



GETTING STARTED

Clarity Software

ENG

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Phone: +420 251 013 400

clarity@dataapex.com

www.dataapex.com

DataApex Ltd.
Petrzilkova 2583/13
158 00 Prague 5
Czech Republic

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Author: LT

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To facilitate the orientation in the **Getting Started** manual and **Clarity** chromatography station, different fonts are used throughout the manual. Meanings of these fonts are:

Open File (italics) describes the commands and names of fields in **Clarity**, parameters that can be entered into them or a window or dialog name.

WORK1 (capitals) indicates the name of the file and/or directory.

ACTIVE (capital italics) marks the state of the station or its part.

Chromatogram (blue underlined) marks clickable links referring to related chapters.

The bold text is sometimes also used for important parts of the text and the name of the **Clarity** station. Moreover, some sections are written in format other than normal text. These sections are formatted as follows:

.....
Note: Notifies the reader of relevant information.
.....

Caution: Warns the user of possibly dangerous or very important information.
.....

█ Marks the problem statement or trouble question.

Description: Presents more detailed information on the problem, describes its causes, etc.

Solution: Marks the response to the question, presents a procedure how to remove it.

1 Getting to know Clarity

Clarity Chromatography Station is an effective tool for the acquisition, processing, and evaluation of data from a wide range of directly controlled chromatographs, and from any gas or liquid chromatograph with an analog output.

Clarity provides tools to comply with the FDA's directive **21 CFR Part 11**.

1.1 Key features

- **Measurement** - Simultaneous data acquisition from up to four 32-signals systems (4×32 signal configuration).
- **Integration** - Clarity includes two advanced integration algorithms, offering extensive customization options for peak detection and quantification. Fine-tuned integration parameters can be easily applied to other chromatograms, ensuring consistent and efficient data processing.
- **Calibration** - Internal and external standard calculation methods, calibration of groups of peaks and reference peaks for better identification.
- **Automated measuring support** - Sequence tables for any set of samples with or without an autosampler.
- **Audit Trail and GLP Compliance** - Built-in audit trails and GLP Options settings ensure compliance with GLP and other regulatory standards.
- **User Account Management** - Includes password policy enforcement, access restrictions, and user-level audit logs for secure and compliant operation.
- **Post-run Options** - Automatically displays, prints, exports and starts other programs after completion of measurement.
- **Summary result tables** - Displays and prints selected results from all simultaneously displayed chromatograms.
- **Customizable Reporting** - Customizable templates and styles for generating detailed, professional reports.
- **Column performance** - Calculations of peaks in terms of symmetry, efficiency, resolution, etc.
- **Batch** - Automatically batch processes, displays, exports or prints any number of chromatograms.
- **User calculations** - User-defined columns in the Result and Summary tables.

1.2 Extensions

Extensions provide features within **Clarity** that are specific to a given type of analysis or for a specific task.

Each extension comes with a specific Demo project, allowing you to explore its features using test data. This can be done in the Demo version of Clarity, which simulates acquisition without requiring a hardware key, letting you evaluate the extension before making a purchase.

Currently available extensions are:

- **SST** (System Suitability Test): Tracks and evaluates measurement quality.
- **GPC** (Gel Permeating Chromatography): Tailored for performing and analyzing GPC/SEC data.
- **PDA** (Photo-Diode Array): Designed for evaluating data from PDA/DAD detectors.
- **MS** (Mass Spectrometry): Tailored for data evaluation from MS detectors.
- **CE** (Capillary Electrophoresis): Adds CE-specific tools and terminology.
- **NGA** (Natural Gas Analysis): Performs calculations for gas analyses based on selected norms.
- **EA** (Elemental Analysis): Provides tools for performing and analyzing elemental analyses.
- **DHA** (Detailed Hydrocarbon Analysis): Specializes in determining components in fuels like PIONA.

For more details see the dedicated manuals, that can be found on www.dataapex.com.

1.3 Control Modules

Software modules that provide an interface for chromatography devices such as GC and HPLC systems, Autosamplers, Fraction Collectors and Valves. Direct control allows the device(s) to be controlled and monitored from the **Clarity**. The instrument method that controls the device is saved in the measured chromatograms.

For full list of supported instruments visit our www.dataapex.com.

1.4 Hardware and software requirements

Basic Hardware and Software Compatibility:

Latest information about hardware and software compatibility can be found in the datasheet **D016** or on the web page www.dataapex.com under section *Products - Clarity - Compatible Windows OS and Hardware*.

Verify that you have:

- Free USB Ports:
 - One for the HW key.
 - One for the installation USB (not needed if downloading the installer from www.dataapex.com).
 - An additional USB port if using an A/D converter for analog acquisition (not connected during installation).
- Microsoft .NET Framework 4.8 or higher installed.
- A free, suitable communication port if connecting a controlled instrument (refer to the module's manual for details).
- For regulated environment:
 - Windows Pro/Professional Edition is required for configuration. See manual [M132: Clarity in Regulated Environment](#) for more details.

Note: When using discontinued hardware such as: INT5, INT7, INT9, CB11, CB20, U-PAD, U-PAD2 or Net-PAD, consult the separate manual for requirements and compatibility issues.

2 Installation

This chapter will guide you through the installation process of Clarity and the initial setup of connected devices.

Caution: Do not connect any devices, such as **Colibrick**, before installing **Clarity**!

2.1 Language selection

Clarity is available in **English** and the following languages: **Chinese, French, German, Spanish,** and Russian.

You can select the preferred language at the beginning of the installation process or change it later using *Help - Languages* menu command from the main **Clarity** window.

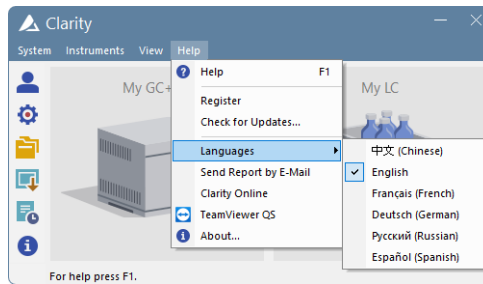


Fig. 1: Switching Clarity into different language

2.2 Software Installation

Setting the Windows environment:

- Ensure you have Administrator access rights in your system before you proceed with the installation. The preferred option is to choose *Run as administrator* under the intended Windows User Account. This ensures that the Windows user has a read/write access to the **Clarity** folders (C:\CLARITY and all subfolders) necessary for operating **Clarity**. Otherwise, the operating system will terminate installation, or **Clarity** will not function properly.
- We recommend to switch off *User Account Control (UAC)* in **Windows** before the installation. In **Windows**, go to *Start - Control Panel - User Accounts - User Accounts* and click on the *Change User Account Control settings*. In the UAC dialog, move the slider down to select the *Never notify* option.
- Ensure that Windows is up-to-date. In case there are pending Windows updates, Clarity installation will be terminated with the following message:

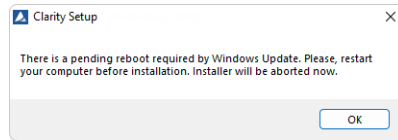



Fig. 2: Pending Windows Update message

- For regulated environment it is required to set up Windows Accounts in specific way to comply the regulations. See manual [M132: Clarity in Regulated Environment](#) for more details.

Installing Clarity:

- Insert the **Clarity** installation medium into the PC or download the latest **Clarity** version from www.dataapex.com/downloads.
- Select the INSTALL.EXE file and run it.
- The installation wizard will take you through the installation process, including the creation of a **Clarity** shortcut in the *Start* menu and a **Clarity** icon  on the Desktop.
- Enter the User code provided during the purchase of your station or start without the User code to activate Trial mode.

Trial mode:

- Select *Enter User Code later* option in the *Clarity User Code* dialog and click the *Next* button. When no User code is provided, **Clarity** will start in the so called Trial mode. Trial mode is valid for 30 days or 100 station starts (whatever comes first), and enables all the functions **Clarity** can offer. When the Trial period expires, you will be asked to fill in your User Code number you received with your station, or enter the trial prolongation code. If none is supplied, Clarity will not start.

Caution: It is highly recommended NOT to install the Clarity software into the PROGRAM FILES directory.

2.3 Hardware Installation

The following chapters describe the installation of the **HW key** and a brief installation of the **Colibrick** A/D converter (not included in case of direct control of the chromatograph).

A detailed description of the hardware and its installation, including troubleshooting, is available in separate manuals (see www.dataapex.com/downloads).

Caution: Install **Clarity** before connecting any external devices to the PC.

2.3.1 Installation of the Colibrick A/D Converter

Caution: Install **Clarity** before connecting the **Colibrick** to the **USB** port. Drivers will be installed automatically during the installation of **Clarity**.

- Install **Clarity** from the provided medium or get the latest version from www.dataapex.com/downloads.
- Connect the **Colibrick** with a cable to a **USB** port on the computer.
- After connecting the **Colibrick**, the device will be automatically detected by the operating system.

Note: Multiple **Colibricks** can be distinguished by their unique serial numbers. Therefore, even when plugged into a different **USB** port, **Clarity** will automatically assign the appropriate **Colibrick** to the corresponding *Instrument*. There is no need to restart the **PC**.

2.4 Device wiring

The wiring strongly depends on the particular configuration. The **Clarity** station package with the **Colibrick** A/D converters contains a **cable set** composed of signal, starting, and digital output cables for connecting **Clarity** to a chromatograph, and a **USB** cable for connecting a **Colibrick** to a computer.

The following subsections contain information regarding the A/D converter wiring. Using directly controlled detectors eliminates the necessity of having an A/D converter - in this case, continue in the chapter "**Clarity Configuration**" on pg. 10. See www.dataapex.com/controls for a list of digitally controlled instruments.

2.4.1 Standard cable for Colibrick

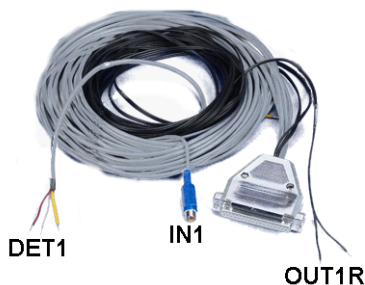


Fig. 3: The standard Colibrick cable for one detector

Signal cables

The cables labeled as "DET1" to "DET4" (corresponding to the number of channels) are supplied without connectors with stripped and tinned endings - red/brown (+), white (-), and shielding (analogue ground).

Starting (marker) cables

The cables labeled as "IN1" to "IN4" (corresponding to the number of channels) come with an RCA connector. Each starting cable contains two more cables: one with either free leads [red (+), shielding (digital ground)] for a direct connection to the chromatograph, or a valve for a valve-mediated connection, and one equipped with a push-button for the cases when there is not a starting contact available and it is necessary to perform a manual start.

Digital output cables

Relay contacts labeled as "OUT 1R" to "OUT 4R" (corresponding to the number of channels) terminate with free leads. These are used for the autosampler (AS) synchronization in an active sequence without the AS Control module.

Each **Colibrick** comes with a female CANNON SUB D 37-pin connector.

2.4.2 Chromatograph

Connect cables according to one of the diagrams in **Fig. 4** on pg. 8. Use a symmetrical connection only if you are sure that the chromatograph/detector is

equipped with a symmetrical output - it is necessary to read the instructions for the corresponding chromatograph.

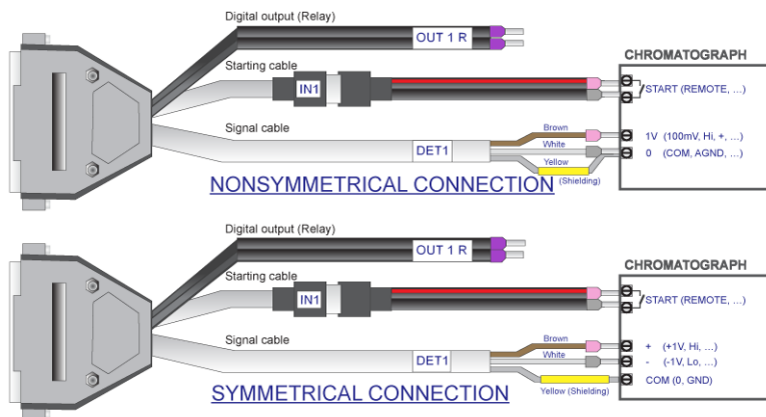


Fig. 4: Possible types of connection between the Clarity station and a chromatograph

Note: Since the introduction of the INT7 converter, all **DataApex** A/D converters use the same standard **INT7 Connector**.

Connecting the signal cables:

Signal inputs of the **Colibrick** are symmetrical: red/brown (+), white (-), yellow shielding (= analogue ground/copper braiding).

Caution: The shielding must be connected since it also serves as the analogue ground for the measurement. In the case of an asymmetrical detector output (only two leads/terminals/pins/screws), the shielding must be connected to the white lead! No lead of the signal cable can remain unconnected.

Try to connect the signal cable to the chromatograph detector output with the largest possible level of signal. This one is usually labeled as **INTEGRATOR** (signal approx. 1 V). The level of the signal on the output marked as **RECORDER** is only about 10 mV.

For an easier modification of the wiring, we supply a **SV9 Terminal board** (p/n **SV9**) with screw contacts.

Connecting the starting cables:

The starting input reacts to a change of the TTL logical level (5 V) or to a connection by any contact (button, contact of relay). It can be used for a remote start from a chromatograph, or from a valve with a contact closure when injecting manually.

The input implicitly reacts to a change from *HIGH* to *LOW* (or closing of a contact). By switching the *Down* item to *Up* in the *Ext. Start/Stop* section from the *Method Setup - Measurement* dialog (accessible from the *Instrument* window using the *Method - Measurement* command), the input function may be changed.

2.4.3 Autosampler

The most typical autosampler connections are described in the chapter "**Connecting Autosamplers (AS)**" on pg. 36. The start synchronization configuration through *Ext. Start Dig. Input* and *Ready Dig. Output* functions is included.

The autosamplers controlled directly using an **AS Control** module (p/n **A26**) are described in their corresponding manuals.

2.5 Clarity Configuration

The following chapter explains how to set the instrument number and type, how to assign **Colibrick** channels to a specific instrument, and how to name those channels and set units.

The configuration of particular control modules is described in the corresponding **Clarity Controls** manuals.

- Start the **Clarity** station with the  icon on the desktop.
- Open the **System Configuration** dialog using the *System – Configuration...* command or via the  icon. See **Fig. 5** on pg. **11**.

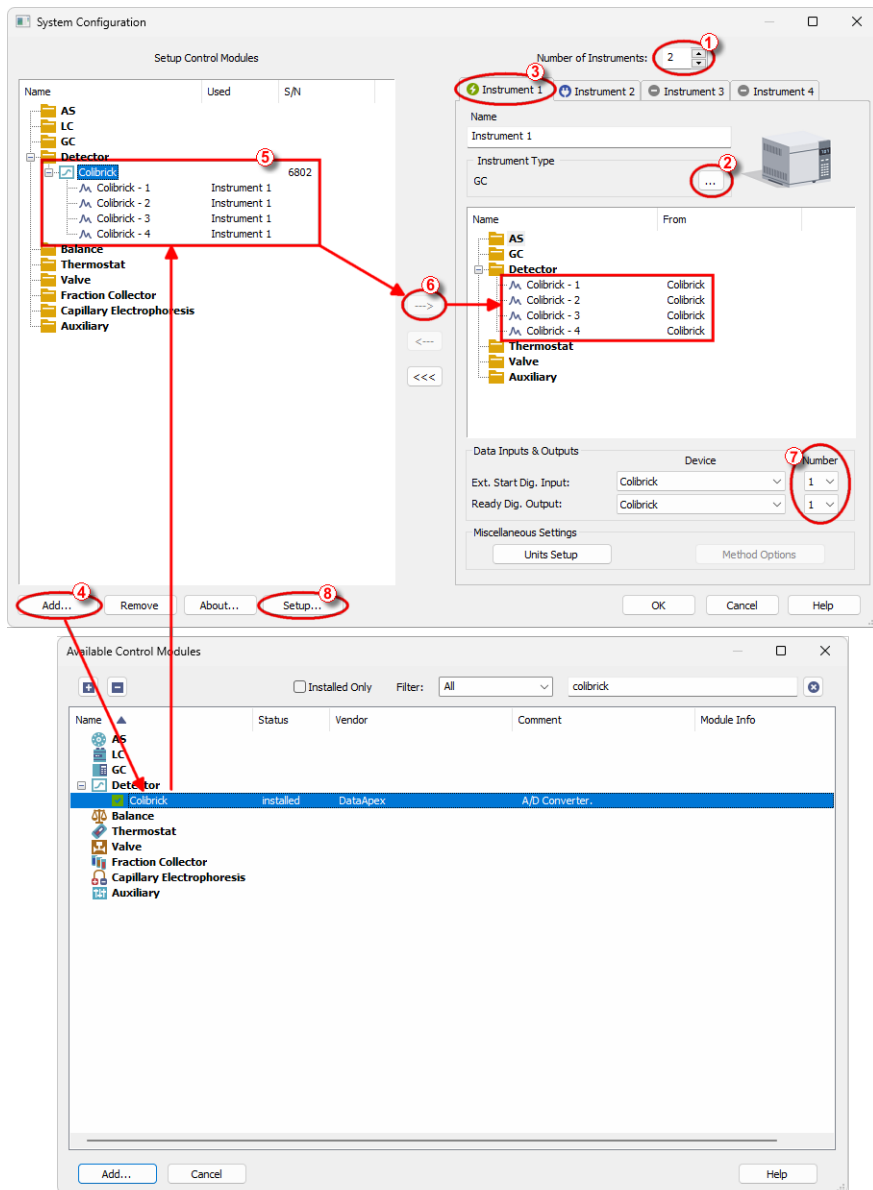


Fig. 5: System Configuration dialog

- Set the *Number of Instruments* field ① .

Note: You can set a larger number of Instruments than you have purchased. You will not be able to measure on the surplus Instruments (indicated by a blue icon on the tab) but you may use them e.g. for “offline” evaluation of chromatograms from other projects.

- Set the corresponding type of chromatograph (GC/LC/EA/GPC...) using the button ② .
- Instruments can be selected on the Instrument tab ③ . Each instrument can have a different configuration depending on your hardware configuration.
- Add devices to the list on the left using the *Add* button ④ in the lower left corner of the dialog. After adding a device, a setup dialog will appear. This dialog varies for each device; an example for a **Colibrick** is shown below.
- To modify the instrument configuration, drag and drop the equipment from the *Setup Control Modules* list on the left to the selected *Instrument* tab on the right. Alternatively, select the device ⑤ and press the button ⑥ .
- For the proper setting of *Numbers* in the *Data Inputs & Outputs* group ⑦ see the chapter "**Connecting Autosamplers (AS)**" on pg. 37.
- The setup dialog of each device can be invoked again by double-clicking on its name or by selecting it and clicking the *Setup* button ⑧ :

Fig. 6: Dialog for the setting of a **Colibrick** converter

- Check and/or change the settings of the converter (e.g. set the names of the detectors, signal polarity, etc.).

Note: You can change the signal units and offset using this dialog. A more accurate description can be found in the **Colibrick** manual.

- Click the **OK** button to save the changes in the configuration.

3 Qualification procedures

Many laboratories place great importance on the quality of their analytical data. One of the requirements for ensuring the reliability of generated results is the validation of all instrumentation and procedures that are used to acquire data. For chromatography data stations, usually three levels of validation (qualification) are relevant:

- [Installation Qualification](#)
- [Operational Qualification](#)
- [Performance Qualification](#)

3.1 Installation Qualification - IQ

The **Installation Qualification (IQ)** is a procedure that confirms the successful installation of the software and verifies the correctness of the file versions. **IQ** is an integral part of the **Clarity** installation procedure.

How to use the Installation Qualification

- Install **Clarity** according to the instructions of the **Installation Wizard**.
- Locate the **IQ Report**: this is dependent on your operating system. You can search for **IQ Report** in the search field of the *Windows Start* menu.
- Click on the **IQ Report** program and the *IQ* window will be opened.

Note: **IQ** can also be started by using IQ.EXE located by default in C:\CLARITY\BIN.

- If the installation has been performed correctly, the status should read: "*Installation Qualification Test: Passed*".

Installation Qualification Report

Date	03.05.2023, 00:18
Serial number of application	
User Code	
Version of application	Clarity version 9.0.0.55
Build date of application	29.04.2023, 05:23
Instruments	3
Extensions	SST; GPC; PDA; EA; CE; IMS; NGA; DHA; GCxGC; MS-TOF
Controls	GC; LC; AS
Certification file	C:\Clarity\Bin\iq.chk
Checksum of cert. file	4494D50B4E0B603E
Date of cert. file	29.04.2023, 06:41
User	Test
System	Microsoft Windows 11 Professional version 10.0 (Build 22000)
Acquisition and hardware devices	Key Rockey 4ND OQ Validation detector

Core Files, Embedded Components: Passed

Files

[Hide files list <](#)

File	Path	Version	Size	File date	Status
advantecchf122scfc.rb	c:\clarity\bin\utils\uni_drivers\advantec	-	35746	29.04.2023, 05:16	Passed
advioncms.dll	c:\clarity\bin	6.4.14.1	487936	29.04.2023, 06:28	Passed
AdvionCommon.dll	C:\Clarity\Bin	6.4.14.1	30208	29.04.2023, 06:28	Passed

Fig. 7: The IQ window

- If the **Installation Qualification** fails, it is recommended to uninstall and then re-install Clarity. If it fails again, contact the DataApex support (support@dataapex.com).

Note: The most common reason for a "Failed" result is when an upgrade is installed over an existing full version of Clarity. While this process does not generate any errors, it can lead to checksum mismatches because some files are retained from the original installation.

- The **Installation Qualification** report can then be printed, copied to a clipboard, sent by an email, etc.

3.2 Operational Qualification - OQ

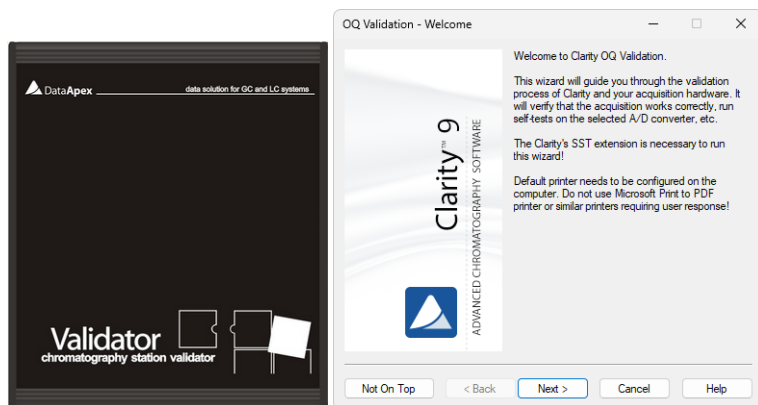


Fig. 8: DataApex Validator 2 and OQ Validation Wizard

The **Operational Qualification (OQ)** is a procedure designed to confirm that the data station is performing according to the manufacturer's specifications. The **Operational Qualification** is provided by the **Validation Kit** (optional), which consists of a precise peak generator and a set of methods and reports used in the validation process. The **System Suitability Test (SST)** module, an optional Extension of **Clarity**, is necessary for running **OQ**.

How to use the Operational Qualification

To perform **OQ**, run the *OQ Validation Wizard* from the CLARITY\BIN\OQ_VALIDATION folder. The Wizard will guide you through the procedure of the **OQ** validation.

It is possible to perform **OQ** in two different ways:

1. Validation with an A/D converter

Colibrick or any other DataApex A/D converter and a **Validator** peak generator (a part of the **Validation Kit**, p/n **CVK**) are required for this type of validation. The **Validator** generates a signal which is received by the A/D converter, and the acquired dataset is compared with expected values. This validation protocol ensures the validity of the entire acquisition chain, starting from analog signal input and ending with result calculation.

2. Validation with a Virtual detector

For systems with digital acquisition, this is the only feasible manner of validation. The input signal is simulated via the **Virtual detector** control module, which is able to simulate signal input into **Clarity** in exactly the same way as a real chromatographic instrument would do. This will ensure that digital signals are processed correctly after being received from a detector. **Virtual detector** is a part of the **Clarity** software, meaning no extra hardware or control module is needed for this type of validation.

Note: **OQ** validation takes approximately 50 minutes to complete and during this time, it is not possible to perform analysis using **Clarity**.

The **Validation kit** (p/n: **CVK**) as well as the **SST Extension** (p/n: **A22**) can be purchased separately. The validation process is described in more detail in the **Validation Kit** manual (M039).

3.3 Performance Qualification - PQ

The **Performance Qualification (PQ)** is a procedure confirming that the analytical system is fit for a given type of analysis. The overall system performance is tested against the requirements of the manufacturer's specification. For this purpose, a dedicated **Clarity** Extension, the **System Suitability Test (SST)** can be used. **PQ** must be done based on the Standard Operating Procedures (SOPs), devices, and procedures used directly on site, therefore, DataApex cannot provide any pre-prepared **PQ** procedures.

The **SST** module (p/n **A22**) can be purchased separately.

4 Program structure and control

Clarity has a hierarchic structure. It works with the so-called Instruments. All detectors connected to the same Instrument share a common time base.

Upon clicking the **Clarity** icon, the main **Clarity** window will be displayed with names of the configured Instruments.

Note: If the **Clarity** is a specific version, such as Demo, Offline, or Distributor, a colored information stripe ③ appears below the tiles representing individual instruments.

The main **Clarity** window is designed to configure chromatography station, select access rights, and choose basic directories for data saving ①. It also shows the status of the logged-in instruments ②.

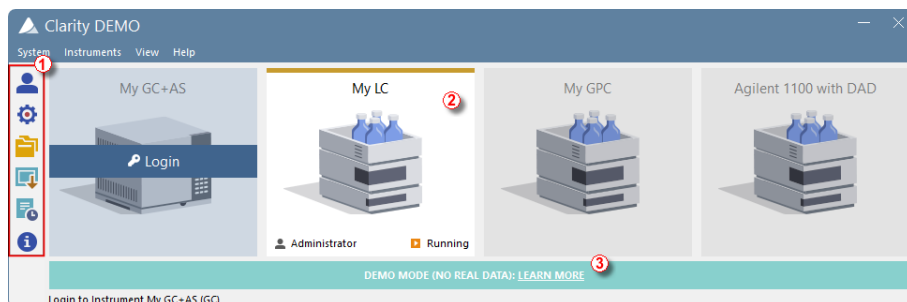


Fig. 9: Clarity main window

Select the *Instrument 1*. After clicking on the chromatograph picture, you will be prompted to log in by entering your *User Name* and selecting a project (this can be later changed). Proceed by pressing the *OK* button.

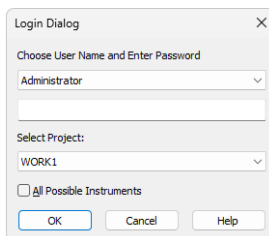


Fig. 10: Login dialog

The dialog about Method Setup adaptation may be displayed. Click *Yes* and adapt the Method in the *Method Setup* dialog. In case you trying out Clarity with demo data, just save the method for now. Alternatively you can press *Help* to learn more about method adaptation. Now the *Instrument* window will be displayed.

The *Instrument* window is used for acquisition and processing of data using the connected chromatograph. Up to four independent *Instrument* windows can be

displayed. As you can see on the example in **Fig. 9** on pg. 18., *Instrument 2* is opened and running.

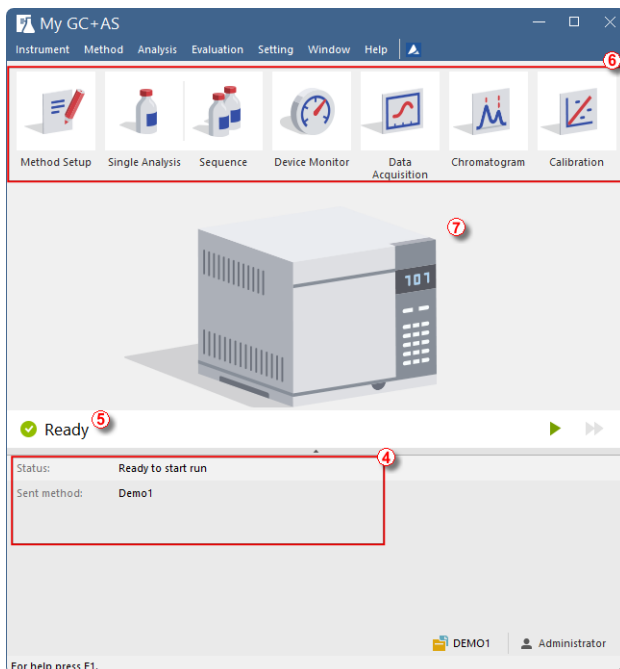


Fig. 11: Instrument window

Each *Instrument* window contains an information table (4), a status line (5), tiles for Method Setup, Single Analysis, Sequence, Device Monitor, Data Acquisition, Chromatogram, and Calibration (6), and lastly an instrument image (7) (image is hidden at default window size).

Instruments are distinguished by the color of the *Instrument* window header and by the instrument name, which is displayed in the header of each *Instrument* window. The name in the header of the *Instrument* window is identical to the name displayed above the corresponding chromatograph in the main *Clarity* window.

All relevant dialogs for performing actions in the *Instrument* window can be easily accessed using appropriate commands from the menu or by clicking on their icons.

5 Tour through the Clarity station

The following two sections will guide you through a single analysis (the chapter "**Running the Single Analysis**" on pg. 21.) and a sequence measurement (the chapter "**Running the Sequence measurement**" on pg. 33.).

These sections provide step-by-step instructions to follow in order. Some sections may be skipped as their output files are already included as examples - notifications will indicate when this applies. Optional procedures are located in Note sections and do not need to be completed to achieve the final goal.

The **Clarity** software is intuitive and easy to master without much training. The first analysis can be run in less than one minute after installing the station and configuring the hardware.

This tour is primarily designed for the users who installed the **Clarity Demo** version, where the configuration is prepared in addition to the demo data that is also in the standard Clarity. To be able to complete the tour in standard Clarity with demo data, it is recommended to set the Demo Detector to the Instrument that will be used (for more details on how to do that see the [Configuration](#) topic).

It is possible to test the **Clarity** functions on other projects, but the files mentioned in this guide will not be present.

Note: Pressing **F1** or the *Help* button shows the help page specific to the window or dialog. In the help, the *Index* tab serves for a keyword search and the *Search* tab serves for full-text searching.

5.1 Running the Single Analysis

There is a simple project DEMO2 aimed on basic functions. It shows the way to start a [Single Analysis](#), monitor the [Data Acquisition](#) and process the resulting [Chromatogram](#).

5.1.1 Instrument window

1. Start the **Clarity** station. The main window will appear.
2. Open **Instrument** which is prepared to test the **Single Analysis**. In Clarity Demo it is **Instrument 2**. Do so by using the *Instrument - Login to Instrument X* command or by clicking on its icon. The *Login Dialog* will open.
3. Let User field filled with the pre-selected *Administrator*. In the *Select Project*: combo-box choose option *DEMO2* and press the *OK* button.

You can also load the desired demo project to the *Instrument* window by using the *Instrument - Project...* command, then use the *Open...* button and select the **DEMO2** project. This will load all the necessary files.

Note: You can create your own User accounts from the main *Clarity* window using the *System - User Accounts...* command.

The *Instrument* window will open. **Fig. 12** on pg. **21**. shows the most important icons in the *Instrument* window. During the tour, we will review all windows belonging to these icons.

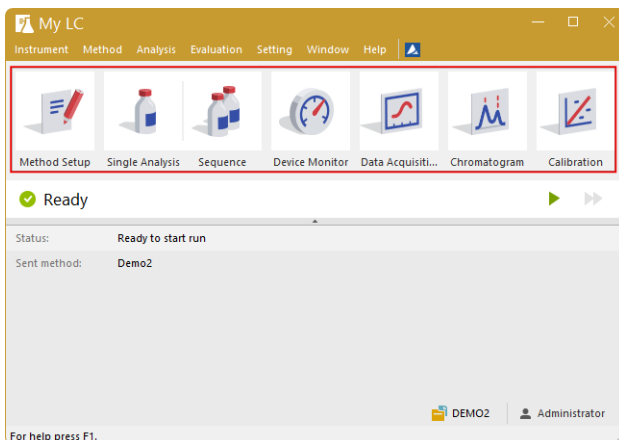


Fig. 12: Instrument window

5.1.2 Single Analysis dialog


Use the *Single Analysis*  button in the *Instrument* window to open the *Single Analysis* dialog.

Fig. 13: The Single Analysis dialog


- The fields in the *Analysis* tab contain information about the sample. You may set the values in the fields as shown in **Fig. 13** on pg. 22., as typical analysis settings.
- *Sample ID* and *Sample* fields ① are only informational, and can be propagated to chromatogram name via variables.
- Values in *Sample Amount*, *Dilution*, *ISTD Amount*, and *Inj. Volume* fields ② can be used for further calculations.
- Choosing the *Standard* from the *Sample Type* drop-down menu ③ and entering a value in the *Level* field would mark this sample as the calibration standard and save the chromatogram into the CALIB subdirectory.
- The measurement of the sample will be performed according to the method selected in the *Method* field. Method can be selected by using ... button.
- The *Edit Method...* button ④ opens the *Method Setup* dialog, where you can edit the parameters of the method. Click the button and check the setting of the *Autostop* parameter (*Autostop* should be enabled) and *Run Time* (7.5 minutes). Return to the *Single Analysis* dialog by pressing the *OK* button.

- **Chromatogram File Name** ⑤ field is used for entering the file name of the resulting chromatograms. It is possible to use plain text together with variables adding the time, date, sample name or other parameters to create a unique chromatogram name. The resulting name can be seen just above the field ⑥ in parentheses.

Note: The complete set of available variables is shown after clicking the field and selecting the ▾ icon.

- After the parameter setup, you can run the analysis by clicking the **Run** button ⑦. The **Single Analysis** dialog will close now. If you open it again, you will see three additional buttons (**Stop**, **Abort**, **Snapshot**) that will allow you to stop or abort the analysis or take snapshots (see the chapter "**Data Acquisition window**" on pg. 23.).
- Close the **Single Analysis** dialog and return to the **Instrument** window.

5.1.3 Data Acquisition window

- In the **Instrument** window look at the **Status line** (see **Fig. 12** on pg. 21.). The acquisition is now signaled by the **RUNNING** state and the actual run time is shown there.
- To see the data acquisition in process and control it if necessary, click the **Data Acquisition**  icon (see **Fig. 12** on pg. 21.) to open the **Data Acquisition** window.
- Depending on your Instrument's configuration, one or more signals may be displayed. The number of detectors (signals) and their names can be seen in the upper right corner of the graph ①.

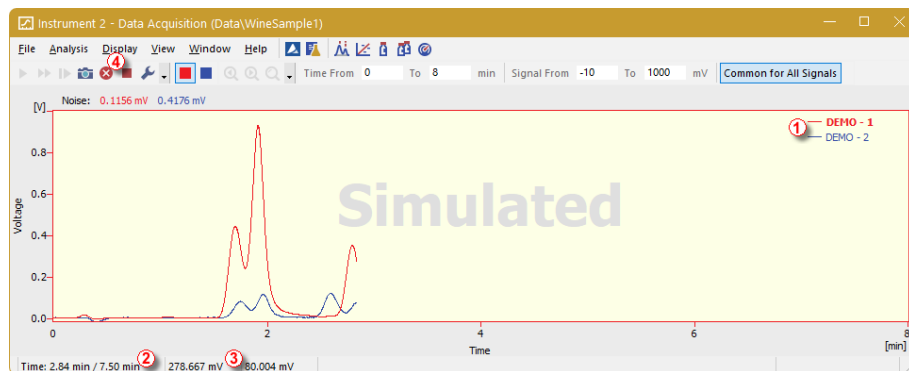








Fig. 14: The Data Acquisition window

- In the **Status bar** on the bottom of the **Data Acquisition** window, the elapsed time of the analysis ② can be seen, as well as the value of the signal for each detector ③ and its units.

- **Stop**  and **Abort**  icons  allow you to cancel the analysis. If stopped, **Clarity** will save all the data acquired so far and stop the analysis. Abort cancels the acquisition without saving any data.
- **Snapshot** icon  creates the preview of the already measured data. After clicking on it, snapshot chromatogram is created and opened in the *Chromatogram* window. If it is not Saved As under new name until the measurement is completed, it is overwritten by the newly created complete chromatogram.
- After 7 minutes and 30 seconds (the run time set in the template method used for the measurement), the analysis will automatically stop and the chromatogram will be opened in the *Chromatogram* window.
- The *Chromatogram* window opens automatically if it was not opened before, because of the settings made in the *Single Analysis* dialog. These settings are available in the *Post-run Options* tab. You can also configure additional post-run actions, such as exporting data or executing external programs, in this tab.

5.1.4 Chromatogram window

- The *Chromatogram* window can be opened also manually by clicking on the *Chromatogram*  icon in the *Instrument* window.
- Here you can evaluate your previously acquired data or open our sample chromatogram to get familiar with the basic functions which will be covered in this chapter.
- Use the *File - Open Chromatogram...* command or click the open icon  and select the WINE_SAMPLE.PRM file and press the *OK* button.
- The *Chromatogram* window is divided into two parts: the *Graph* (upper) pane and the *Results* (lower) pane.
- Zoom in any part of the chromatogram by selecting the area while holding the left mouse button. Restore the default chromatogram view by double-clicking in the graph.

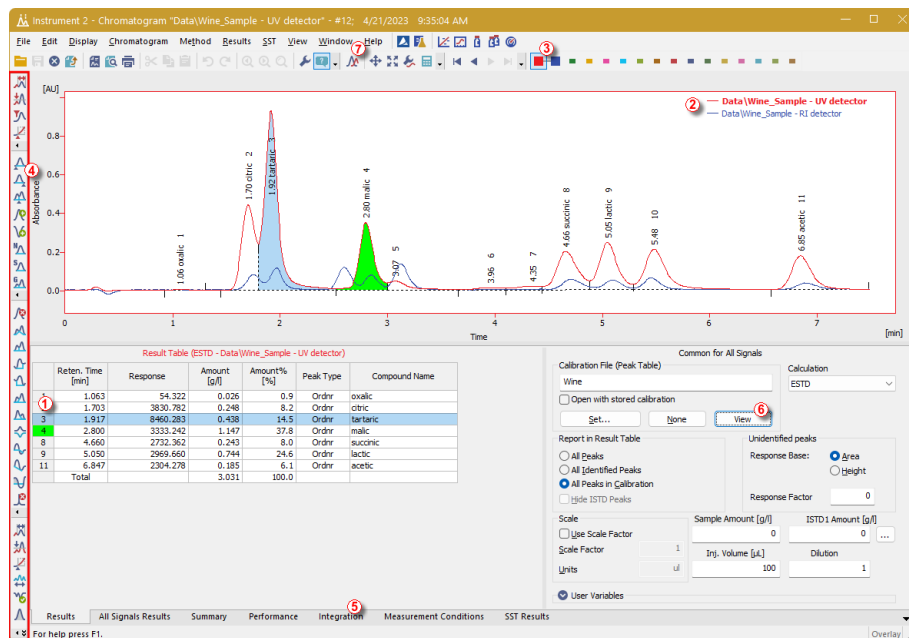




Fig. 15: The Chromatogram window

- Clicking on a cell in the *Result table*  will highlight the peak (or peaks when selecting multiple cells) corresponding to the row(s) you just selected.
- Only one detector signal can be active at a time. The active signal can be identified in three ways:

- in the legend section at the upper right corner of the graph ② , where the active signal is displayed in bold text
- in the *Overlay* toolbar ③ , where it is marked with a debossed icon 
- by noting the color of the graph outline and table headers.
- Try to change the active signal by double clicking on its name in the legend section. You will notice that the **Result table** has changed.
- To change the color of the active signal click on the desired color in the *Overlay* toolbar.
- You can change the integration of peaks using the interactive icons on the toolbar on the left side of the *Chromatogram* window ④ , selecting the Integration operation in the Chromatogram menu, or directly in the *Integration* tab ⑤ . Any changes made either way will change the **Integration table** and can be copied to the template method.
- By clicking the *View* button ⑥ , you can open the calibration linked to this chromatogram.
- To display more than one chromatogram you can enable the *Overlay mode* ⑦ .


Note: Already measured chromatograms can be reprocessed in the *Batch* dialog using the newly created method to apply the adjusted Integration table.

6.1 Creating calibration


This chapter and the prepared **DEMO1** project will guide you through the creation of a calibration and linking it to the methods and chromatograms. After this you can continue in the same project with [Running sequence measurement](#), to try how the automatic calibration/recalibration from the sequence works.


In Clarity, when calibration is prepared (Compounds Names, Retention Times, and Amounts for every used level are filled in), you can load the responses of standard chromatograms manually in the Calibration window or automatically when running a sequence. Doing so will lead to creation or recalculation of calibration curves of individual compounds.

6.1.1 Calibration window

- In the main *Clarity* window, open the **Instrument** on which you want to test the functions of Sequence. In Clarity Demo it is **Instrument 1**. Do so by using the *Instrument - Login to Instrument X* command or by clicking on its icon. The *Login Dialog* will open.
- Let User field filled with the pre-selected *Administrator*. In the *Select Project*: combo-box choose option *DEMO1* and press the *OK* button.
- Use the Calibration  button in the *Instrument* window to open the *Calibration* window.

Note: If you wish to use prepared demo calibration instead of creating a new one, in the *Calibration* window, open (via the *File - Open...* command) the calibration file DEMO1.CAL and test the functions of the *Calibration* window on it. In this case you can skip the following section and continue with the chapter "**Linking the calibration to a chromatogram**" on pg. 30.

- Use the *New Calibration*  icon ① to create a new calibration file. Save the calibration under a name of your choosing.

Note: The calibration can be saved either using the *Save Calibration*  icon ②, *File - Save*, or *File - Save As...* command.

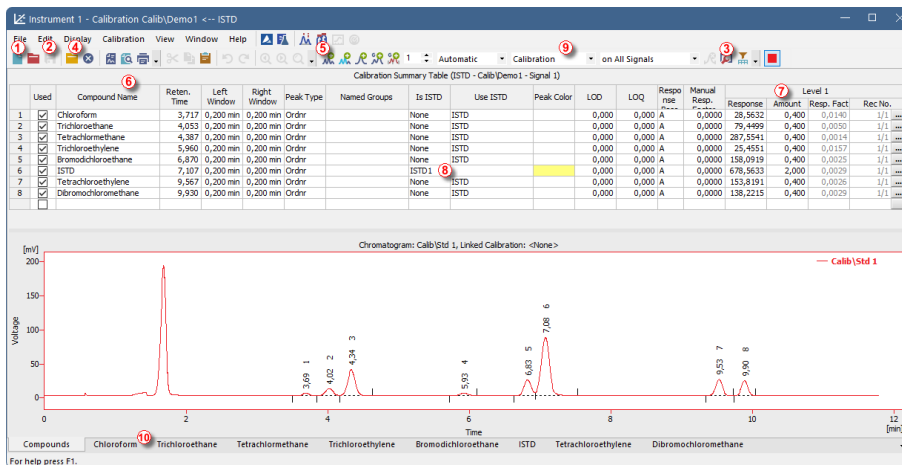


Fig. 16: The Calibration window - loaded standard


- Use the **Calibration Options** icon (3) and change the **Display Mode** (top right corner of the dialog) to **ISTD** as our example is calculated by internal standard, then press the **OK** button.


Now, the calibration standards need to be imported into the calibration. This is done in a series of successive steps:






- Use the **Open Standard** icon (yellow) (4) to open the STD 1.PRM data file. The lower part of the **Calibration** window now displays the chromatogram of the standard.
- Use the **Add All** icon (blue) (5) to add all identified peaks to the Calibration Summary Table. The Table appears in the **Calibration** window, ready to be completed as shown on **Fig. 16** on pg. 28.
- As demonstrated in the Calibration Summary Table and the Chromatogram, individual peaks are now identified according to their retention times only. To label the peaks, click and edit the fields in the **Compound Name** column (6) to the names shown on **Fig. 16** on pg. 28.
- You may also set the color of a specific peak in the **Peak Color** column, for example, try to set the ISTD peak color to yellow.


Note: The changes made in calibration immediately affects the chromatograms that have this calibration linked (so it is not influences the opened standard as it is not have this calibration linked).

- Fill the **Amount** column (7) with the concentration of the particular compounds. In this standard mixture, all compounds except for the peak number 6 (ISTD) have the amount of 0.4.

- Peak number 6 is our internal standard. So in the *Is ISTD* column, change its type to ISTD1  and then set its amount in the *Amount* column to 2.

The first calibration level is now completed. On the tabs of the individual compounds  (labeled according to the *Compound Name* field), graphs with a single-point linear calibration can be viewed.

- Proceed to completing the other calibration levels: the operation is quite simple and straightforward
 - Use the *Open Standard*  icon (yellow)  again to open another calibration standard named STD 2.PRM.
 - Make sure that *Calibration*  is selected and use the *Add All*  icon (blue)  (response will be added to first empty *Level*).
 - In the *Amount* column, enter the value of 1.0 for all peaks, except for ISTD peak 6, where you should enter a value of 2 instead.
- Set the third calibration level analogously using the STD 3.PRM file and the *Amount* of 3.0, and subsequently the fourth level (file STD 4.PRM, *Amount* 5.0). Again, the ISTD peak should always have the *Amount* of 2.




As the result, on the tabs of the individual compounds , the linear four-point calibration graphs can be viewed.

- Now, save the calibration file using the *Save Calibration*  icon.

6.1.2 Linking the calibration to a method

If you have a large number of samples to be measured and subsequently evaluated using a particular calibration, linking the calibration to each chromatogram separately would be a time-consuming process. To avoid this, link the calibration to a method used for the measurement beforehand.

In the case you want to use same calibration but want the calibration to be constructed only with responses of standards measured in each sequence, it is possible to use calibration cloning - for more details see *Calibrating using clone on first recalibration* topic in the User Guide.

- Return to the *Instrument* window and use the *Method - Calculation...* command to open the *Method Setup* dialog directly on the *Calculation* tab  as shown on **Fig. 17** on pg. 30. Alternatively, open the *Method Setup* by clicking on the icon  and then move to the *Calculation* tab.
- Use the *Set...* button  to select the calibration file and link it to the method.
- Exit the *Method Setup* dialog using the *OK* button. Clicking this button saves this change to the method.
- Any chromatograms measured using this method in the future will be automatically linked to the chosen calibration.

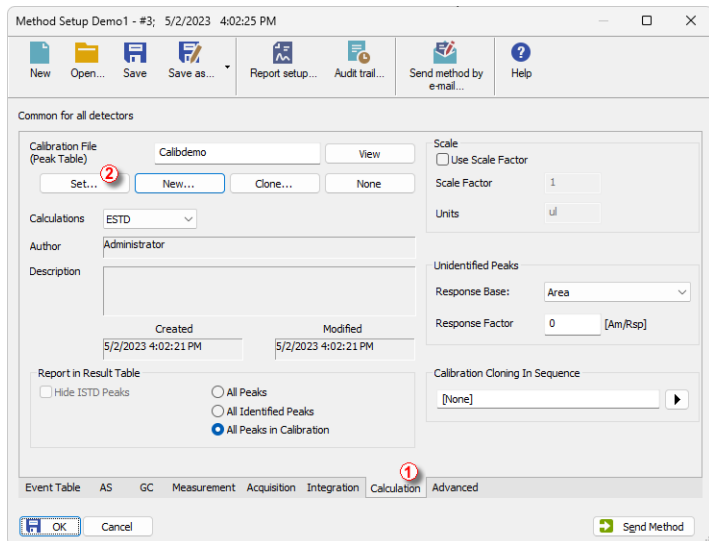




Fig. 17: Method Setup - the Calculation tab

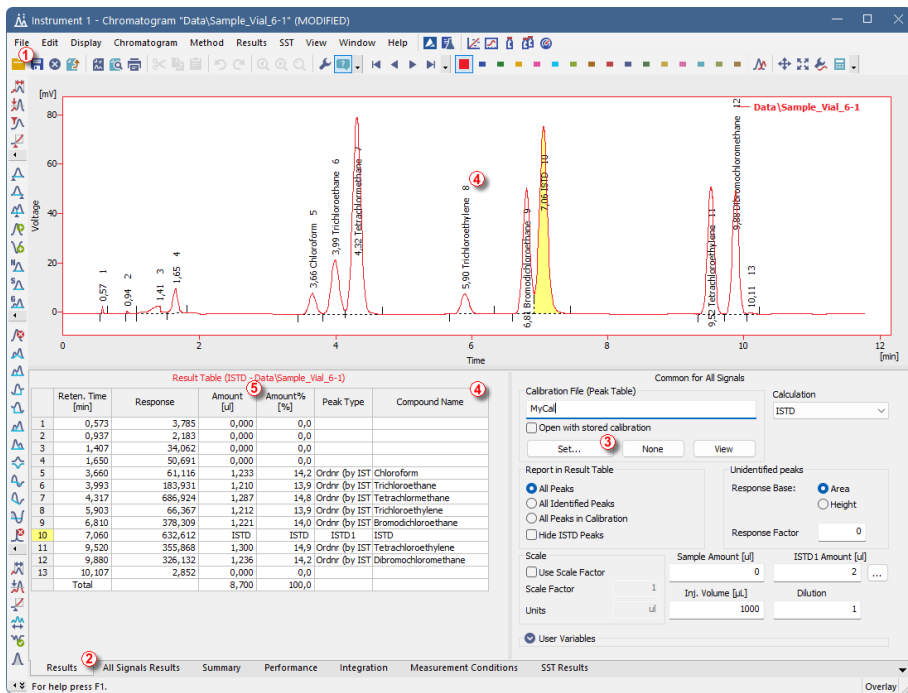
6.1.3 Linking the calibration to a chromatogram

Any chromatogram can be linked to a calibration file, thus automatically providing calibrated results.

- In the *Instrument* window use the *Chromatogram*  icon to open the *Chromatogram* window.
- Use the *Open Chromatogram*  icon ① to open chromatogram you want to link the calibration to. We will use the SAMPLE_VIAL_6-1.PRM file, because it is the sample chromatogram to the standards we used to create the calibration.

Upon opening the chromatogram, the data are uncalibrated and no information about the names of individual compounds is available; the peaks in the *Result Table* are just described according to their retention times. To change this, the appropriate calibration should be linked to these data.

- Select the *Results* tab ② (it should be opened automatically) and look at the section on the right side of the screen. Use the *Set...* button ③ in the *Calibration File (Peak Table)* section to select the calibration file created in the previous section. Any peaks present in the calibration are now identified ④ and have the amounts calculated ⑤.



Note: In case you skipped the process of making your own calibration, please use the DEMO1.CAL instead.

6.1.4 Linking the calibration to a series of already measured chromatograms

If you have already measured chromatograms and wish to change the linked calibration, you can do so easily using the *Batch* reprocessing feature.

This command is especially useful when you have a large number of already measured chromatograms and you want to modify them.

Steps below will describe how to change the calibration of already measured chromatograms.

- Go to the *Instrument* window and use the *Analysis - Batch...* command.
- Select the files to be reprocessed in the left part of the dialog (1) (Fig. 18 on pg. 32.); multiple files can be selected by left-clicking them while holding the **Ctrl** or **Shift** key. For the demonstration, select all files with the names SAMPLE_VIAL_X-Y to be reprocessed.
- Check the *Reprocess by Method* (2) checkbox, select the method to be used for the reprocessing (the one that has the correct calibration linked), and in

Calibration part of the Options select the *Update*.

- Click the *Proceed*  button.

All selected chromatograms will now be linked to the calibration based on the selected method.

Note: You can reprocess files only from the currently opened project.

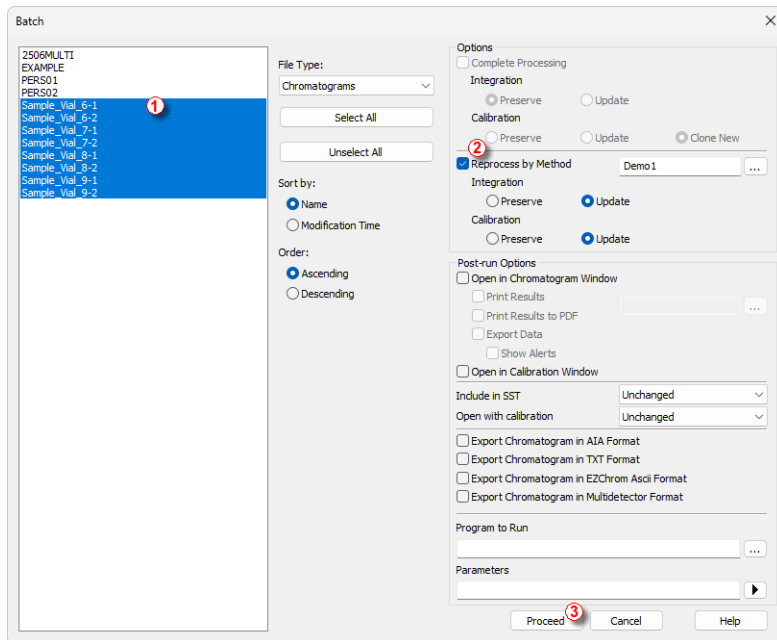





Fig. 18: Batch dialog with selected chromatograms

- After the reprocessing is complete, open the *Chromatogram* window and load any reprocessed file (e.g. SAMPLE_VIAL_7-2.PRM) and look at the *Result Table*. All peaks present in the calibration are now identified and calibrated.
- Multiple chromatograms may be displayed at once. Switch to the *Overlay* mode by pressing the *Overlay*  button found on the *Overlay* toolbar ( in **Fig. 15** on pg. 25.) and then open all reprocessed chromatograms altogether. You can click the *Overlay*  button again to close all the chromatograms except the currently active one.

7.1 Running the Sequence measurement


This chapter and the prepared **DEMO1** project will guide you through *Sequence* window used for automated measurement.

Sequence operation allows automated measurement of large number (depending on PC and autosampler configurations) of samples using chromatographs equipped with autosamplers. **Clarity** provides the possibility to select an *ACTIVE* (start controlled by the station) or *PASSIVE* (start controlled by the autosampler) sequence.

It is also possible to re-process the already measured sequences in the *Batch* dialog.

Note: It is not necessary to have the **Autosampler (AS) Control** module to use the autosampler; start synchronization can be performed even without it. However, the control module can add direct control from **Clarity**, enabling automated actions such as sending vial positions, injection volumes, etc., all without requiring programming the AS through the instrument panel.

7.1.1 Sequence window

- In the main *Clarity* window, open the **Instrument** on which you want to test the functions of Sequence. In Clarity Demo it is **Instrument 1**. Do so by using the *Instrument - Login to Instrument X* command or by clicking on its icon. The *Login Dialog* will open.
- Let User field filled with the pre-selected *Administrator*. In the *Select Project:* combo-box choose option *DEMO1* and press the *OK* button.
- Use the *Sequence*  icon in the *Instrument* window to open the *Sequence* window.

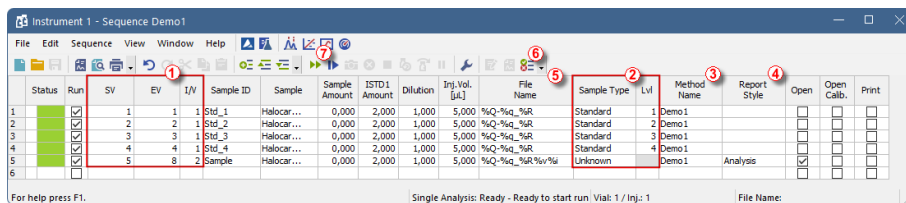




















Fig. 19: The Sequence window

- Look at the *Sequence Table*. Each row of this table defines one or more analyses, depending on the fields *SV* (Starting vial), *EV* (Ending vial) and *I/V* (Injections per vial) . As shown, the first four rows each represent a single measurement (*SV* and *EV* is the same, *I/V* is 1), while row 5 represents eight analyses (*SV* is 5, *EV* is 8; thus measuring 4 samples from 4 successive vials and as *I/V* parameter is 2, each sample vial will be measured twice).



- Also note that in the fields *Sample Type* and *Lvl* , the first four samples are marked as standards on levels 1-4. Chromatograms measured from those rows will be automatically used for the calibration that is linked to the method.
- The *Method Name* column  sets the method used for measuring the row.
- The *Report Style* column  sets the print style used for reporting.
- In the *File Name* column , the name of the resulting chromatogram file is specified. It is recommended to use variable parameters to form the chromatogram filename, for example %Q means that the file name will use the text from the *Sample* field. The complete set of available variables can be listed after clicking in the field and selecting the  icon. It is possible to combine several of these variables with plain text or symbols to create a unique file name for each chromatogram.
- To verify the sequence setup, click on the *Check Sequence*   icon . The **Clarity** station will change all symbols at the beginning of the row to green fields () , meaning the rows are ready, or display an error/warning   message if a problem is detected. The error/warning   message is accompanied with a list of corrections for each case, guiding you on what needs to be fixed before proceeding.

Note: For demonstration purposes only, try to make a mistake and check the sequence once more. For example, check the *Print* checkbox on the first row. You can see that a warning sign appeared on the corresponding row 1. After pressing the   icon, the warning message appears, informing that you are trying to Print the chromatogram with no Report Style selected. Holding the mouse above either field will display the tooltip with the cause of the problem. Set the sequence back to its original state and continue to the next step.




- Start measuring the sequence using the  icon . The state of the *ACTIVE* sequence will change to *WAITING FOR INJECTION*. As soon as the *Ready* signal from the autosampler is detected, the measurement will start.

Note: Even if the autosampler is not connected, **Clarity** will get the *Ready* signal, thus starting the sequence. However, it is not possible to generate separate demo data for each chromatogram, as all chromatograms would be the same. For the demonstration purposes, there are examples of the resulting files in the project folder. You may stop or abort the sequence now or later either from the *Data Acquisition* window or directly from the *Sequence* window. Close the *Sequence* window before proceeding.

- After the first row of the *Sequence table* is measured, the Instrument will once again switch to the *WAITING FOR INJECTION* state, and the autosampler will start a new measurement by sending the *Ready* signal.

Stop the sequence from the *Data Acquisition* window or *Sequence* window at any time by pressing the **Stop**  button (single-click means that the currently measured analysis will be finished and the sequence will stop subsequently, after double-clicking, the sequence will stop immediately). All data measured will be saved. Instead of stopping, you can also abort the measurement with the **Abort**  button (does not produce any chromatogram).

Note: It is possible to edit the sequence even during the measurement. However, if it pauses due to an error, it is necessary to resume the measurement after the error is resolved.

- Already measured rows will change their *Status* from green field () to blue icon with small chromatogram (). During the measurement, the icon is orange.
- A small triangle will appear in the icon  if a chromatogram is produced by the particular measurement in the row. Left mouse click on the triangle will open the menu where you can open the measured chromatogram(s). You can click on the name of the chromatogram to open it or select option to open all chromatograms in overlay as seen in **Fig. 20** on pg. 35.

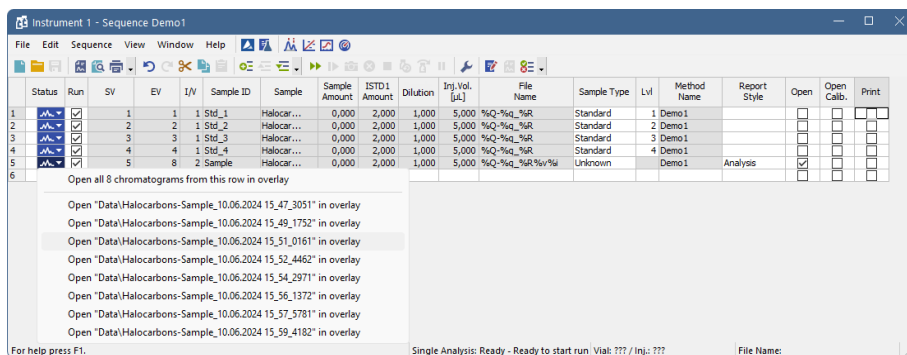


Fig. 20: Opening chromatograms in overlay

- On the right side of the *Sequence Window* you can check at each row whether corresponding chromatogram should be opened, printed or loaded into the calibration window. These columns are part of the so-called *Post-run Options*.
- In the *Sequence*, there are many more hidden columns including the rest of the *Post-run Options*, they can be displayed by right-clicking the sequence table and selecting *Setup Columns*. In the following dialog move columns that should be displayed to *Show Columns* list.

8 Connecting Autosamplers (AS)

This chapter describes the most common wiring of autosamplers. The configuration varies depending on the type of chromatograph (GC or LC), sequence mode (*ACTIVE* or *PASSIVE*), and presence of optional control modules in your **Clarity** station.

Typical configurations are:

- [AS + GC set - ACTIVE sequence](#)
- [AS + LC set - ACTIVE sequence](#)
- [AS + GC set - PASSIVE sequence](#)
- [AS with Clarity control module - ACTIVE sequence + A/D converter](#)
- [AS with Clarity control module - ACTIVE sequence + digital acquisition](#)

All of the aforementioned configurations are described in more detail in the following chapters. If your device configuration does not correspond to any of these cases, contact us at support@dataapex.com.

In an *ACTIVE* sequence, the start is controlled by the station. **Clarity** sends the permission signal to the autosampler and waits until the sampler acknowledges the injection. Data acquisition will be started after the confirmation signal has been sent back to **Clarity** and the permission to another injection is disabled.

In a *PASSIVE* sequence, the start is controlled by the autosampler. **Clarity** waits for an external start signal from the autosampler and only after receiving the signal, it starts the sequence and data acquisition.

The START synchronization between **Clarity** and the autosampler is controlled via cable pins for inputs and outputs, or by serial (RS 232) / USB / LAN port communication. The communication line is defined in the *System Configuration* dialog, which is accessible from the *Clarity* main window through the *System - Configuration...* command. The *System Configuration* dialog operates the communication line via the *External Start Digital Input* and *Ready Digital Output* functions, as described in the following text.

Data Inputs & Outputs group:

- **External Start Digital Input** ① should be set to the device and its specific pin that gives **Clarity** the information about injection being performed. Subsequently, **Clarity** starts Data Acquisition.
- **Ready Digital Output** ② defines the device and its specific pin through which **Clarity** informs other parts of the system that sequence can be run.

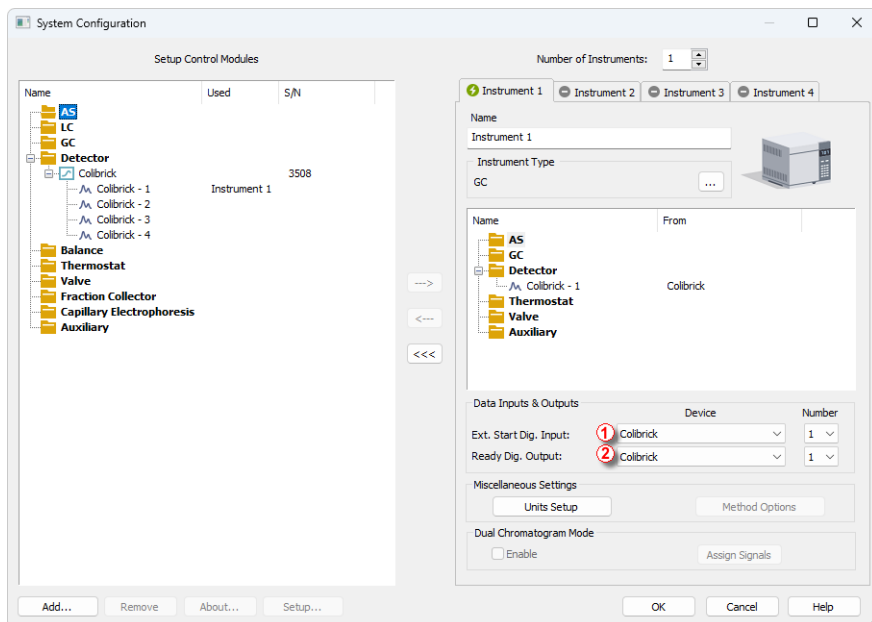


Fig. 21: System Configuration

8.1 AS + GC set - Active Sequence

In GC systems, the sample cycle is typically controlled by the GC, as the cool-down time of different systems varies due to the generally used temperature gradient. The sampler is thus synchronized with the GC by a signal wire (READY), allowing the next injection only after the GC gets to the READY state. The autosampler performs the injection and starts the GC using another signal wire (START). Any autosampler that is used in the **Active Sequence** without an **AS Control** module must be synchronized by cable with **Clarity** as well as with the chromatograph. The **IN_n** starting cable should be plugged into the synchronization output (INJECTION) of the autosampler or GC. The **OUT_nR** cable should be connected to the synchronization input between GC and autosampler.

All commonly used autosamplers may be divided into two groups:

- Variant A: Autosamplers started by **closing** the contacts on the input ($\overline{\text{READY}}$).
- Variant B: Autosamplers started by **opening** the contacts on the input (READY).

Variant A - started by closing the contacts

The first diagram shows the wiring of an autosampler that will initiate the injection after its input contact has been closed.

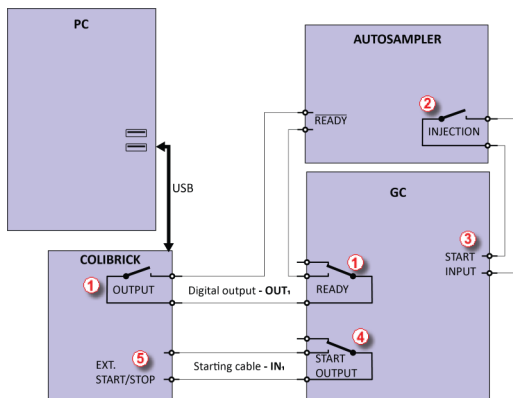


Fig. 22: Wiring of the autosampler - variant A

The injection will start only after the both serially connected contacts (**Clarity** and GC) has been closed (1). After an injection, the autosampler will close the INJECTION contact (2) and thus the command to start the temperature gradient program will be given (3). At the same time, the chromatograph will close the START contact (4), and thus the command to start acquisition will be given (5).

If the chromatograph does not have a START OUTPUT contact, then the starting cable **IN_n** must be connected directly to the INJECTION output on the autosampler (this way, in fact, parallel to the START INPUT contact of the chromatograph).

To have the contact on the **Colibrick** A/D converter opened in the initial state, it is necessary to set the *Output Initial State* item to *HIGH* in the *Digital Outputs of Colibrick* dialog as shown on **Fig. 23** on pg. **40**.. This dialog is accessible from the *Clarity* main window through the *System - Digital Outputs...* command.

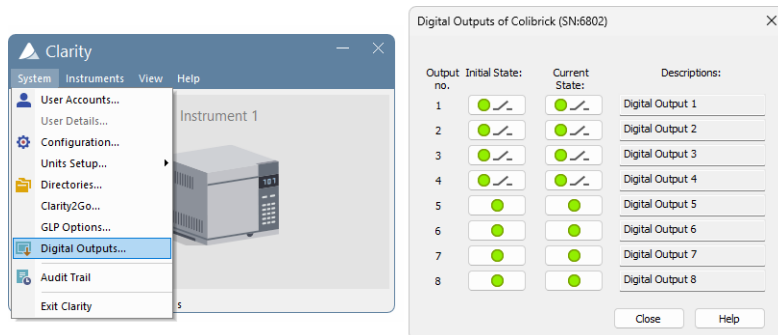


Fig. 23: The Digital Outputs dialog

The start output, mapping of **Clarity** to individual digital outputs of the **Colibrick** A/D converter, can be set in the bottom-right corner of the *System Configuration* dialog, see **Fig. 21** on pg. **37**. Use the following settings.

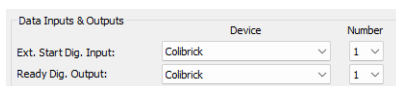


Fig. 24: System Configuration - Data Inputs & Outputs for a GC set

Variant B - started by opening the contacts

In the second diagram, there is an autosampler wiring that conversely waits for output contacts to be opened. This requires different connection (marked by a circle).

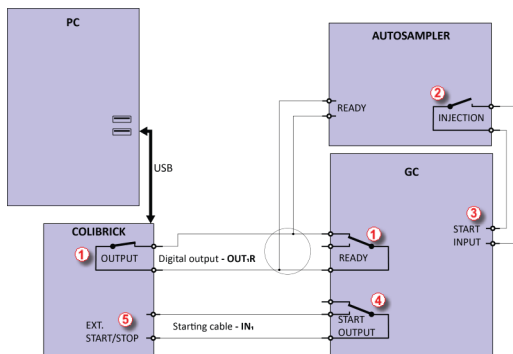


Fig. 25: Wiring of the autosampler - variant B

The **OUTPUT** and **READY** contacts are connected in parallel, and the autosampler will start its operation after both contacts have been opened ①. After an injection, the autosampler will close the **INJECTION** contact ② and thus the command to start the temperature gradient program will be given ③. At the same time, the chromatograph will close the **START** contact ④ and thus the command to start acquisition will be given ⑤.

If the chromatograph does not have a **START OUTPUT** contact, then the starting cable **IN_n** must be connected directly to the **INJECTION** output of the autosampler.

To have the contact on the **Colibrick** A/D converter closed in the initial state, it is necessary to set the *Output Initial State* item to **LOW**.

External Start Digital Input and *Ready Digital Output* settings in the **System Configuration** dialog are the same as for Variant A.

8.2 AS + LC set - Active Sequence

In LC systems, the autosampler typically governs the timings. The eventual pump gradient and detector programs are set independently. Any autosampler that is used in the **Active Sequence** without an **AS Control** module must be synchronized with **Clarity** by cables. The **IN_n** starting cable should be plugged into the synchronization output (INJECTION) of the autosampler, and the **OUT_{nR}** cable should be plugged into the synchronization input (READY) of the autosampler.

The autosampler will initiate the injection after its input contact has been closed ①. After the injection, the autosampler will close the INJECTION contact ②, and the command to start acquisition will be given directly back ③. When using additional devices (Detectors, LC Pumps, etc.) it is recommended to connect these devices independently to other digital outputs of the A/D converter ④. Each device will then need a dedicated row in the **Event Table** (Fig. 28 on pg. 43.) to be started or stopped by **Clarity**.

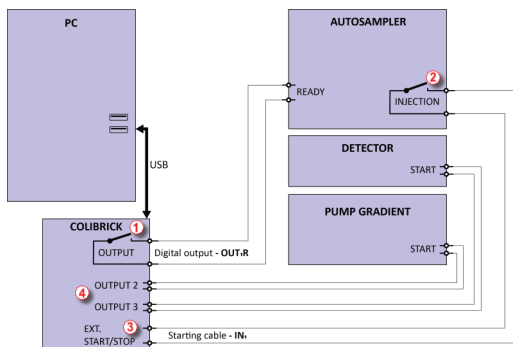


Fig. 26: Wiring of the autosampler in an LC set without the AS Control module

Note: The labels on the input and output contacts may vary depending on the type of the autosampler.

Note: When the detector or pump start inputs are connected in parallel to the **Clarity** start input, make sure to ground the device properly.

The start output, mapping of **Clarity** to individual digital outputs of the **Colibrick** A/D converter, can be set in the bottom-right corner of the **System Configuration** dialog, see **Fig. 21** on pg. **37**. Use the following settings.

Data Inputs & Outputs	Device	Number
Ext. Start Dig. Input:	Colibrick	1
Ready Dig. Output:	Colibrick	1

Fig. 27: System Configuration - Data Inputs & Outputs LC set

Events to start additional detectors and pumps from **Clarity** must be set in the **Event Table** accessible from the **Method Setup** dialog. In the most typical setup (shown in **Fig. 26** on pg. **42**.) use the setting as displayed in **Fig. 28** on pg. **43**.

Method Setup Demo1 - #4; 26.05.2023 12:26:56

Common for all detectors

	Name	Input					Output			
		Type	Source	Input	Value	Units	Output Type	Output	Parameter	Store
1	Start detector	Acq Begin	---	---	---	---	Colibrick	Digital Output 2	Pulse	<input type="checkbox"/>
2	Start pump	Acq Begin	---	---	---	---	Colibrick	Digital Output 3	Pulse	<input type="checkbox"/>
3										

Event Table Measurement Acquisition Integration Calculation Advanced

OK Cancel Send Method

Fig. 28: Event Table for starting detector and pump from Clarity

8.3 AS + GC set - Passive Sequence

The autosampler used in the **Passive Sequence** does not need the **OUT_nR** digital output cable to be connected. All timings are controlled by the chromatograph and autosampler. **Clarity** performs only one analysis for each start signal received. Synchronization includes only external start of data acquisition in **Clarity** using the **IN_n** starting cable.

The sequence must be started in **Clarity** before the autosampler. The autosampler initiates the injection after manual start on the device. The sampler is synchronized with the GC by a signal wire (READY), allowing the next injection only after the GC gets to the **READY** state. After an injection, the autosampler will close the INJECTION contact ① and thus the command to start GC will be given ②. At the same time, the chromatograph will close the START contact ③ and thus the command to start acquisition will be given ④.

Caution: It is necessary to set timings in the autosampler and **Clarity** to ensure the next injection will be performed after the previous run is finished.

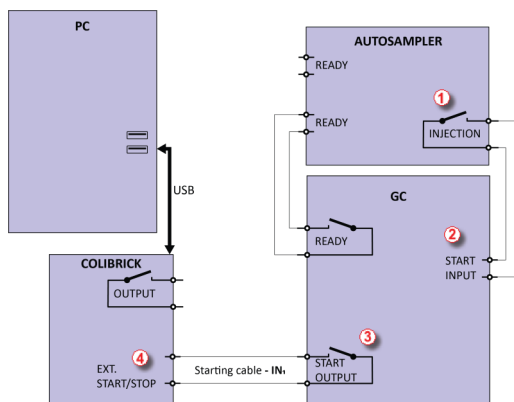


Fig. 29: Wiring of the autosampler in Passive Sequence

Passive Sequence must be used for example in the sets with Headspace autosamplers (without **AS Control** module).

Caution: It is not recommended to use the **Passive Sequence** together with the Control modules.

The start output, mapping of **Clarity** to individual digital outputs of the **Colibrick** A/D converter, can be set in the bottom-right corner of the *System Configuration* dialog, see **Fig. 21** on pg. **37**. Use the following settings.

Data Inputs & Outputs	Device	Number
Ext. Start Dig. Input:	Colibrick	1
Ready Dig. Output:	Colibrick	1

Fig. 30: System Configuration - Data Inputs & Outputs for Passive Sequence

8.4 AS with Clarity control module - Active Sequence + A/D converter

When using the optional **AS Control** (p/n **A26**) module, all communication is performed through a separate data cable (usually a serial cable connected to a COM port).

Caution: Refer to the corresponding **Clarity Control** manual (found on your installation media or at www.dataapex.com) for the wiring specific to your instruments.

The following diagram shows a directly controlled autosampler with external digital acquisition by the **Colibrick** A/D converter. In this case the digital output cable **OUT_nR** does not need to be connected. For any controlled autosampler in **Clarity**, the synchronization via starting cable is possible. Some autosamplers, however, do not need the connection of the starting cable, but can send the start of an injection over the communication line.

The autosampler initiates an injection after **Clarity** receives the command sent through a serial cable ①. After the injection, the autosampler will close the INJECTION contact ② and thus the command to start acquisition will be given ③.

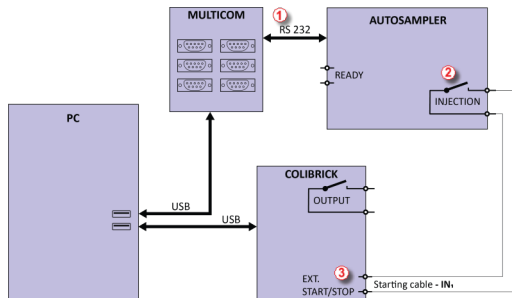


Fig. 31: Wiring of the autosampler with AS Control module + A/D converter

The start output, mapping of **Clarity** to individual digital outputs of the **Colibrick** A/D converter, can be set in the bottom-right corner of the **System Configuration** dialog, see **Fig. 21** on pg. **37**. Use the following settings.

Data Inputs & Outputs		Device	Number
Ext. Start Dig. Input:	Colibrick	1	1
Ready Dig. Output:	Colibrick	1	1

Fig. 32: System Configuration - Data Inputs & Outputs AS + A/D converter

8.5 AS with Clarity control module - Active Sequence + digital acquisition

When using optional **AS Control** module in combination with digital acquisition detectors (e.g., the Agilent 6890 module), the connection should be as follows.

All communication with **Clarity** is performed through separate data cables (usually a serial cable connected to a COM port). The autosampler initiates the injection after **Clarity** receives the command sent through a serial cable ①. After the injection, the autosampler will close the INJECTION contact ② and thus the command to start the temperature gradient program will be given ③. At the same time, the chromatograph will send the command ④ through a serial cable to start acquisition ⑤.

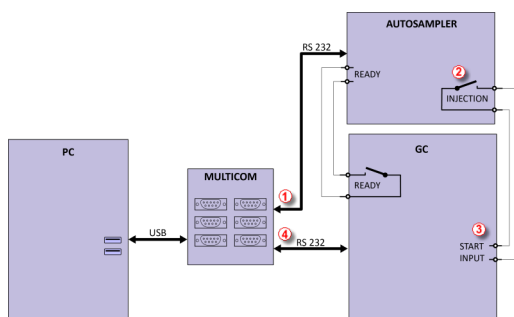


Fig. 33: Wiring of the autosampler with AS Control module and digital acquisition

The start output for specific autosamplers can be set in the bottom-right corner of the *System Configuration* dialog, see **Fig. 21** on pg. 37. Refer to the corresponding **Clarity Control** manual for the wiring to your instruments.

9 Navigating Early Challenges: Common Beginner Missteps

This chapter explains a few most common issues you may encounter while learning how to use Clarity. For a more comprehensive list of potential issues and their solutions, please refer to the *Troubleshooting* section in the User Guide manual where additional issues and explanations are provided.

When troubles occur, the fastest way to find a solution is to read the context help (accessible by pressing F1), or search our online Clarity [documentation](#). You can search there using keywords such as the name of the **dialog** or **window** where the problem occurred, the text of **error messages** that appeared, or the used **hardware**.

9.1 Missing HW key

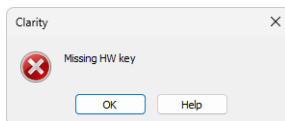


Fig. 34: Missing HW key error dialog

If you try to start **Clarity** without the key, an error message saying "Missing HW key" is displayed and **Clarity** will not start. The key must be plugged into a USB port and its driver must be properly installed. Under normal circumstances, USB drivers are automatically installed upon inserting the key into a USB port.

Reason 1: Your HW key may not be connected correctly.

Solution: Check if the key is properly inserted in the USB port. Check whether the USB port is working (e.g., try to connect a different device, etc.), check if the HW key diode is lighting steadily, if blinking or is dimmed try another USB port.

If this does not help, continue to *Missing HW key* topic in the User Guide, where also more complex reasons for this issue are explained.

9.2 The User Code is not accepted

The User Code is not accepted and thus Clarity cannot be started. In the case the User Code is intended for unlocking additional extensions/add-ons for the station, the previously used accepted one is still saved.

If necessary, contact the manufacturer or your distributor to request the correct User Code. In this case, be prepared to provide the serial number (S/N) of the workstation.

Note: The *User Code* dialog does not distinguish between upper case and lower case letters. However, be careful not to confuse the letter "l" with the number "1".

9.2.1 The User Code is not valid for version x.y

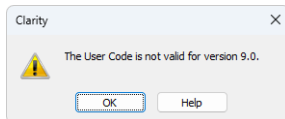


Fig. 35: The User Code not valid for version error dialog

Reason: You have probably entered a User Code for a different version.

Solution: You have to enter the User Code corresponding to your current version. For example, when you purchase additional extensions/control licenses, a new User Code is generated for your station. The new User Code is valid only for the most recent Clarity major version, so you will probably need to install the latest version of the software.

9.2.2 Wrong User Code

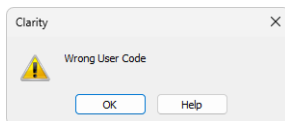


Fig. 36: Wrong User Code error dialog

The User Code of the workstation does not match the code in the HW key.

Reason: You have entered a User Code that does not match the serial number of the HW key plugged into the PC.

Solution: Submit a correct User Code. The User Code can be found on the back of the plastic card provided with the installation USB.

9.2.3 Wrong Software Version

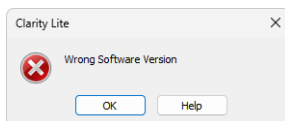


Fig. 37: Wrong Software Version error dialog

Reason: You have probably installed a different application than you had purchased. For example, you installed Clarity Lite instead of Clarity.

Solution: Install the correct application you had purchased. If you are not able to locate the correct installer, contact the manufacturer or your distributor.

9.3 Trial Expired

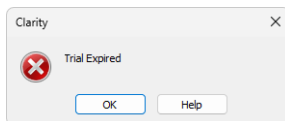


Fig. 38: Trial Expired error dialog

The Trial period (time period when Clarity works without a User Code filled in) expired. You are prompted to enter a User Code or a Trial Prolongation Code.

Reason: Your Clarity station just ended its trial period.

- Solution:*
- Enter the correct User Code, which switches Clarity from the Trial mode into the full mode ①
 - Or switch to section ② and enter a Trial Prolongation Code to extend the trial mode period. Trial Prolongation Codes must be requested from your distributor or DataApex.
- Once a correct User Code or Trial Prolongation Code has been provided, click the **OK** button to start Clarity.

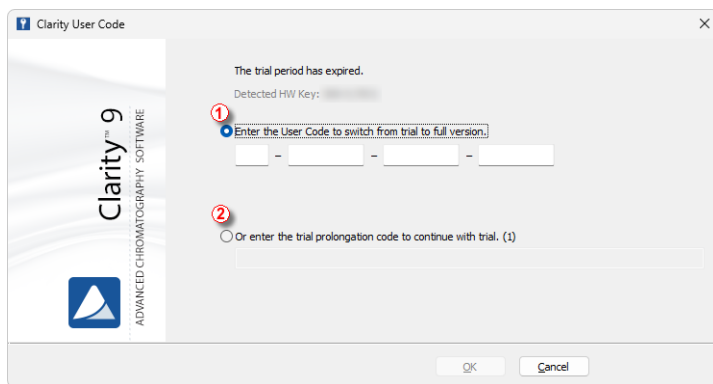


Fig. 39: Clarity User Code

9.4 Data Acquisition - Disabled

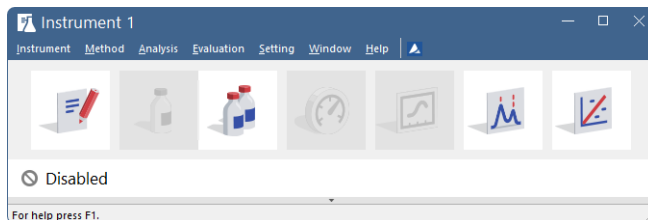


Fig. 40: Data Acquisition disabled

The "Disabled" label appears, and the *Single Analysis* dialog and *Data Acquisition* windows are not available. Other manifestations of this error are also: *Method Setup - Acquisition* tab missing, *Run*, *Stop*, and *Abort* commands non-functional in the *Sequence* window.

Reason 1: No detector is allocated to the Clarity Instrument.

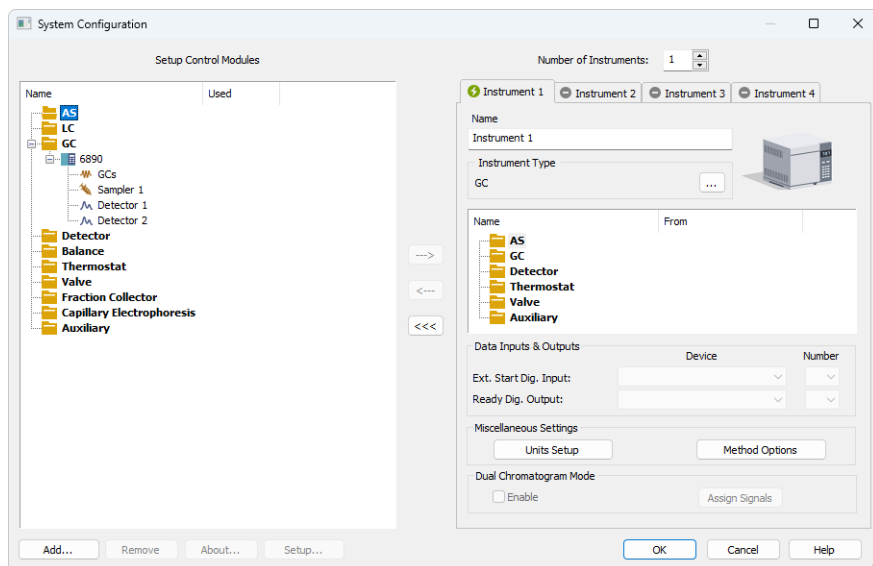


Fig. 41: Detector not allocated to the Instrument

Solution: Open the *System Configuration* dialog from the *Clarity* window using the *System - Configuration...* command and check the tab of the corresponding Instrument - **Instrument X**. If it has no allocated detectors, add them.

In the list on the left side of *Setup Control Modules*, select the correct detector, and drag it to the corresponding instrument section on the right.

If the appropriate detector is not in the list, add it using the *Add* button and repeat the previous step.

If this does not help, continue to *Data Acquisition - Disabled* topic in the User Guide, where also more complex reasons for this issue are explained.