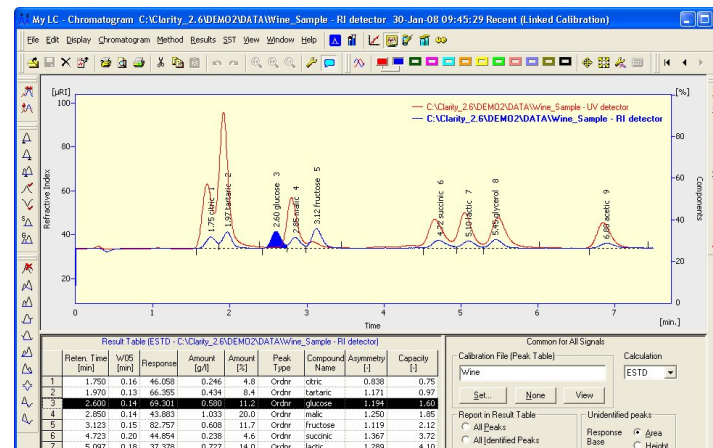


This is not a tutorial.....

- In this presentation the concept of Clarity is explained with a special focus on organisational structure of the software
- For detailed information how to use the software, we refer to the tutorials and manuals.



- *What is Clarity data system?*
- Clarity data system is a fully featured acquisition software, with all the tools for automated data acquisition, calibration, processing and reporting.



- *I know about data acquisition and instrument control. But what should I know about Clarity, before getting started?*
- Before getting started you should know about how Clarity has organized data acquisition, analysis, calibration and processing.



Clarity structure

- Clarity uses several windows:
 - Main Clarity window
 - Configuration window
 - Instrument method
 - Data acquisition window
 - Sequence window
 - Chromatogram window
 - Calibration window



- The structure of Clarity windows will be highlighted on the basis of common questions about software use
 1. *How can I set up the communication with the hardware?*
 2. *How can I set the application parameters?*
 3. *How can I run samples?*
 4. *How can I evaluate chromatograms?*
 5. *How can I extract the results from the analyses?*



1. How can I set up the communication with the hardware?



Start up Clarity

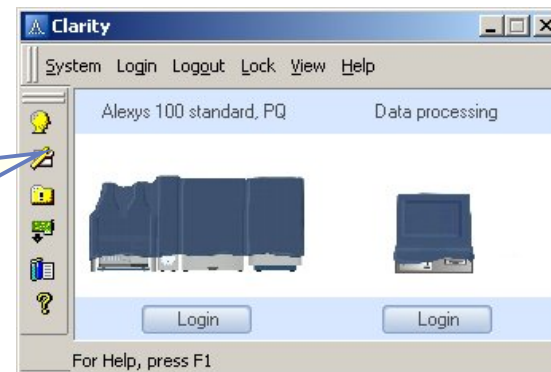
- Use one of the two different types of Clarity shortcuts
 - General start-up shortcut present on the desktop
 - Customized Antec start-up shortcut, activating preconfigured Clarity files for a particular application (ALEXYS system solution)



Main window

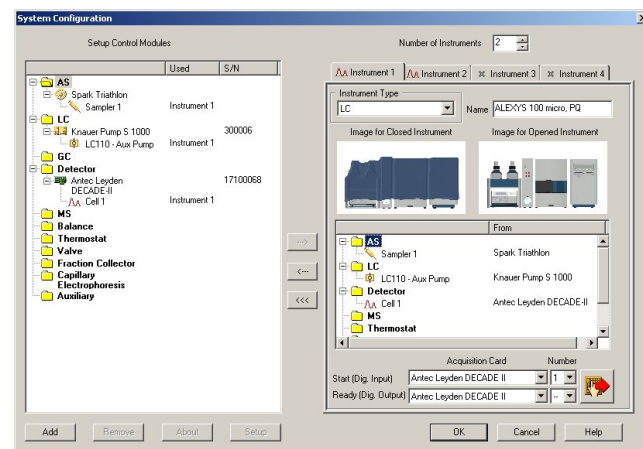
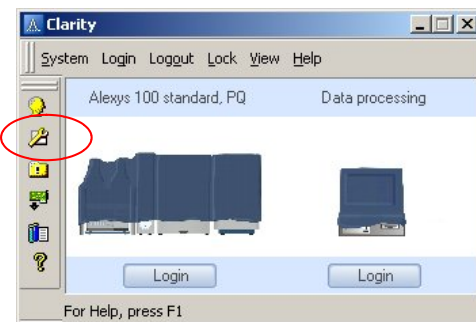
- This window opens at startup

Button to access the hardware configuration window



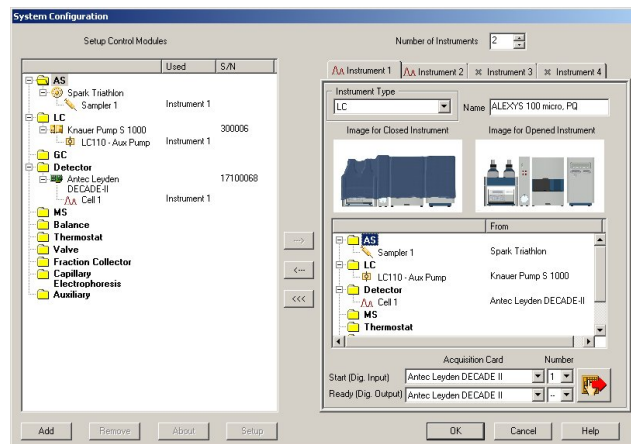
Configuration window

- This window is necessary to:
 - select different hardware drivers for the system elements.
 - set-up general settings, like
 - detector oven temperature
 - sample tray types present in autosampler
- Identify the ports through which the hardware should communicate with the computer



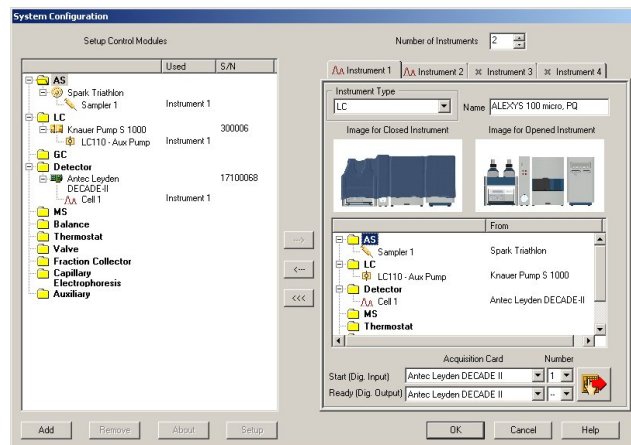
Configuration window

- After a correct set-up, this window does not need to be accessed any more



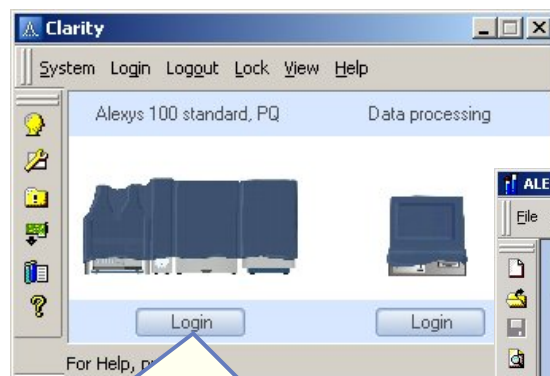
Customized short-cut from Antec

- One click direct start-up!
- Antec provides pre-configured configuration and method files for different ALEXYS system solutions

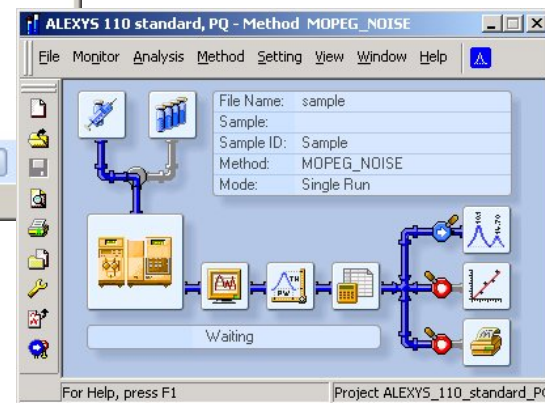


Main window

- Use the Login button in the main window to open communication
- The instrument window will open

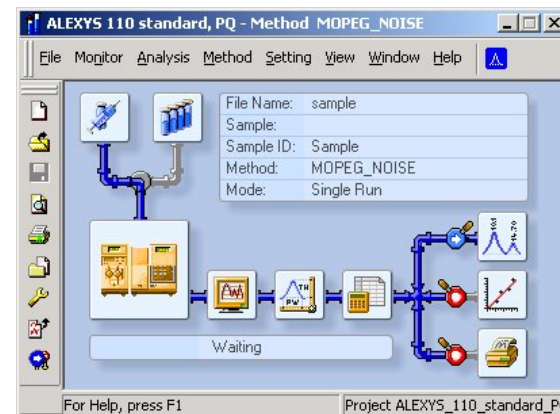


Button to activate the communication between software and hardware



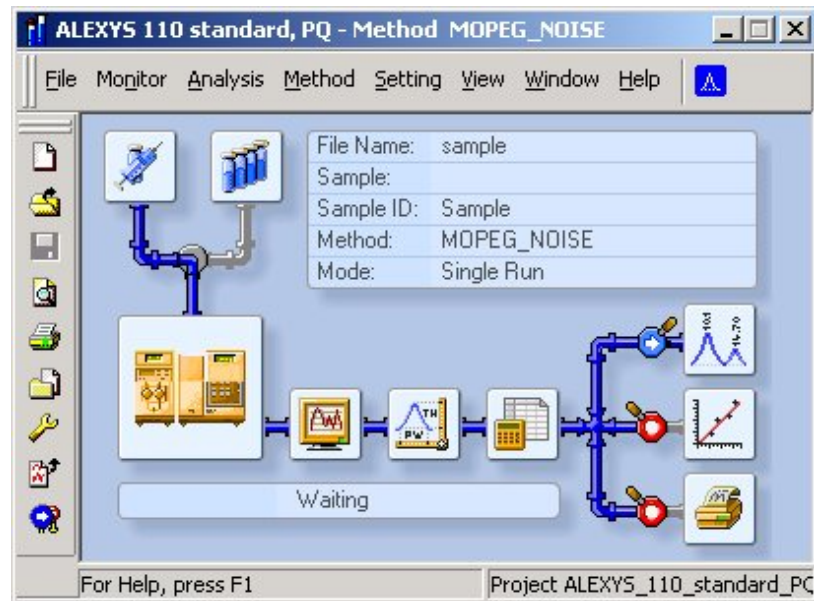
Instrument window

- Icons/menu are present to access all the other windows:
 - method window with the application settings
 - calibration window
 - sequence window for automated sampling
 - data acquisition window (actual run)
 - chromatogram window (processed data)
 - general settings
 - data storage folder
 - appearance of chromatograms
 - ...



Instrument window

- This window is a collection of buttons through which to access the different features of the software
- Centre of the software

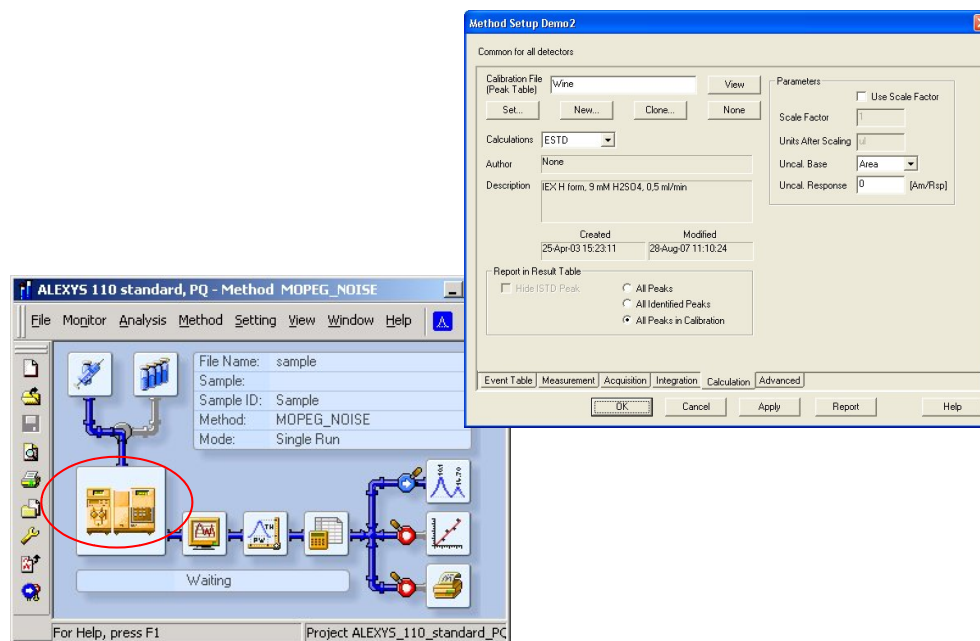


2. How can I set the application parameters?



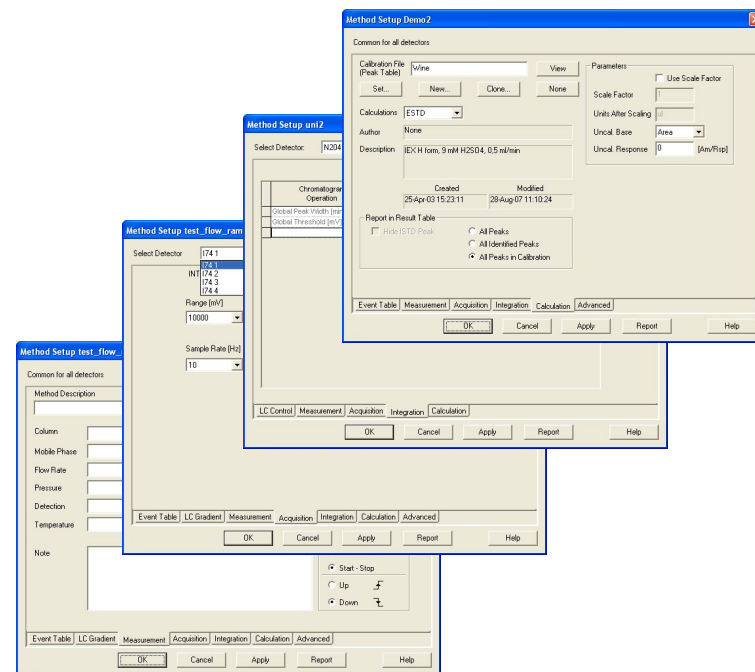
Method window

- In the Instrument window, the method window opens by clicking the instrument buttons



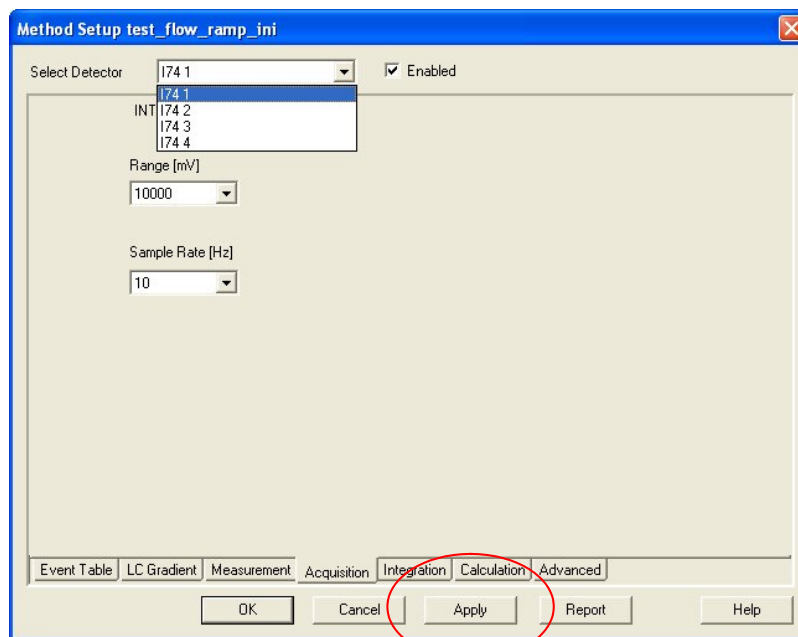
Method files

- The method file uses tabs for a structured organization
- Method files contain:
 - device settings (detector, pump, autosampler)
 - run duration
 - automatic integration settings
 - Link (!) to a specified calibration file, containing peak names



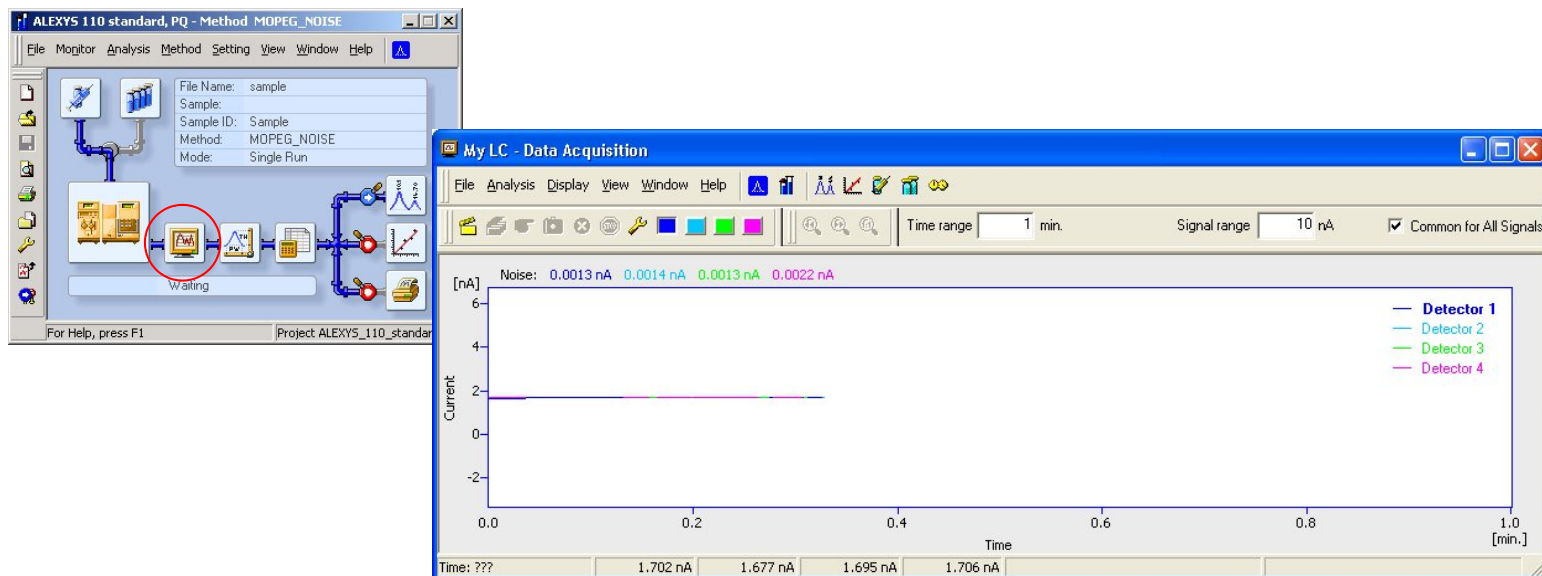
Method window

- By clicking the Apply button, all settings in the different tabs are sent to the hardware



Data acquisition window

- Active monitoring of the actual situation
 - for evaluation of baseline or running application



3. How can I run samples?



Sequence window

- To program an autosampler with analysis details for each injection

The screenshot displays two windows from the ALEXYS 110 software. The top window, titled 'ALEXYS 110 standard, PQ - Sequence PQ', shows a table of 18 injection runs. The bottom window, titled 'ALEXYS 110 standard, PQ - Method MOPEG_NOISE', shows the method configuration for a single run, with a red circle highlighting the autosampler icon in the method diagram.

Sts.	Method Name	Run	SV	Sample ID	Sample	Inj.Vol [µl]	File Name	Std	Lvl	Report Style	Oper	Open Calib	Print
1	MOPEG_INJ	✓	1	cal_1	0.5 µM MOPEG	5	%q_%R	Y	1	PQ-calib			
2	MOPEG_INJ	✓	1	cal_2	0.5 µM MOPEG	10	%q_%R	Y	2	PQ-calib			
3	MOPEG_INJ	✓	1	cal_3	0.5 µM MOPEG	15	%q_%R	Y	3	PQ-calib			
4	MOPEG_INJ	✓	1	cal_4	0.5 µM MOPEG	20	%q_%R	Y	4	PQ-calib			
5	MOPEG_INJ	✓	1	cal_5	0.5 µM MOPEG	25	%q_%R	Y	5	PQ-calib			
6	MOPEG_INJ	✓	1	cal_6	0.5 µM MOPEG	30	%q_%R	Y	6	PQ-calib			
7	MOPEG_INJ	✓	1	cal_7	0.5 µM MOPEG	35	%q_%R	Y	7	PQ-calib			
8	MOPEG_INJ	✓	1	cal_8	0.5 µM MOPEG	40	%q_%R	Y	8	PQ-calib		✓	✓
9	MOPEG_INJ	✓	2	repro_1	0.5 µM MOPEG	20	%q_%R	N		PQ-repro	✓		
10	MOPEG_INJ	✓	2	repro_2	0.5 µM MOPEG	20	%q_%R	N		PQ-repro	✓		
11	MOPEG_INJ	✓	2	repro_3	0.5 µM MOPEG	20	%q_%R	N		PQ-repro	✓		
12	MOPEG_INJ	✓	2	repro_4	0.5 µM MOPEG	20	%q_%R	N		PQ-repro	✓		
13	MOPEG_INJ	✓	2	repro_5	0.5 µM MOPEG	20	%q_%R	N		PQ-repro	✓		
14	MOPEG_INJ	✓	2	repro_6	0.5 µM MOPEG	20	%q_%R	N		PQ-repro	✓		
15	MOPEG_INJ	✓	2	repro_7	0.5 µM MOPEG	20	%q_%R	N		PQ-repro	✓		
16	MOPEG_INJ	✓	2	repro_8	0.5 µM MOPEG	20	%q_%R	N		PQ-repro	✓		
17	MOPEG_NOISE	✓	2	repro_8	0.5 µM MOPEG	20	%q_%R	N		PQ-repro	✓		
18	MOPEG_NOISE	✓	2	noise	no injection	0	%q_%R	N		Full	✓		

Sequence files

- Single injection
 - one line

Alexys 100 standard, PQ - Sequence PQ_test-injection

Sts.	Method Name	Run	SV	Sample ID	Sample	Inj.Vol. [µl]	File Name	Std	Lvl	Report Style	Open	Open Calib.	Print
1	MOPEG_INJ	<input checked="" type="checkbox"/>	1	test injection	0.5 µM MOPEG	20	%q_%R	N		Test-injection	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
2		<input type="checkbox"/>									<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>

For Help, press F1 ??? - Stop Vial: ??? / Inj.: ??? File Name:

- Multiple injections
 - several lines

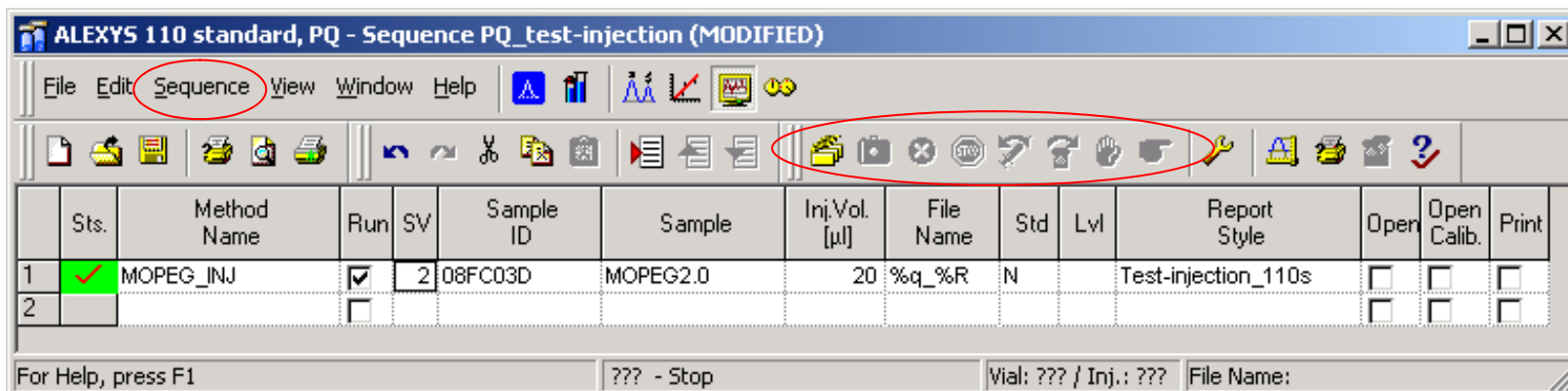
ALEXYS 110 standard, PQ - Sequence PQ

Sts.	Method Name	Run	SV	Sample ID	Sample	Inj.Vol. [µl]	File Name	Std	Lvl	Report Style	Open	Open Calib.	Print
1	MOPEG_INJ	<input checked="" type="checkbox"/>	1	cal_1	0.5 µM MOPEG	5	%q_%R	Y	1	PQ-calib	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
2	MOPEG_INJ	<input checked="" type="checkbox"/>	1	cal_2	0.5 µM MOPEG	10	%q_%R	Y	2	PQ-calib	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
3	MOPEG_INJ	<input checked="" type="checkbox"/>	1	cal_3	0.5 µM MOPEG	15	%q_%R	Y	3	PQ-calib	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
4	MOPEG_INJ	<input checked="" type="checkbox"/>	1	cal_4	0.5 µM MOPEG	20	%q_%R	Y	4	PQ-calib	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
5	MOPEG_INJ	<input checked="" type="checkbox"/>	1	cal_5	0.5 µM MOPEG	25	%q_%R	Y	5	PQ-calib	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
6	MOPEG_INJ	<input checked="" type="checkbox"/>	1	cal_6	0.5 µM MOPEG	30	%q_%R	Y	6	PQ-calib	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
7	MOPEG_INJ	<input checked="" type="checkbox"/>	1	cal_7	0.5 µM MOPEG	35	%q_%R	Y	7	PQ-calib	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
8	MOPEG_INJ	<input checked="" type="checkbox"/>	1	cal_8	0.5 µM MOPEG	40	%q_%R	Y	8	PQ-calib	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
9	MOPEG_INJ	<input checked="" type="checkbox"/>	2	repro_1	0.5 µM MOPEG	20	%q_%R	N		PQ-repro	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
10	MOPEG_INJ	<input checked="" type="checkbox"/>	2	repro_2	0.5 µM MOPEG	20	%q_%R	N		PQ-repro	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
11	MOPEG_INJ	<input checked="" type="checkbox"/>	2	repro_3	0.5 µM MOPEG	20	%q_%R	N		PQ-repro	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
12	MOPEG_INJ	<input checked="" type="checkbox"/>	2	repro_4	0.5 µM MOPEG	20	%q_%R	N		PQ-repro	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
13	MOPEG_INJ	<input checked="" type="checkbox"/>	2	repro_5	0.5 µM MOPEG	20	%q_%R	N		PQ-repro	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
14	MOPEG_INJ	<input checked="" type="checkbox"/>	2	repro_6	0.5 µM MOPEG	20	%q_%R	N		PQ-repro	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
15	MOPEG_INJ	<input checked="" type="checkbox"/>	2	repro_7	0.5 µM MOPEG	20	%q_%R	N		PQ-repro	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
16	MOPEG_INJ	<input checked="" type="checkbox"/>	2	repro_8	0.5 µM MOPEG	20	%q_%R	N		PQ-repro	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>
17	MOPEG_NOISE	<input checked="" type="checkbox"/>	2	noise	no injection	0	%q_%R	N		Full	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
18		<input type="checkbox"/>									<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>

For Help, press F1 ??? - Stop Vial: ??? / Inj.: ??? File Name:

Running a sequence

- a queue can be started
 - from the menu (sequence/Run)
 - using the icons

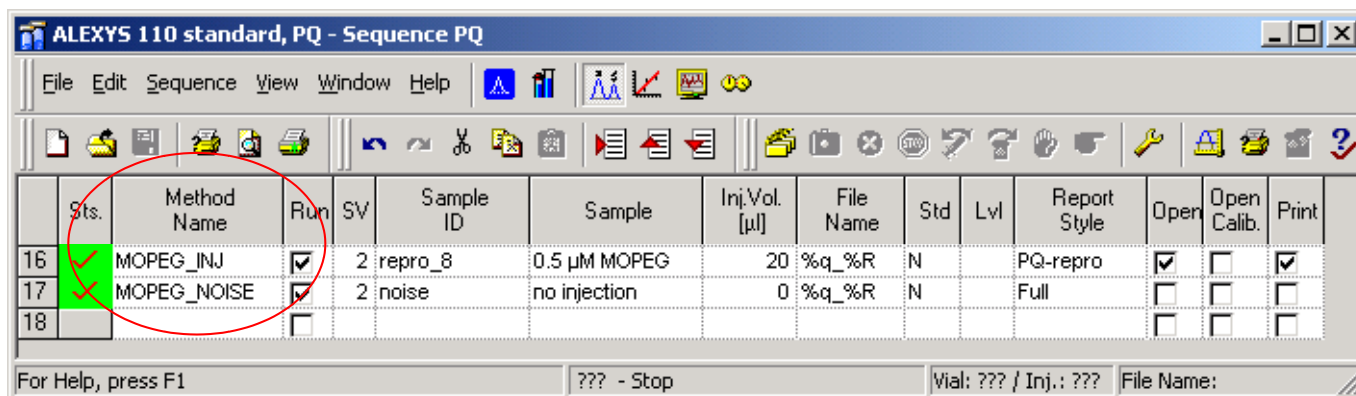


The screenshot shows the ALEXYS 110 software interface. The title bar reads "ALEXYS 110 standard, PQ - Sequence PQ_test-injection (MODIFIED)". The menu bar includes "File", "Edit", "Sequence", "View", "Window", and "Help". The "Sequence" menu is circled in red. Below the menu bar is a toolbar with various icons, including a red circle around a set of control icons (stop, play, pause, etc.). The main window displays a table with the following data:

	Sts.	Method Name	Run	SV	Sample ID	Sample	Inj. Vol. [μl]	File Name	Std	Lvl	Report Style	Open	Open Calib.	Print
1	✓	MOPEG_INJ	<input checked="" type="checkbox"/>	2	08FC03D	MOPEG2.0	20	%q_%R	N		Test-injection_110s	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
2			<input type="checkbox"/>									<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>

At the bottom of the window, there is a status bar with the text "For Help, press F1", "??? - Stop", "Vial: ??? / Inj.: ???", and "File Name:".

- *Is there anything special about the sequence files?*
- Each line can be individually defined for many parameters. This allows you for example,
 - record a baseline trace as part of the sequence (use different methods)
 - to print only certain chromatograms



ALEXYS 110 standard, PQ - Sequence PQ

File Edit Sequence View Window Help

	Sts.	Method Name	Run	SV	Sample ID	Sample	Inj.Vol. [μl]	File Name	Std	Lvl	Report Style	Open	Open Calib.	Print
16	<input checked="" type="checkbox"/>	MOPEG_INJ	<input checked="" type="checkbox"/>	2	repro_8	0.5 μM MOPEG	20	%q_%R	N		PQ-repro	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>
17	<input checked="" type="checkbox"/>	MOPEG_NOISE	<input checked="" type="checkbox"/>	2	noise	no injection	0	%q_%R	N		Full	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
18	<input type="checkbox"/>		<input type="checkbox"/>									<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>

For Help, press F1

??? - Stop

Vial: ??? / Inj.: ???

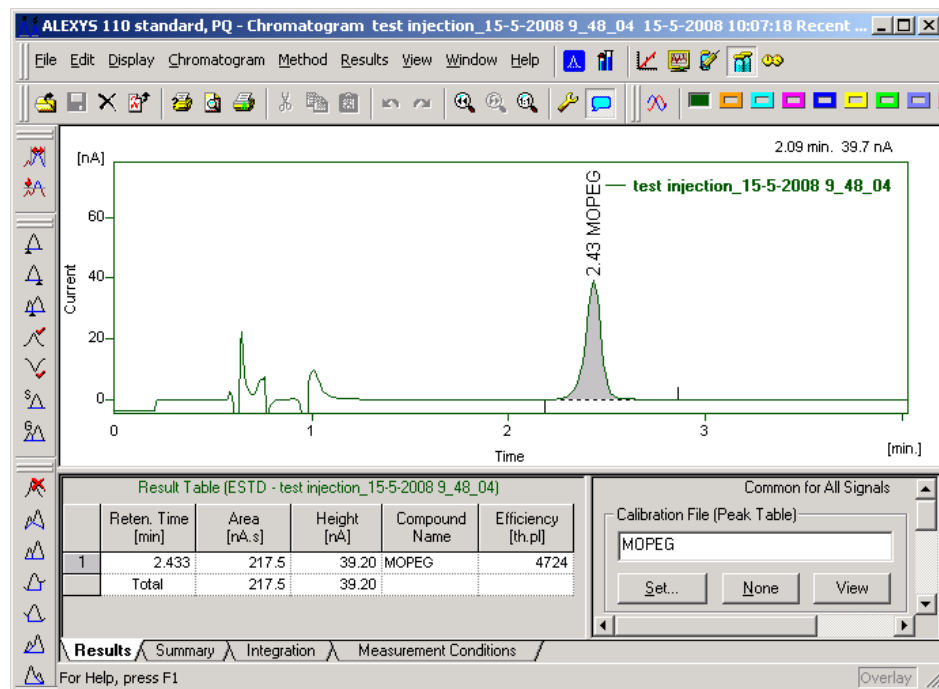
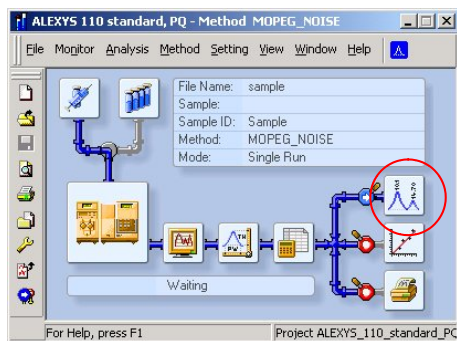
File Name:

4. How can I evaluate chromatograms?



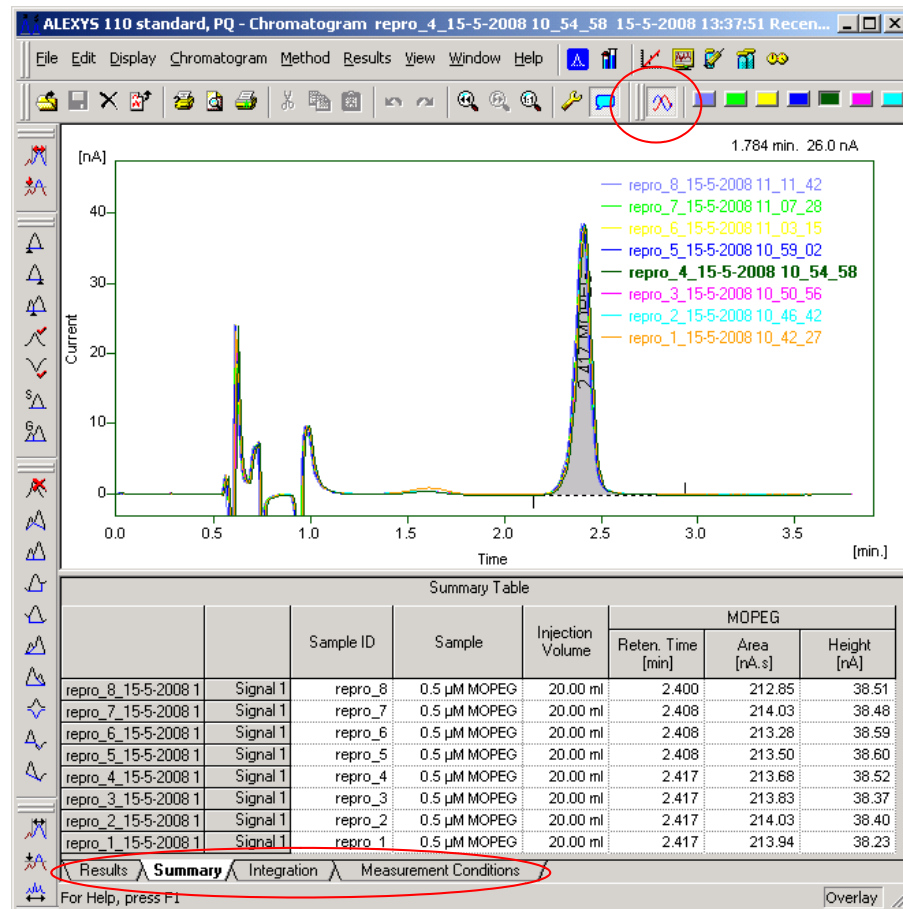
Chromatogram window

- To access completed/stored chromatograms



Chromatogram window

- Overlay mode
- Zoom in/out
- Peak integration
- Results summary
- Copy of the method settings during analysis
- Link to calibration file (peak table)

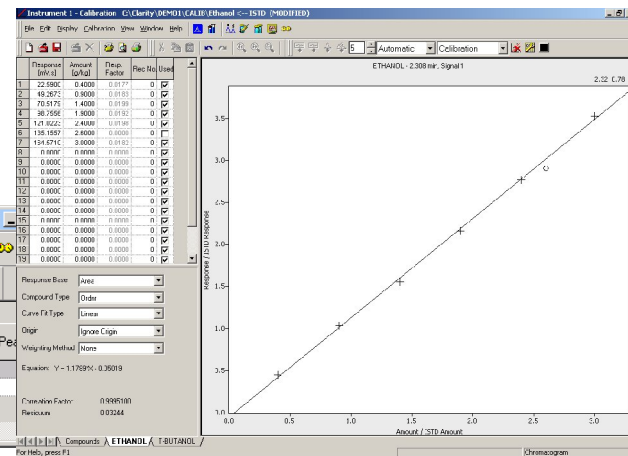
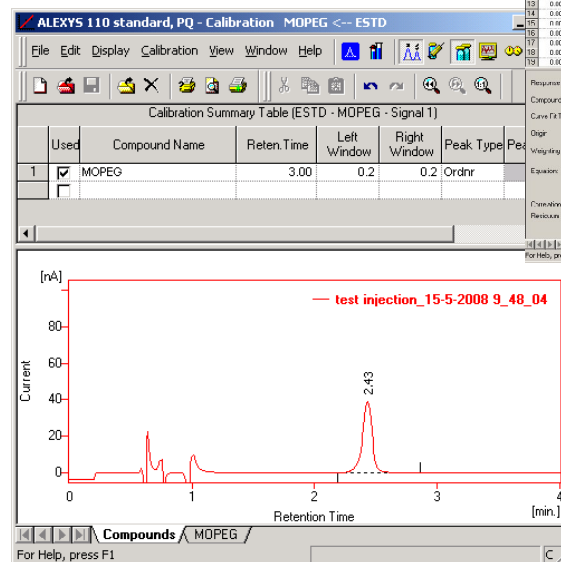
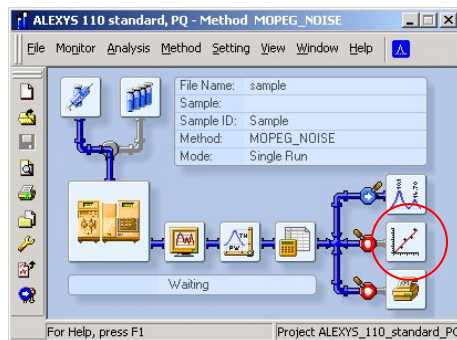


- *How can I access the calibration file?*



Calibration window

- Calibration files contain different tabs
 - compound table (peak names)
 - calibration graph for each compound

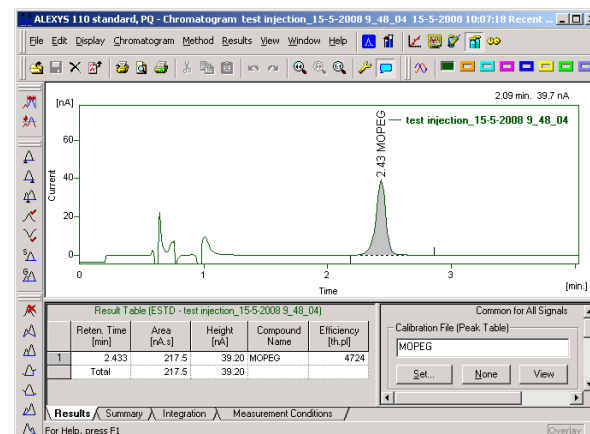


- *What does it mean that the calibration file is linked to a chromatogram?*



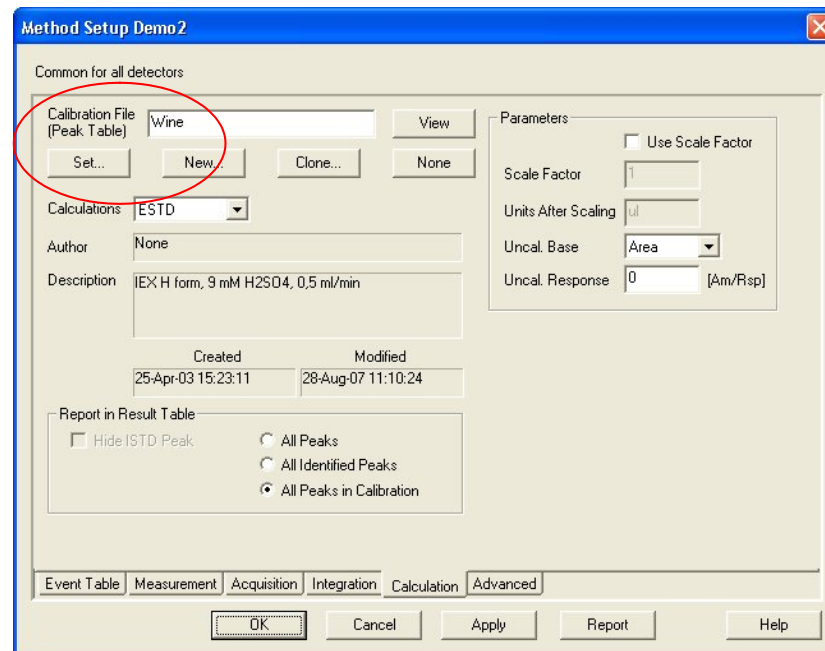
Chromatogram link to calibration file

- Calibration file is common to all chromatogram files linked to it
- All changes in calibration file are immediately progressed to all opened chromatogram files linked to it
- History is traceable as a copy of actual calibration state is stored within chromatogram, when saved



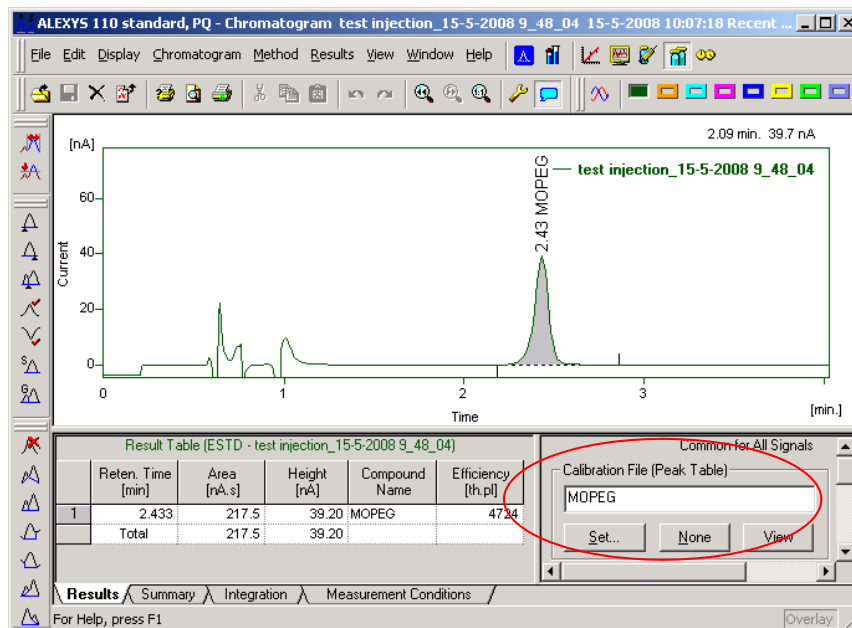
Chromatogram link to calibration file

- Before analysis
 - Link can be set in the method file



Chromatogram link to calibration file

- After analysis
 - Link can be changed in chromatogram

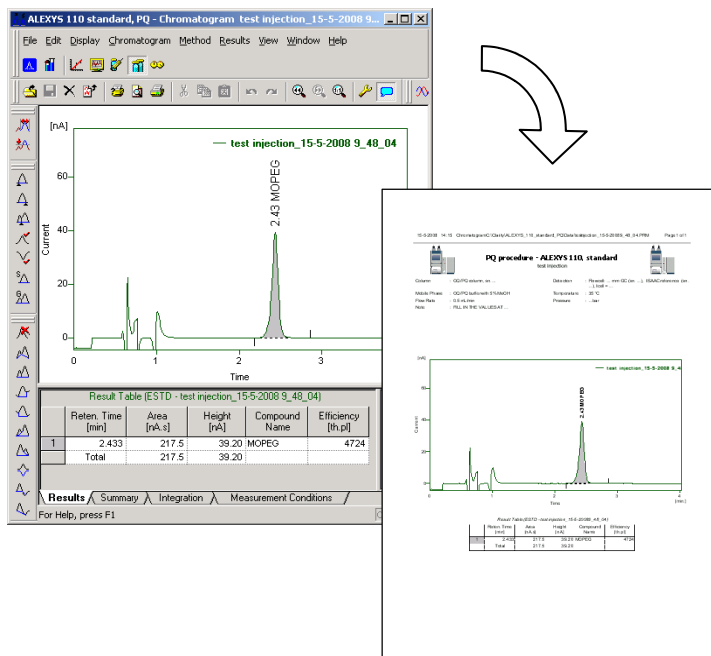


5. How can I extract the results from the analyses?

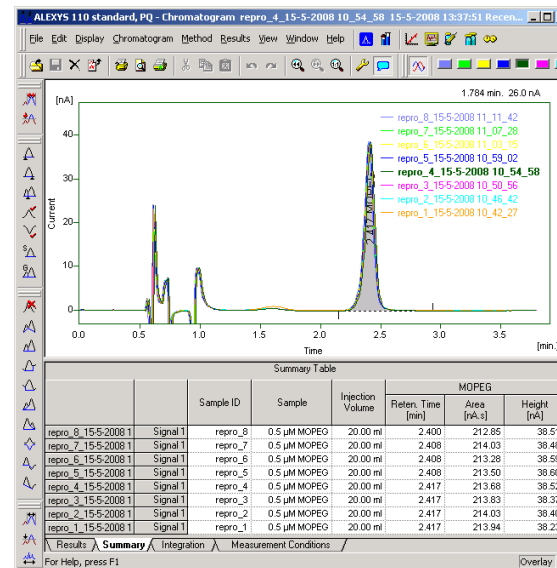


Report options

- Chromatograms can be printed individually or exported as figure

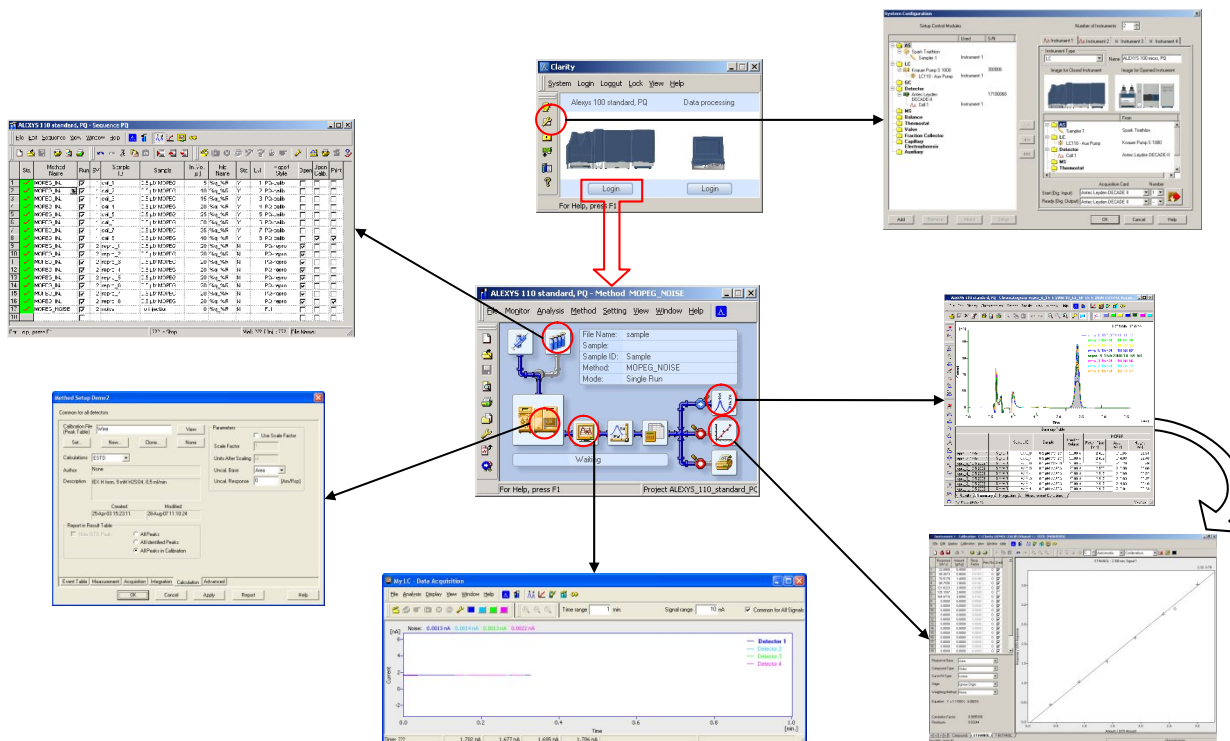


- Data of multiple chromatograms (summary table) can be copy-pasted to for instance Excel



Summary

- Clarity is a modular organised software program, with the Instrument window at the centre.



More information....

For more details on the Clarity Chromatography software:

- Clarity manuals
- Antec web site: www.myantec.com
- Data Apex website: www.dataapex.com

