DataApex
Clarity™
CHROMATOGRAPHY SOFTWARE

DUAL CHROMATOGRAM MODE

Clarity Extension ENG

Code/Rev.: M251/100A
Date: 2024-10-29

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To facilitate the orientation in the **Dual Chromatogram Mode** 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 Dual Chromatogram Mode

The **Dual Chromatogram Mode** is a mode of operation with autosamplers in **Clarity Chromatography Software**. It can be used also in **Clarity Offline** to prepare files for measurement or to evaluate chromatograms previously measured in Clarity.

The **Clarity Dual Chromatogram Mode** enables the processing of data acquired by systems with dual-tower samplers if the option to set the *Back Injector Offset* is implemented in the sampler method (e.g., Agilent ICF Autosamplers). It can also split detector signals into two separate chromatograms if needed.

2 Specification

The **Dual Chromatogram Mode** is a specific operation mode mainly used with autosamplers in **Clarity Chromatography Software**.

Conditions for enabling the mode:

- AS Control (p/n A26) enabled in **Clarity**
- At least two detector signals configured on the Instrument

The **Dual Chromatogram Mode** is compatible with GC and LC *Instrument Types*, as well as the DHA, NGA, and PDA Extensions.

3 Installation & Setup

The *Dual Chromatogram Mode* is already available in the installed Clarity.

To enable the *Dual Chromatogram Mode* on an Instrument, set a supported *Instrument Type* ⓐ (e.g., GC) in the *Instrument Type Setting* dialog. Assign at least two detector signals to the Instrument ⓑ and check the *Enable* checkbox in the *Dual Chromatogram Mode* section ⓒ .

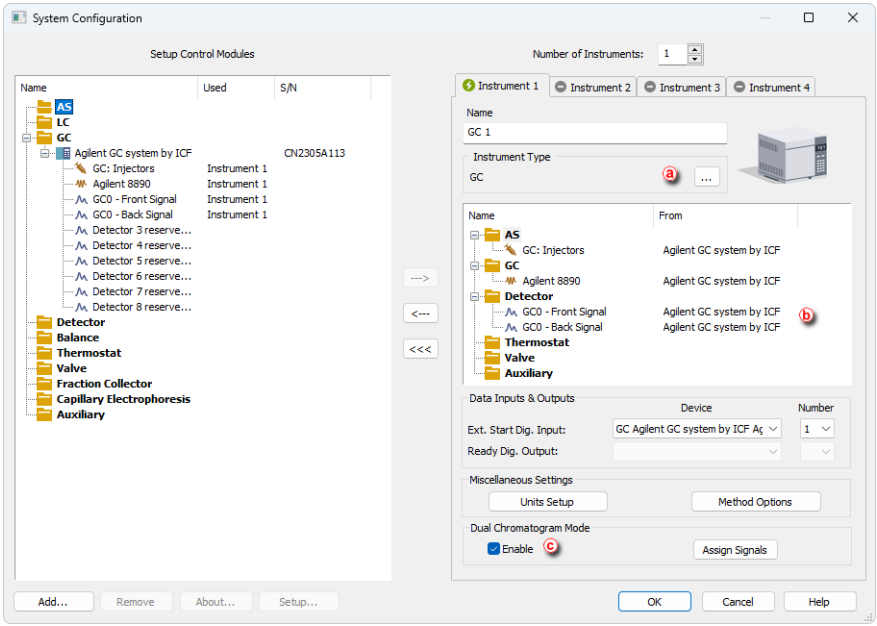


Fig. 1: System Configuration - Dual Chromatogram Mode

It is also necessary to assign at least one signal to both the *Front* and the *Back position* in the *Dual Chromatogram Mode - Assign Signals* dialog.

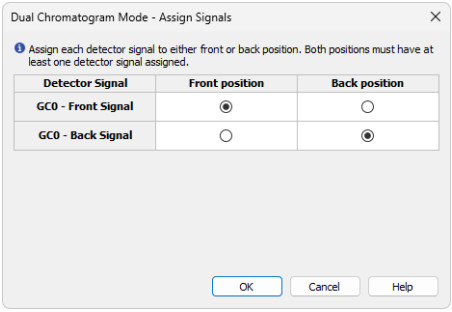


Fig. 2: Dual Chromatogram Mode - Assign Signals

4 Dual Chromatogram Mode Description

This chapter lists and describes the features changed in or added into Clarity by the *Dual Chromatogram Mode*.

4.1 Method Setup

When the *Dual Chromatogram Mode* is enabled, every signal in the ***Method Setup*** is also labelled by the position which it has been assigned to (for example, on the *Integration* or *Acquisition* tabs). The *Calculation* and *Advanced* tabs are divided to two sub-tabs, one for each position.

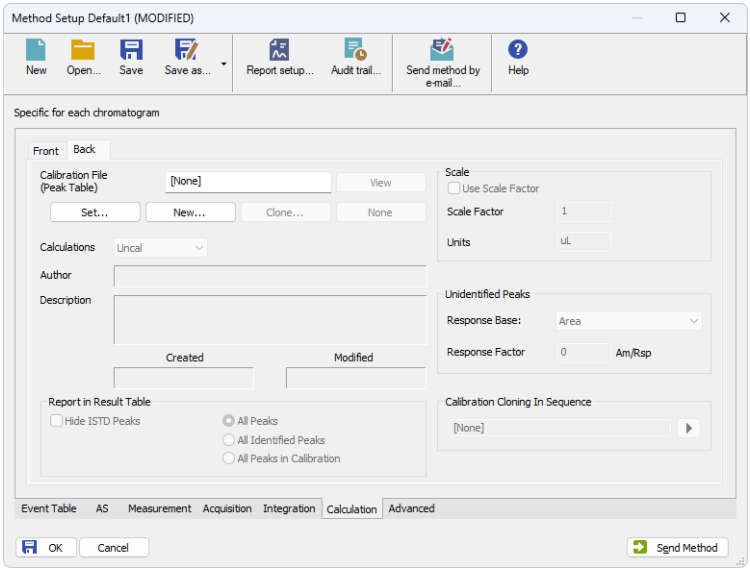


Fig. 3: Method Setup - Calculation tab - Back position sub-tab

In order to save a method:

- in the *Calculation* tab, the *Calibration File* has to be set for both position to a different file, or not set at all
- in the *Calculation* tab, the name of the cloned calibration in the *Calibration Cloning in Sequence* also has to be set for both, or not at all

In the reports, there are always printed sections for both positions. They are identified by the *Front* and *Back* labels.

As the *Subtraction Chromatogram* (on the *Advanced* tab) is set for each position separately, the option *File - Show Subtraction Chromatogram* in the *Data Acquisition* window is not available. Individual chromatograms can still be displayed using the *Set Background Chromatogram* option.

4.2 Single Analysis

The *Dual Chromatogram Mode* is not intended for use with *Single Analysis*. The sampler cannot be operated from this window. If a measurement without a sampler is carried out from the *Single Analysis* window, all settings (e.g., *Sample ID* and *Sample* fields) will be applied to both created chromatograms . The inputted name is appended by the identification of the detector signal position (-Front or -Back).

4.3 Sequence

In the ***Sequence*** window, the columns meant for sample and chromatogram identification are duplicated so it is possible to input different values for the *Front* and *Back* position chromatograms. The duplicated columns are: *SV*, *EV*, *Sample ID*, *Sample*, *File Name*, and *Line Info*.

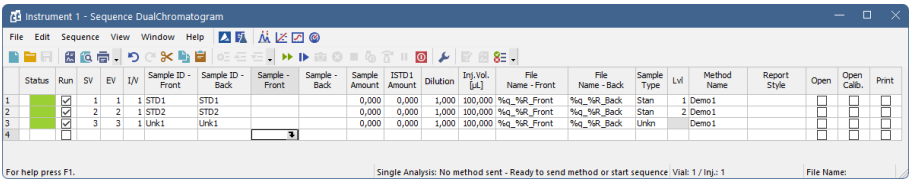
Caution: The *SV - Back* and the *EV - Back* columns are hidden by default and serve only as informative columns for the user. They do not influence which vial is used for the *Back* position, it is still determined by the vial for the *Front* position and the offset set in the used method. The *SV - Back* and *EV - Back* columns can be left empty, in which case the variable *%v* is filled based on vial set for the *Front* position for both positions.

Note: The *EV - Back* column is not modifiable. It is calculated based on *SV - Back* and values for the front position. If the *SV - Back* is left empty, *EV - Back* is empty as well.

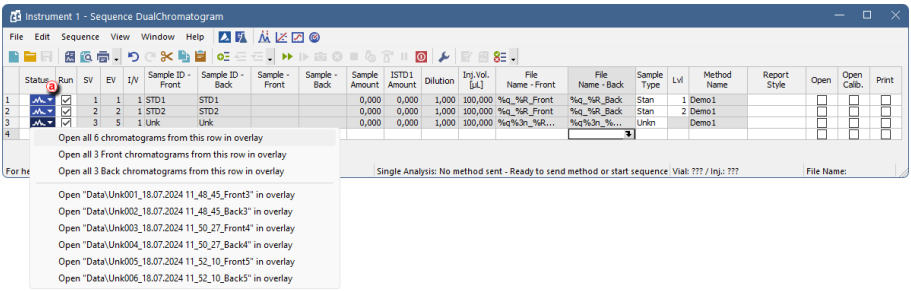
It is possible to quickly display only the *Front* or *Back* position columns or both by the *Front Only*, *Front & Back*, and *Back Only* commands in the *View* menu. This does not affect the columns not distinguished by the detector position.

Note: The variable *%f* (vial barcode) is not allowed in the *Dual Chromatogram Mode* (the sequence validation fails if *%f* used).

The sequence created within the *Dual Chromatogram Mode* cannot be opened in the standard mode and vice versa. It is necessary to create a new sequence or export the sequence, turn the Dual Chromatogram Mode ON/OFF, import it back, and make necessary changes.



It is possible to open all *Front* or *Back* chromatograms at once. In the *Sequence* window, a menu appears by clicking the arrow in the status cell of a measured line ⓐ . Here you can select which chromatograms to open.



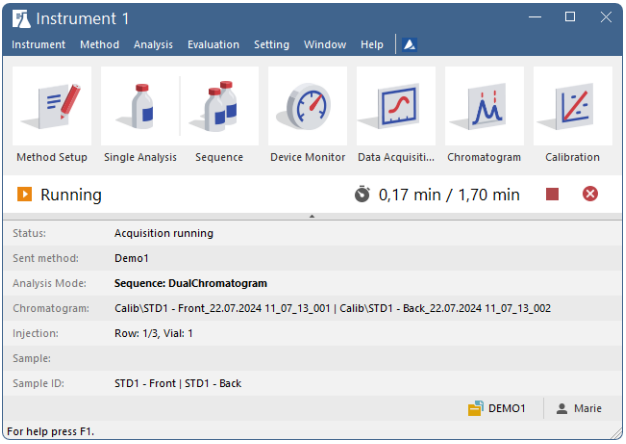
Sequence import is adjusted to consider the duplicated *Front*/*Back* columns present in the *Dual Chromatogram Mode*.

4.4 Instrument

During measurement, in the *Instrument* window, the *Chromatogram*, *Sample*, and *Sample ID* rows are divided in half to display both the *Front* and the *Back* position contents. If the content for both position is the same, it is displayed only once.

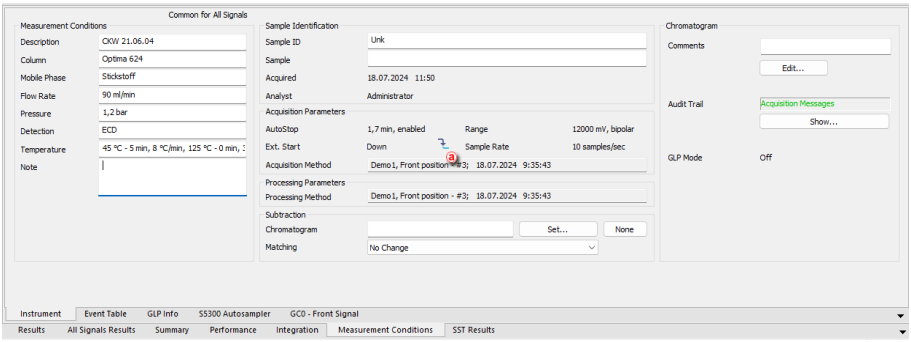
Caution: The *Injection* row only displays the vial used for the *Front* position.

Note: The display of the analysis works the same way in Clarity2Go: the rows are divided in half to display both the *Front* and *Back* position content.



4.5 Chromatogram

In the *Chromatogram - Measurement Conditions* pane, *Instrument* sub-tab, the position in which the chromatogram was acquired is included in the *Acquisition* and *Processing Method* info ⓐ .



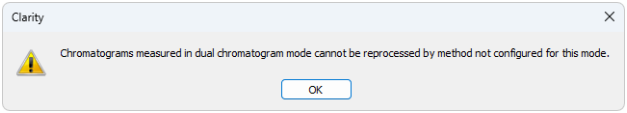
Import of chromatogram and mathematical operations always apply the setting for the *Front* position of the method.

If the *Report Header - Chromatogram Info* checkbox is selected in the *Report Setup*, the reports contain an additional item *Dual Mode*, which states *Front/Back*, depending on the position in which the chromatogram was created.

4.6 Reprocessing

Reprocessing by method is possible in the standard manner using the *Batch* dialog or directly in the *Chromatogram* window using the *Method* menu. Integration tables can also be copied into the method directly in the *Method Setup* dialog.

In general, if you reprocess by a method from any location, both files have to be saved in the *Dual Chromatogram Mode* (or both in the standard mode). In the case of the *Dual Chromatogram Mode*, the *Front* position signals of source are mapped to *Front* position signals of the target (and analogously for the *Back* position).



On the contrary, if you reprocess using a chromatogram (e.g., by *Copy from Chromatogram*), it does not matter whether it originates from the *Front* or *Back* position. The part that is used as the processing method in this chromatogram (meaning the part that is visible in the user interface) will be used in the target file.

5 Clarity Dual Chromatogram Mode operation

This chapter describes the basic operating principles for working within the **Clarity** *Dual Chromatogram Mode*. Some operations overlap with the standard mode procedures; in such cases, you will be referred to detailed descriptions of the standard operations in the **Clarity User Guide**.

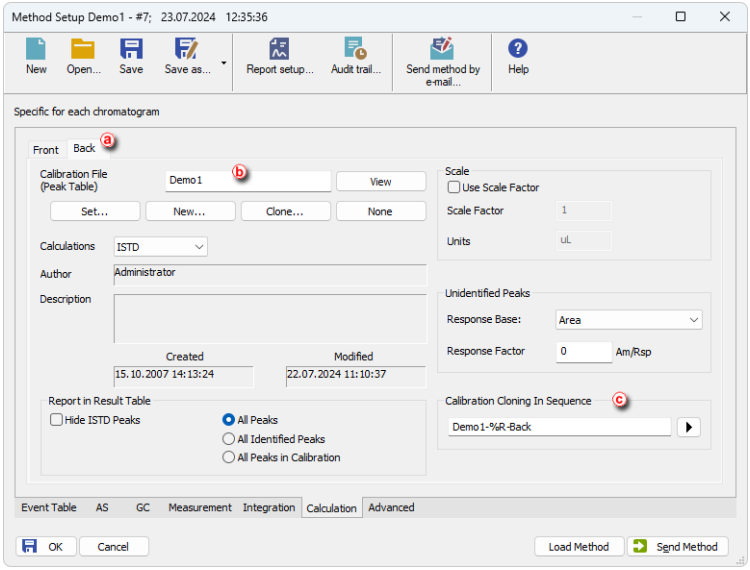
The typical workflow for individuals conducting routine analyses in the *Dual Chromatogram Mode* should include:

1. Setting the Instrument to the Dual Chromatogram Mode

In the *System Configuration*, enable the *Dual Chromatogram Mode* and assign *Detector Signals* to the *Front* and *Back* positions. For more details, see Installation & Setup - Dual Chromatogram Mode topic.

2. Creating a method

- In the *Method Setup* dialog, create a new method, or adapt an already existing one to the *Dual Chromatogram Mode* configuration.
- Set the acquisition parameters for all controlled devices.
- Fill in the *Run Time* on the *Measurement* tab.
- If you want to calibrate the results, for each detector signal position ⓐ , set different *Calibration Files* ⓑ . Also, fill in the name of cloned calibration ⓒ for both positions if calibration cloning will be performed.



The *User Guide - Create Calibration* topic contains detailed instructions on how to create a calibration.

- Fill in any other necessary method parameters (e.g., auxiliary signals settings).

The method development is in principle the same as described in the *User Guide - Setting up a method* topic.

3. Creating & running a Sequence

Prepare sequence according to your needs. Do not forget to fill in a unique file name for both detector signal positions.

Preparation of a sequence is in principle the same as described in the *User Guide - Creating and running a sequence* topic.