topic
 See

 Logon
 A.1

 UNICORN access
 A.2

 Methods and method runs
 A.3

 Evaluation
 A.4

Logon A.1 In this section This section describes how to solve the following log on problems: Unable to log on to UNICORN • Error message "Strategy file error". The table below describes some log on problems and their solutions: Unable to log on to UNICORN Solution **Problem description** You have forgotten your password. Ask the system administrator to supply a new password. Username and password not accepted • Restore the file USERS30.MPM from the latest back-up copy You cannot log on although you use your correct username and password. or Reason: The file USERS30.MPM in the • reinstall the default user. folder \UNICORN\SERVER\FIL could be corrupt. No user names: Remote station Make sure that the computer is logged on to the network before you start Both these conditions must apply: UNICORN. • The **User name** drop-down box in *Note*: A remote station accesses the the **Logon** dialog box is empty. user list directly from the network • You are trying to log on from a reserver. mote station in a network installation No user names: Local station Make sure that the computer is logged on to the network before starting The user list on a local station in a net-UNICORN. work installation is not up to date. *Note*: The user list is stored locally on a local station, and is updated automatically from the network server if the computer is logged on to the network.

Error message "Strateau file er-	The table below describes some problems and their solutions:		
ror"	Problem description	Solution	
	Stand-alone installation If you receive the error message "Strategy file error" in a <i>stand-alone</i> in- stallation, the strategy file is probably corrupt.	Reinstall the strategy as described in the Administration and technical manual "Install selected software com- ponents after the initial installation".	
	Network installation In a <i>network</i> installation, the error message "Strategy file error" may ap- pear if you try to create a method for a system not physically connected to the computer.	Make sure that the computer is logged on to the network before UNICORN is started, so that the strategy file on the server disk is accessible.	

A.2 UNICORN access

In this section

This section describes how to solve the following UNICORN access problems:

- Unable to access certain UNICORN functions
- Connection problems
 - Connections are not available
 - System is not available
 - Error message in a network installation
 - You cannot control the system
- Run data Connection in System Control displays a "NO [1]", "NO [2]" or "NO [3]".

Unable to access certain UNICORN functions

ess The table below describes an access problem and its solution:

Problem description	Solution
UNICORN functions to which you do not have access appear grey in the menu and cannot be used.	Choose Administration:User Setup in the UNICORN Manager to change the user profile.
	<i>Note</i> : Contact the system administrator if you are not authorized to change your user profile.

Connection prob- The table below describes some connection problems and their solutions:

lems

Problem description	Solution
The connections are not available.	• Check the connection between the PC and the oligonucleotide system.
	• Check that the power to the chroma- tography system is turned on.
 The connections are not available even though the connection between PC and oligonucleotide system appears to be correct the power is turned on. 	 Quit UNICORN. Shut down and switch off the computer. Switch off the oligonucleotide system. Restart the entire system.

Problem description	Solution
A system is not available when you at- tempt to establish a connection.	Check that you have access rights to the system. Access rights are not auto- matically assigned for a newly defined system.
You receive the error message "Cannot connect to system" in a network install- ation.	• Check that the local computer to which the system is connected is turned on and logged on to the network.
	 Check that the computer where you try to establish a connection is logged on to the network.
	• Check that the limit of 8 connections to the system has not been exceeded.
You can establish a connection but cannot control the system, that is the	• Check that no other user has a con- trol mode connection.
Manual menu commands in the Sys- tem Control are grey.	 Check that you have sufficient access rights to control the system manually.

The Connection field in System Control displays a "NO [X]"

Problem Description Solution The **Connection** field in Check that the UNICORN PC Control board is con-• the **Run data** pane in figured according to the settings made during the System Control says installation of the program. The same Control unit "NO [1]" or "NO [2]". number, Address and IRQ must be set at the Control board, see the Administration and technical manual "Hardware installation". • The communication may also fail if there is a conflict between the UNICORN PC Control board configurations and other boards in the PC. If so, select a free Address and a free IRQ during UNICORN installation and at the Control Board, see the Administration and technical manual "Hardware installation".

The table below describes some connection problems and their solutions:

Problem Description	Solution
The Connection field in the Run data pane in	 Choose Administration:System Setup in the UNICORN Manager.
System Control says "NO [3]".	 Select the system with problems in the dialog box and click the Edit button.
	- Check that the strategy, computer name and the control number are correct according to the installation at the local station which is physically connected to the system. See the Administration and technical manual "System definitions".
	 If you connect remotely to a system
	 check that the local station which is physically connected to the system is turned on
	 check that the network is functioning at both the remote and the local station.
	• Check that the limit of eight connections to the system has not been exceeded.

A.3	Methods and method runs			
In this section	This section describes how to solve the following method and method run problems:			
	Cannot perform Quit or Logoff			
	• Monitor signals do not appear in the C	Curves pane in System Control		
	• Error message "Couldn't create result	file Destination path could not be found"		
	 The Method-System Connection dialog box keeps appearing 			
	The Method Editor window does not fit on the screen			
	There are red instructions in a method			
	After Windows® logout and login you cannot get a system connection			
	• The Print screen command does not s	send a copy of the screen to the printer		
Cannot perform	The table below describes a problems an	d its solutions:		
Quit of Logon	Problem description	Solution		
	You are unable to perform Quit or Lo- goff from UNICORN for a connection.	You might be running a MethodQueue . This function requires a control mode connection in order to start subsequent cycles correctly.		
		Action: Stop the MethodQueue before you quit or log off.		

A.3 Mathods and mathod

not appear in the Curves panel in System Control			
	Problem description	Solution	
	Monitor signals do not appear in the Curves pane in System Control .	Choose System:Settings in System Control	
		<i>Result</i> : The System Instructions dialog box opens.	
		Choose the Curves group in the In- structions field.	
		• Set the Store option to ON .	
		Store	
		Signals for which Store is set to ON can be selected from the View:Proper- ties:Curves dialog box in Sustem Con-	
		trol.	

Monitor signals do The table below describes a problem and its solution:

The table below describes a problem and its solution:

Problem description	Solution
If you receive the error message "Couldn't create result file Destination path could not be found" at the end of a method, the local computer was un- able to access the folder specified in the result file path.	This may happen if the specified folder is on the network server and network communication has been lost. The res- ult file is saved in the Failed folder on the local station.

The Method-Sys- tem Connection	The table below describes a problem and its solution:		
dialog box keeps appearing	Problem description	Solution	
	If the Method-System Connection dia- log box keeps appearing you have some method(s) which is not connected to a system.	Connect the method(s) to the appropri- ate system.	
	<i>Reason</i> : Most likely you have imported some method(s) with the command File:Copy from External in the UNICORN Manager .		

The Method Editor	The table below describes a	problem and its solution:
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wir	ndow	does	not
fit	on th	e scre	en

Problem description	Solution
The Method Editor window does not fit the screen and has scroll bars. <i>Reason</i> : The incorrect font size might be installed.	 The display screen resolution may be set to "1024x768x65536" with "Large fonts". You need to install the "Small fonts". This requires that you have the Windows 2000 or Windows XP CD-ROM that was shipped with your Compaq computer. Insert the CD-ROM and follow the directions on the screen.

Note: Always install the latest service pack after you have installed something from the Windows 2000/XP CD-ROM.

There are red in-	The table below describes some solutions to syntax error problems:		
method	Problem description	Solution	
	 Red instructions (instructions with a red dot) in a method are syntax errors and may be due to the following: The method was connected to the wrong system, that is the strategy of the system is incompatible with the method. The method instructions do not correspond to the components you have chosen for your system. Check your system components under Administration:System Setup in the UNICORN Manager. The Copy function was used instead of Copy from external when a method was imported from a diskette. The wrong system may have been selected in the Save As dialog box in the Method Editor. You may also have templates not intended for your system, which might be the case for custom designed systems. The systems strategy has been updated with a new strategy that differs in the instruction set. 	 There are several actions that you can take: Check that the method has been connected to the correct system in either of these ways: in the System Method Connection dialog box when you use the Copy from external dialog box in the Save As dialog box in Method Editor. If the system is custom designed, open the Method Editor, select the red instruction and either delete it or replace it with a corresponding instruction (if available) from the Instructions before saving the method. 	

After Windows logout and login you cannot get a system connection

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The table below describes a system connection problem. This applies only to local systems, not remote systems:

Problem description	Solution
You have logged out of Windows 2000 and then logged in again, but you can- not get a system connection in UNICORN.	Restart the computer in order to obtain a system connection in UNICORN.
<i>Reason</i> : If you shut down Windows 2000 with the command Start:Shut- down:Close all programs and log in as a different user , you will not be able to obtain a System Control connection in UNICORN the next time you or anoth- er user logs on. This is because the de- scribed shutdown procedure automat- ically shuts down a number of pro- cesses, including those needed for sys- tem connection. The services are only started when the computer is booted up.	

Print screen does not send a copy of the screen to the printer

Print screen does The table below describes how to solve a printing problem:

Problem description	Solution
The Print screen command only makes a copy of the screen to the clipboard and not to the default printer.	If you want to print the view on the screen, press the <print scrn=""></print> key and paste the image from the clipboard into an appropriate program, such as Microsoft® Paint, and then print out the image.

A.4	Evaluation		
In this section	 This section describes how to solve the following evaluation problems: Incorrect date and time in the result file Evaluation procedure aborts 		
Incorrect date	The table below describes a problem and its solution:		
result file	Problem description	Solution	
	The result file shows incorrect date and time.	Check the system clock setting.	
		The date and time recorded in the result file are taken from the PC system clock setting.	
Evaluation proced- The table below describes a problem and its solution:		its solution:	
	Problem description	Solution	
	The evaluation procedure aborts.	Instructions in an evaluation procedure refer to curves by identification number irrespective of the curve names. Make sure that the curves processed when the procedure is executed are compat-	

ible with those processed when it was recorded. An evaluation procedure aborts if you try to store resulting curves at the position of an original raw

data curve.

Introduction This appendix describes the functions that are implemented in the **Evaluation** module.

In this chapter

This chapter contains the following sections

Торіс	See
Smoothing algorithms	B.1
Baseline calculation theory	
Peak table column components	B.3
Procedure instructions	

B.1 Smoothing algorithms

IntroductionThis section describes how the smoothing functions are calculated. ChooseOperations:Smooth in the Evaluation module to view and edit the options.

Moving Average The table below describes the process when the **Moving Average** smoothing algorithm is used.

Stage	Description
1	For each data point in the source curve, the processed curve is calcu- lated as the average of the data points within a window centered on the source data point.
	• The width of the window is determined by the parameter value, expressed as number of data points.
2	When the source point is less than half the window size from the be- ginning of the end of the curve, the average is calculated symmetrically round the source point over as many data points as possible.
	• If you increase the window width, the smoothing effect is also in- creased.

Note: The filter algorithm only accepts odd integer parameter values between 1 and 151. If an even number has been given, it is incremented by one (1).

Autoregressive The table below describes the process when the Autoregressive smoothing algorithm is used:

Stage	Description
1	The first data point in the source curve is copied to the processed curve.
2	For each subsequent data point, the previous processed point is mul- tiplied with the parameter value and added to the current source data point.

Stage	Description		
3	The result is then divided by the parameter value plus 1 according to the following formulae:		
	$t_1 = S_1$		
	$t_{n} = \frac{(p * t_{n-1} + S_{n})}{(p+1)}$		
	Where:		
	t _n = current processed point.		
	t _{n-1} = previous processed point.		
	S _n = current source point.		
	p = smoothing parameter value.		
	<i>Note</i> : If you increase the parameter value, the smoothing effect is also increased.		

Note: The filter algorithm only accepts integer parameter values between 1 and 25.

Median

The table below describes the process when the **Median** smoothing algorithm is used.

Stage	Description	
1	For each data point in the source curve, the processed curve is calculated as the median of the data points within a window centered on the source data point.	
	• The width of the window is determined by the parameter value, expressed as number of data points.	
2	When the source point is less than half the window size from the be- ginning of the end of the curve, the median is calculated symmetrically round the source point over as many data points as possible.	
	• If you increase the window width, the smoothing effect is also increased.	
	• To completely remove a noise spike, the window width should in effect be slightly more than twice the width of the spike.	

Note: The filter algorithm only accepts odd integer parameter values between 1 and 151. If an even number has been given, it is incremented by one.

B.1 Smoothing algorithms

Savitzky-Golay

The table below describes the process when the **Savitzky-Golay** smoothing algorithm is used.

Stage	Description
1	The algorithm is based on performing a least squares linear regression fit of a polynominal of degree k over at least k+1 data points around each point in the curve to smoothen the data.
	The derivate is the derivate of the fitted polynominal at each point.
	The calculation uses a convolution formalism to calculate 1st through 9th derivatives.
2	The calculation is performed with the data in low X to high X order. If the input trace goes from low to high, it is reversed for the calculation and is re-reversed afterwards.

Note: See Gorry, Peter A, General Least-Squares Smoothing and Differentation by the Convolution (Savitsky-Golay) Method (Analytical Chemistry 1990, Volume 62, 570-573) for more information on the Savitzky-Golay algorithm.

B.2 Baseline calculation theory

Overall process	The table below describes the overall process of a baseline calculation.		
	Stage	Description	
	1	The baseline segments are defined.	
	2	The baseline points are selected.	
	3	The baseline is drawn.	
Baseline segment definition	eline segmentBaseline parameters are used to find the baseline segments. The defaul the parameters are determined from the source curve. The baseline seg found by different parameters that are based on the type of algorithm tha <i>Note</i> : The parameters can be displayed in the Evaluation module if you		
	Integrate:C	Calculate baseline function. You can also click the Baseline settings button grate:Peak integrate dialog box.	
Morphological al-	The Morph	ological algorithm searches for all parts of the source curve where:	
gorithm	• The curve parts come into contact at both ends of a horizontal line of the length defined in the Structure width parameter. The default value of this parameter is based on the widest detected peak in the curve. The horizontal line is moved along the curve up the peak until it reaches the contact points. The curve parts below the horizontal line and the line will now form a "curve" with a plateau. The center point in the plateau formed by the horizontal line will be the data point for the baseline.		
	The data reduces	a points fulfil the Minimum distance between data points . This parameter the total number of data points that are created from a curve.	

B.2 Baseline calculation theory

Classic algorithm The **Classic** algorithm searches for all parts of the source curve where: The curve parts are longer than the Shortest baseline segment. This parameter determines the minimum length for a part of the source curve to be considered a possible baseline segment. • The curve has no point outside the **Noise window**. The noise window is defined as a rectangular corridor parallel to the slope of the curve and centered on the first and last points within the currently inspected segment. • The slope is less than the Slope limit. This limits the maximum slope of the baseline to differentiate baseline segments from peaks. • The curve parts are lower than the Max baseline level. This parameter determines the highest acceptable signal level for the baseline. Baseline paramet- The baseline parameters can be illustrated as a rectangular box that the source curve ers has to fit into in order to be identified as a baseline segment, where: The length of the box corresponds to the **Shortest baseline segment**. • The height of the box corresponds to the maximum level of noise on the baseline ٠ segments. This is referred to as the **Noise window**. • The box is allowed to be tilted with a maximum slope corresponding to the **Slope** limit. • The box is not allowed to move up above the Max baseline level. Baseline paramet-The illustrations below shows the baseline parameters graphically. ers - illustration Shortest baseline segment Noise Window



Baseline segment The table below describes the baseline segment identification process: identification Stage Description 1 The box is virtually moved along the source curve in steps of one th

Stag	е	Description
1		The box is virtually moved along the source curve in steps of one third of the Shortest baseline segment length to look for baseline segments.
2		A baseline segment is found whenever the currently examined part of the source curve fits completely within the box.
3		The found baseline segments are joined by connecting adjacent seg- ments, provided that the slope of the joining lines does not exceed the Slope limit .

Baseline pointsWhen the baseline segments have been defined and joined, they are replaced by(Classic algorithm)baseline points at the start and end of each segment. The line between these is also
filled with points.

Note: The baseline points are shown as green squares in the **Integrate:Edit baseline** function of the **Evaluation** module.

Baseline drawingThe baseline points are used to create the baseline curve using a spline interpolation.
The spline function ensures that the baseline curve is guided by the baseline points.
However, the curve does not necessarily pass through the baseline points. The baseline
will be a smoothly curved function passing close to or through the points.

To reduce the effect of noise at the peak integration, the created baseline is forced equal to the source curve in every position where the difference between the baseline and the source curve is small enough. Choose **Integrate:Calculate Baseline**. If the **Accept negative peaks** option is off, the baseline will be forced down to the level of the source curve whenever the created baseline goes above the source curve.

How to measure the baseline segment (Classic algorithm)

You can try to measure the **Shortest baseline segment** length directly on your chromatogram. The table below describes how to do this:

Step	Action
1	Locate the shortest segment of the curve that you consider a part of the baseline.
2	Use the marker box on the chromatogram to measure the length of the segment.
3	Choose Integrate:Calculate Baseline and insert this value as the Shortest baseline segment value.

How to measure noise level (Classic algorithm)

Curve coordinates can also be used to measure noise levels on the source curve. The table below describes how to do this:

Step	Action	
1	Use the Zoom function to focus on a part of the curve that is representative for the baseline noise.	
2	Select an appropriate Y-axis scale.	
3	Measure the Y-axis coordinates.	
4	• Calculate the noise range as the difference between the max. and min. values.	
	Add an extra 20%.	
	Choose Integrate:Calculate Baseline and insert this value as the Noise window value.	

How to measure the slope limit	The table below describes how to measure the slope at any part of the curve.		
(Classic algorithm)	Stage	Description	
	1	Select Operations:Differentiate in the Evaluation module.	
		<i>Result</i> : The Differentiate dialog box opens.	
	2	Select the desired source curve.	
		Select the First order calculation option.	
		• Click OK .	
		<i>Result</i> : The differentiated curve will appear in the active chromatogram.	
	3	Select an appropriate Y-axis scale, right-click and select Marker to measure the Y-axis values for the differentiated curve with the curve coordinates function.	
		<i>Result</i> : The Y-axis value is interpreted as the UV curve slope at the selected retention point.	
	4	• Determine the highest slope value of the baseline (non-peak) part of the curve.	
		• Add 10%.	
		 Select Integrate:Calculate Baseline and use this value as the Slope limit. 	

Note: If the differentiated curve is very noisy, it can be filtered with a light **Moving average** filter in the **Operations:Smooth** function.

B.3 Peak table column components

Introduction This section contains a list of peak parameters with explanations and calculation formulae when applicable.

Peak parametersThe diagram below illustrates the peak parameters. See the parameter list below for
explanations.



Peak parameter descriptions

The list below contains descriptions of the peak parameters.

Parameter	Description
Area	Calculated as the area between the curve and baseline, between the peak start and peak end, time or volume base. (Gray area in the diagram above.)
Asymmetry	Peak asymmetry (indicator of column packing). See definition below this table.
Baseline height	Baseline amplitude at peak start, peak maximum and peak end. (A, F and G in the diagram above.)

Parameter	Description
Capacity factor	The capacity factor will only be calcu- lated when the chromatogram is in volume base. The total liquid volume, Vt, must be entered in the Integrate dialog box for this parameter to be cal- culated. See definition below this table.
Height	Maximum amplitude above the baseline. (C-F in the diagram above)
Καν	Gel phase distribution constant in gel filtration. Kav will only be calculated when a gel filtration column was used and when the chromatogram is in volume base. The void volume, V0, must be entered in the Integrate dialog box for this parameter to be calculated. See definition below this table.
Plate height (HETP)	Height equivalent to theoretical plate and plates/meter. The column height must be entered in the Integrate dialog box for this parameter to be calculated. See definition below this table.
Peak endpoint heights	Amplitude above the baseline at left (A in the diagram above) and right peak limits (E-G in the diagram above).
Peak endpoint retention	Retention value at peak start and peak end, time or volume base. (A and G in the diagram above.)
Peak name	Name of the peak.
Percent of total area	Peak area as a percent of the total area under the curve above the baseline. Time or volume base. <i>Note</i> : This value can differ in time and volume base if the flow rate is not con- stant throughout the method.

Parameter	Description
Percent of total peak area	Peak area as a percent of the sum of all integrated peaks.
	<i>Note</i> : This value can differ in time and volume base if the flow rate is not constant throughout the method.
Resolution	Peak resolution. See definition below this table.
Retention	Retention at the peak maximum, time or volume base. (C in the diagram above.)
Sigma	Standard deviation for a Gaussian- shaped peak. See definition below this table.
Type of peak limits	Identifies the criteria for peak start and peak end as either the baseline intersec- tion or dropline to the baseline.
Width	Difference in retention between the peak end and peak start, time or volume base. (G-A in the diagram above.)
Width at half height	Calculated by taking the maximum height of the peak above the baseline, then determining the peak width at half this value above the baseline. Time or volume base. (B-D in the diagram above, where BD bisects CF.)

Note: In the **Options** dialog box in the **UNICORN Manager** you can select if negative retentions should be displayed or not. The default selection is that negative retention is not displayed.

Sigma formula

The formula below is used to calculate **Sigma**.

Sigma =
$$\sqrt{\frac{\sum_{i=1}^{n} (y_i (x_i - x_{ymax})^2)}{A_{peak}}}$$

Where:

- *n* is the number of data points.
- *x* is the volume or time value.
- x_{ymax} is the volume or time value at the maximum amplitude value.
- A_{peak} is the area of the peak.

Note: The peak width for a Gaussian peak is (4 x Sigma).

Peak resolution	The peak resolution is calculated with one of the following three algorithms:			
algorithms	1. $(V_{R2} - V_{R1}) / ((W_{b2} + W_{b1}) / 2)$			
	2. (V _{R2} - V _{R1}) / ((Sigma ₂ + Sigma ₁) × 2)			
	3. ((V _{R2} - V _{R1}) / (2 × (W _{h2} + W _{h1}))) / 2.354			
	Where:			
	 V_{R1}, W_{b1}, Sigma₁ and W_{h1} are the retention, width, Sigma and width at half height of the previous peak. 			
	- V_{R2} , W_{b2} , Sigma ₂ and W_{h2} are the retention, width, Sigma and width at half height of the current peak.			
	<i>Note</i> : The Resolution algorithm variable in the Options dialog box in the UNICORN Manager determines which of the three algorithms is used. If this variable has the value 1, 2 or 3, then the algorithm with the corresponding number in the list above is used. The default value is 3.			
How to change the peak resolu- tion algorithm	The table below describes how to change the peak resolution algorithm in the UNICORN Manager .			
	Step	Action		
	1	Choose the Administration:Options menu item.		

Result: The **Options** dialog box opens.

Step	Action
2	• Select the desired algorithm number described as described in Peak resolution algorithms above, in the Resolution algorithm droplist.
	Options Image: Construct of the system o
	• Click OK . <i>Result</i> : The dialog box closes and the peak resolution algorithm is changed.

Note: You must repeat the peak integrations after the change to update the values based on the new algorithm.

Capacity factorThe formula below is used to calculate the Capacity factor.formula $V_{D-1}V_{1}$

$$\mathbf{k}^{1} = \frac{\mathbf{V}_{R} - \mathbf{V}_{t}}{\mathbf{V}_{t}}$$

Where:

- V_R = retention volume.
- V_t = total liquid volume.

Kav formula

The formula below is used to calculate **Kav**.

$$k_{av} {=} \frac{V_R \text{ - } V_0}{V_C \text{ - } V_0}$$

Where:

- V_R = retention volume.
- $V_0 = void volume$.
- V_C = column volume.

Asymmetry formula The formula below is used to calculate the Asymmetry.

Asymmetry = B / A

Where:

- A is a partial peak width, measured at a percentage of the peak height, for the leading part of the peak.
- B is a partial peak width, measured at a percentage of the peak height, for the tailing part of the peak.



How to change the Asymmetry Ratio

The **Asymmetry Ratio** is selected in the **Options** dialog box in the **UNICORN Manager**. The table below describes how to select a value:

Step	Action
1	Choose the Administration:Options menu item.
	<i>Result</i> : The Options dialog box opens.
2	 Type a ratio value in the Asymmetry Ratio at text box. Click OK.
	<i>Result</i> : The ratio value is changed and the dialog box closes.

Note: You must repeat the peak integrations after the change to update the values based on the new asymmetry ratio. The default ratio is 10%.

HETP formula The formula

The formula below is used to calculate the **HETP** value.

HETP = L/N

 $N = 5.54 \times (V_R/w_h)^2$ assuming a Gaussian peak.

Where:

- N = no. of theoretical plates.
- L = bed height in cm.
- V_R = peak retention (elution) volume or time.
- w_h = peak width at half height expressed in the same units as V_R .

B.4 Procedure instructions

IntroductionThis section contains lists of procedure instructions with descriptions. These
instructions are used in the Procedure Editor. Choose Procedures:Edit:New in the
Evaluation module to view the Instruction list.

Curve operation The table below contains a list of instructions for curve operations.

Instruction	Description
ADD	Adds two curves to produce a third curve, which is the sum of the two curves. The two source curves must have the same Y-axis unit and not be fraction or injection curves, or else a run time error will occur.
AMP_MUL	Multiplies the amplitude of the source curve by the multiplication factor and stores the result in the target curve po- sition.
AMP_SHIFT	Shifts the amplitude of the source curve by the shift factor and stores the result in the target curve position.
CLEAR	Clears the specified curve from the working memory of the computer.
СОРҮ	Copies the source curve to the target curve position.
CUT	Cuts out the part of the source curve between the Left and Right limits and stores the result in the target curve po- sition.
DERIVATE	Differentiates the source curve (first or second order) and stores the result in the target curve position. The Y-axis of the target curve position will be a nor- malized scale without unit.

Instruction	Description
DIV	Divides two curves to produce a third curve, which is the quotient of the two curves. The two source curves can have any Y-axis unit. The Y-axis of the target curve position will be a normalized scale without unit.
HISTOGRAM	Creates a histogram from any non- fraction curve (source curve 1) and a fraction curve (source curve 2_frac), and stores the result in the target curve position. If source curve 2 is not a frac- tion curve a run time error will occur. The Y-axis of the target curve position will be the same as that of the first source curve.
INTEGRATE	Performs a mathematical integration of the source curve and stores the res- ult in a Result curve. This instruction is not the same as Peak integrate , which performs a real peak integration.
RET_MUL	Multiplies the retention of the source curve by the Multiplication factor and stores the result in the target curve po- sition.
RET_SHIFT	Shifts the retention of the source curve by the Shift factor and stores the result in the target curve position.
SMOOTH_AR	Smooths the source curve with an autoregressive filter and stores the result in the target curve position. The Filter parameter decides the strength of the filter.
SMOOTH_MA	Smooths the source curve with a mov- ing average filter and stores the result in the Resulting Curve . The Filter width parameter decides how many samples wide the filter is.

Instruction	Description
SMOOTH_MEDIAN	Smooths the source curve with a medi- an filter and stores the result in target curve position. The Filter width para- meter decides how many samples wide the filter is.
SMOOTH_SG	Smooths the curve with the Savitzky- Golay algorithm.
SUB	Subtracts two curves to produce a third curve, which is the difference of the two curves. The two source curves must have the same Y-axis unit and not be fraction or injection curves.
TDIV	Divides two curves to produce a third curve, which is the quotient of the two curves. The two source curves can have any Y-axis unit. The threshold values are used to avoid division of numbers close to zero. At those points where source curve 1 has an amplitude less than Threshold1 , or the source curve 2 has an amplitude less than Threshold2 , the result of the division is defined to be 1.0.

Integration

The table below contains a list of instructions for integration.

Instruction	Description
CALCULATE_BASELINE	Calculates a baseline from the source curve. The baseline is stored in the tar- get curve position. DEFAULT can be selected in the Baseline parameters, which will then calculate default baseline parameters for each new curve.

Instruction	Description
CALCULATE_BASELINE_MORPH	Calculates a baseline from the curve crvSrc using a morphological method. DEFAULT can be selected in the Baseline parameters, which will then calculate default baseline parameters for each new curve. The baseline is stored in curve crvDst.
CLEAR_PEAKTABLE	Clears the peak table in Peak table source from the computer memory.
COPY_PEAKTABLE	Copies a peak table from Peak table source to Resulting peak table .
NEGATIVE_PEAKS	Controls the baseline behavior in sub- sequent baseline calculations. If ONOFF is ON then the baseline can be drawn above the curve and negative peaks can be detected by PEAK_INTEGRATE . If ONOFF is OFF then the baseline is never drawn above the curve.
PEAK_INTEGRATE	Performs a peak integration on the source curve and stores the resulting peak table in Resulting peak table . It is assumed that the baseline is subtrac- ted.
PEAK_WINDOW	Specifies which part of the source curve that will be integrated. Peaks between retention Left limit and Right limit will be detected if the ONOFF parameter is set to ON . If ONOFF is set to OFF , the whole curve will be used for integration.
REJECT_PEAKS	Any combination of conditions is al- lowed. If all parameters are OFF then every detected peak is included in the peak table.

Instruction	Description
SET_COLUMN_HEIGHT	Sets the column height for the peak in- tegration calculation of the HETP value. The Column height parameter is the height of the column in centimetres. If Column height is OFF then the HETP value is not calculated for the following integrations.
SET_COLUMN_V0	Sets void volume for Kav peak integra- tion calculation.
SET_COLUMN_VT	Sets the total liquid volume for peak in- tegration calculation of the capacity factor.
SET_SKIM_SIZE_RATIO	Sets the Skim size ratio to be used in the following peak integration(s).
WINDOW_PEAK_INTEGRATE	Integrates the curve within the peak window. All curve parts outside the peak window remain unchanged.

File operation

The table below contains a list of instructions for file operations.

Instruction	Description
CURVE_OPEN	Opens the curve specified in the Result file defined in File name and stores it in target curve position. If "*" is entered as File name the current result file will be used. The File name parameter may include a path from the users root folder.
IMPORT_CURVE	Imports a curve to the current chroma- togram from another chromatogram (in the current file) and stores it in the target curve position.
IMPORT_PEAKTABLE	Imports a peak table to the current chromatogram from another chroma- togram (in the current file) and stores it in the target curve position.

Instruction	Description
PEAKTABLE_OPEN	Opens the specified Peak table in the Result file defined in File name and stores it in the Resulting peak table . If "*" is entered as File name the current Result file will be used. The File name parameter may include a path from the current users root folder.

Export

The table below contains a list of instructions for export operations.

Instruction	Description
EXPORT_CURVE_AIA	Exports the curve in AIA format.
EXPORT_CURVE_ASCII	Exports the Source curve to the file defined in Export to File in ASCII format. If "*" is entered as File name the current Result file will be used. If "?" is entered followed by text, e.g. "Enter a file name", as File name, a full search path must be entered in answer to the question. In the part of the source curve limited by the Left limit and Right limit every <n> sample is exported.</n>
EXPORT_CURVE_WKS	Exports the source curve to the file defined in Export to File in WKS format. If "*" is entered as File name the current Result file will be used. If "?" is entered followed by text, e.g. "Enter a file name", as File name, a full search path must be entered in answer to the question. In the part of the source curve limited by Left limit and Right limit every <n> sample is exported</n>
Instruction	Description
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EXPORT_EVAL_LOG_ASCII	Exports an evaluation log in ASCII format to the file defined in Export to file . If "*" is entered as File name the current Result file will be used. If "?" is entered followed by text, e.g. "Enter a file name", as File name , a full search path must be entered in answer to the question.
EXPORT_EVAL_LOG_WKS	Exports an evaluation log in WKS format to the file defined in Export to file . If "*" is entered as File name the current Result file will be used. If "?" is entered followed by text, e.g. "Enter a file name", as File name , a full search path must be entered in answer to the question.
EXPORT_EVAL_LOG_XLS	Exports an evaluation log in XLS format to the file defined in Export to file . If "*" is entered as File name the current Result file will be used. If "?" is entered followed by text, e.g. "Enter a file name", as File name , a full search path must be entered in answer to the question.
EXPORT_METHOD_ASCII	Exports a method to the file defined in Export to file in ASCII format. If "*" is entered as File name the current Result file will be used. If all parameters are OFF then no method is exported. If Main is ON then the main method is included and if Blocks is ON then all blocks are included in the exported file.

Instruction	Description
EXPORT_METHOD_WKS	Exports a method to the file defined in Export to file in WKS format. If "*" is entered as File name the current Result file will be used. If "?" is entered followed by text, e.g. "Enter a file name", as File name, a full search path must be entered in answer to the question. If all parameters are OFF then no method is exported. If Main is ON then the main method is included and if Blocks is ON then all blocks are included in the expor- ted file.
EXPORT_METHOD_XLS	Exports a method to the file defined in Export to file in XLS format. If "*" is entered as File name the current Result file will be used. If "?" is entered followed by text, e.g. "Enter a file name", as File name, a full search path must be entered in answer to the question. If all parameters are OFF then no method is exported. If Main is ON then the main method is included and if Blocks is ON then all blocks are included in the expor- ted file.
EXPORT_MULTI_CURVES_ASCII	Exports multiple curves (previously defined with EXPORT_SEL_CURVES in- structions) in ASCII format to the file defined in Export to file . If "*" is entered as File name the current Result file will be used. If "?" is entered followed by text, e.g. "Enter a file name", as File name , a full search path must be entered in answer to the question.

Instruction	Description
EXPORT_MULTI_CURVES_WKS	Exports multiple curves (previously defined with EXPORT_SEL_CURVES in- structions) in WKS format to the file defined in Export to file. If "*" is entered as File name the current Result file will be used. If "?" is entered followed by text, e.g. "Enter a file name", as File name, a full search path must be entered in answer to the question.
EXPORT_MULTI_CURVES_XLS	Exports multiple curves (previously defined with EXPORT_SEL_CURVES in- structions) in XLS format to the file defined in Export to file. If "*" is entered as File name the current Result file will be used. If "?" is entered followed by text, e.g. "Enter a file name", as File name, a full search path must be entered in answer to the question.
EXPORT_NORMALISE_RETENTION	Normalizes retention when exporting multiple curves.
EXPORT_PEAKTABLE_ASCII	Exports the peak table in Peak table source to the file defined in Export to file in ASCII format. If "*" is entered as File name the current Result file will be used. If "?" is entered followed by text, e.g. "Enter a file name", as File name, a full search path must be entered in an- swer to the question.
EXPORT_PEAKTABLE_WKS	Exports the peak table in Peak table source to the file defined in Export to file in WKS format. If "*" is entered as File name the current Result file will be used. If "?" is entered followed by text, e.g. "Enter a file name", as File name, a full search path must be entered in an- swer to the question.

Instruction	Description
EXPORT_PEAKTABLE_XLS	Exports the peak table in Peak table source to the file defined in Export to file in XLS format. If "*" is entered as File name the current Result file will be used. If "?" is entered followed by text, e.g. "Enter a file name", as File name, a full search path must be entered in an- swer to the question.
EXPORT_PEAKTABLE_XML	Exports the peak table in Peak table source to the file defined in Export to file in XML format. If "*" is entered as File name the current Result file will be used. If "?" is entered followed by text, e.g. "Enter a file name", as File name, a full search path must be entered in an- swer to the question.
EXPORT_SEL_CURVES	Selects a curve for subsequent export (using the EXPORT_MULTI-CURVES_* instruction). The curve is cut according to the right and left cut limit and the number of points to be exported may be set by the Export parameter (for example, every fifth point).
EXPORT_DOC_400_ASCII	Exports the documentation in the cur- rent result file in ASCII format to the file defined in Export to file . If "*" is entered as File name the current Result file will be used. If "?" is entered followed by text, e.g. "Enter a file name", as File name , a full search path must be entered in answer to the question. If all parameters to this function are OFF then no documentation is exported. If at least one of them is ON then the documentation will be exported and the corresponding parts will be included in the exported file.

Instruction	Description
EXPORT_DOC_400_WKS	Exports the documentation in the cur- rent result file in WKS format to the file defined in Export to file . If "*" is entered as File name the current Result file will be used. If "?" is entered followed by text, e.g. "Enter a file name", as File name , a full search path must be entered in answer to the question. If all parameters to this function are OFF then no documentation is exported. If at least one of them is ON then the documentation will be exported and the corresponding parts will be included in the exported file.
EXPORT_DOC_400_XLS	Exports the documentation in the cur- rent result file in MS Excel XLS format to the file defined in Export to file . If "*" is entered as File name the current Result file will be used. If "?" is entered followed by text, e.g. "Enter a file name", as File name , a full search path must be entered in answer to the question. If all parameters to this function are OFF then no documentation is expor- ted. If at least one of them is ON then the documentation will be exported and the corresponding parts will be included in the exported file.

Instruction	Description
EXPORT_DOC_WKS	Exports the documentation in the cur- rent result file in WKS format to the file defined in Export to file . If "*" is entered as File name the current Result file will be used. If "?" is entered followed by text, e.g. "Enter a file name", as File name , a full search path must be entered in answer to the question. If all parameters to this function are OFF then no documentation is exported. If at least one of them is ON then the documentation will be exported and the corresponding parts will be included in the exported file.
EXPORT_DOC_XLS	Exports the documentation in the cur- rent result file in XLS format to the file defined in Export to file . If "*" is entered as File name the current Result file will be used. If "?" is entered followed by text, e.g. "Enter a file name", as File name , a full search path must be entered in answer to the question. If all parameters to this function are OFF then no documentation is exported. If at least one of them is ON then the documentation will be exported and the corresponding parts will be included in the exported file

Instruction	Description
EXPORT_DOC_ASCII	Exports the documentation in the cur- rent result file in ASCII format to the file defined in Export to file . If "*" is entered as File name the current Result file will be used. If "?" is entered followed by text, e.g. "Enter a file name", as File name , a full search path must be entered in answer to the question. If all parameters to this function are OFF then no documentation is exported. If at least one of them is ON then the documentation will be exported and the corresponding parts will be included in the exported file.

Chromatogram

The table below contains a list of instructions for chromatogram functions.

Instruction	Description
COPY_CHROM	Creates a copy of the specified chroma- togram. If "*" is used as source then the current (default) chromatogram is used. If "*" is used as destination then a de- fault name will be created for the copy.
CREATE_NEW_CHROM	Creates a new chromatogram with the given name. If "*" is used for the chro- matogram name a default name will be generated and used. <i>Note</i> : It is a recommendation not to use only numbers as names for new chro- matograms.
DELETE_CHROM	Deletes the named chromatogram. If trying to delete the current (default) chromatogram a run time error will be caused.
OPEN_CHROM	Opens the specified chromatogram from the specified file.

Instruction	Description
RENAME_CHROM	Renames the specified chromatogram. If "*" is used as From then the current (default) chromatogram is used.
RESTORE_DESTINATION_CHROM	Resets the destination for the sub- sequent curve and peak table opera- tions to the default chromatogram. Used in pair with the SET_DESTINA- TION_CHROM instruction.
SET_DESTINATION_CHROM	Opens the named chromatogram as destination for the subsequent curve and peak operations. Used in pair with the RESTORE_DESTINATION_CHROM instruction.

Other instructions The table below contains a list of instructions for other operations.

Instruction	Description
BASE	Sets the X-axis base that the following calculations will be made in. If the value of the X-axis base is DEFAULT , then the default base is used (usually the base the method was run in). This instruction should be the first in the evaluation procedure, otherwise it will have no ef- fect at all.
Comment	Inserts a comment below the marked instruction.
ENDLOOP	Marks the end of a LOOP statement.
LOOP	The instructions between this statement and the ENDLOOP statement are re- peated n times. It is possible to have loops within loops as long as the num- ber of LOOP statements matches the number of ENDLOOP statements.

Instruction	Description
MOLSIZE	Calculates the molecular sizes from a molecular size curve. A Mol. size column will be added to the Peak table .
QC_TEST	Performs a QC test.
QUANTITATE	Calculates the concentration and amounts in the sample from a quantit- ation table.
	Amount and Concentration columns will be added to the Peak table .
REPORT	Prints a report with the specified named report layout and title. If Title is "*" then the title in the report layout is used. If Report Layout is "*" then a default lay- out is used.
RUN_PROGRAM	Starts a program as a separate process. The Program name string contains the program name and parameters to start it with.
UPDATE	Updates a Quantitation table with new data from one standard concentration level. The default Limit(+/-) value of 12.5% will be used.

Test instructions The **Instruction** field also contains a group of test instructions. These instructions are only available for the UNICORN software development team.

Instruction	Description
AUTOSAMPLER_PEAK_INTERVALS	Sets the area intervals for the AUTO-SAMPLER_PEAK_TEST .
AUTOSAMPLER_PEAK_TEST	Locates the first peak in the peak table. Compares the area of the peak in the peak table with the specified maximum and minimum areas.

Instruction	Description
EXPORT_TEST_RESULT_TO_FILE	Finishes the current result and saves the output file as an ASCII file in a des- tination and with a file name specified in the variable DestFilename (.txt). A complete search path may be incluede in the file name.
GRADIENT_TEST_INTERVALS	Sets the level intervals for the GRADI-ENT_TEST .
GRADIENT_TEST	The theoretical straight line between the 0% and 100% levels are calculated. The deviation between the curve and the ideal straight line is compared in both directions from the center position (50%) until the deviation exceeds the defined maximum deviation. The calcu- lated deviation points are checked against the defined limits.
STEP_RESPONSE_INTERVALS	Sets the level intervals for the STEP_RESPONSE_TEST .
STEP_RESPONSE_TEST	The relative amplitude is calculated at the specified retentions (The 0% and 100% amplitudes are used for refer- ence). The calculated relative amp- litudes are checked against the spe- cified error margins. The 0% level amplitude is verified to be within the specified interval from the absolute 0 level.
TEST_CURVE_AMPLITUDE_CHANGE	Verifies that the curve amplitude has changed more than or equal to the value of the Delta parameter between the defined to and from retention points. A print parameter may be set to On to generate printed results.

Instruction	Description
TEST_CURVE_AMPLITUDE_STABLE	Verifies that the curve amplitude is stable between the defined to and from retention points. The actual curve value is compared to a set amplitude para- meter. If the difference exceeds a set Delta value, the test is failed. A print parameter may be set to On to gener- ate printed results.
TEST_INFO	Adds selected information items to the output file, e.g. system name, UNICORN version etc. Also, a specified free text can be added. A print parameter may be set to On to generate printed results.
TEST_LOGBOOK_EVENT	Verifies if a specified text is present in the logbook curve between the defined to and from retention points. The test can be defined to be passed either if the text is present or not. A failed or passed text will be added to the output file. A print parameter may be set to On to generate printed results.
UV_RESPONSE_INTERVALS	Sets the level intervals for the UV_RE- SPONSE_TEST .
UV_RESPONSE_TEST	The amplitudes for the 0% and 100% levels are calculated and the difference between the values are calculated. The results of (1) Curve2_Difference / Curve1_Difference and (2) Curve2_Dif- ference / Curve3_Difference are calcu- lated. The calculated points are checked if they are outside the defined limits from the 50% level.

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