Clarity (Lite)

2.4 vs 2.3

ENG

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About this manual

This manual introduces main differences in the **Clarity** and **Clarity Lite** stations between the versions **2.4** and **2.3**.

For complete documentation it is recommended to download the updated **Reference Manual** in PDF format from our website www.dataapex.com (section **Downloads – Manuals**).

Passages concerning the full version only are distinguished by the following logo ✓Full version in the manual and marked with a grey stripe to the right of the text.

Protection of Clarity

Protective key

Clarity (since version **2.4**) will always require the protective key - dongle (USB or LPT port).

The **User Code** does not have to correspond to a specific serial code of the A/D converter.

Caution! *When you upgrade to **Clarity** version **2.4** you will not be able to use previous versions of **Clarity**!*

30 day TRIAL version

With a hardware key, the user has a possibility to test the station without entering the proper User Code - the station will work in the full mode for **30 days** or **100 sessions** (whatever comes first).

Chromatogram

Global Peak Width

From interactively selected interval calculates the *Peak Width* parameter for the whole chromatogram. The 🏔 **Global Peak Width** can be set also manually in the first row of the **Integration Table** found in the **Chromatogram – Integration** window).

The interval has to contain the narrowest peak that should be still integrated.

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Note: *To see the value of the automatically set **Global Peak Width** parameter switch to the Integration tab.*

Global Threshold

From interactively selected interval calculates the *Threshold* parameter for the whole chromatogram. The 🖾 **Global Threshold** can be set also manually in the second row of the **Integration Table** found in the **Chromatogram – Integration** window)

This interval must contain only noise!

Note: *To see the value of the automatically set **Global Threshold** parameter switch to the Integration tab.*

Local Peak Width

Defines the method of integration of peaks (icon 🖾) on a specified interval.

The **Peak Width** parameter is determined by the narrowest identified peak and influences the number of points used in the evaluation. The value must be within the range of *0.001 - 10* minutes.

Caution!   *Setting an excessively high value will distort the results.*

Local Threshold

Determines the noise threshold (icon 🖾) on a specified interval.

The **Threshold** parameter determines the sensitivity of the integration algorithm while detecting the beginning and end of a peak.

Caution!   *The height of all peaks (measured from the baseline to the top) which you wish to detect should be at least <u>twice this parameter</u>. The value must be within the range of* $1 \mu V - 10 V$.

The Local Peak Width /Threshold command procedure:

- You will be prompted to place the cursor lines to the beginning and end of the interval and mark each by left-clicking the mouse. The 🖾 **Local Peak Width / Threshold** parameter will be applied within this interval only.
- Then the **Peak Width**/**Threshold** dialog will open in which you may adjust the graphically set interval in

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the **Start Time** and **Stop Time** fields and enter the required peak width into the **Value** field.

- By clicking the **Suggest Value** button user can interactively select:

    For **Local Peak Width** - interactively select the narrowest peak that still has to be integrated

    For **Local Threshold** - the highest "peaks" that still should not be integrated (again using the cursor lines).

- Suggested value will be transferred to the **Value** field.

Note: *Keep in mind that the suggested* **Local Threshold** *value will be half of these "highest" peaks because only peaks twice the size of the noise threshold will be detected.*

Note: *The* **Peak Width** *value is not critical, so narrower peaks than the set value are also detected, but this may lead to an imprecise definition of the beginning and end of the peak and incorrect interlining of the baseline.*

- Click **OK** to apply the selected value to the specified interval.

Note: *The value as well as the interval can be later edited in the* **Integration Table**.

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Fast browsing through chromatograms

The new **File - Open Chromatogram Sequentially** command from the **Chromatogram** window opens chromatograms from the last folder opened using **Open Chromatogram** command.

Caution!   *The **Sequential Opening** will be active only if the **Overlay** mode is **OFF**.*

◄| **First**   Opens first chromatogram from current folder (CTRL + F7)

◄   **Previous**   Opens the previous chromatogram from current folder (F7)

►   **Next**   Opens the next chromatogram from current folder (F8)

►| **Last**   Opens the last chromatogram from current folder (CTRL + F8)

Filters and sorting applied in the **Open Chromatogram** dialog can limit the list of chromatograms for the **Sequential Opening** that will be performed later using the icons in the **Chromatogram** window.
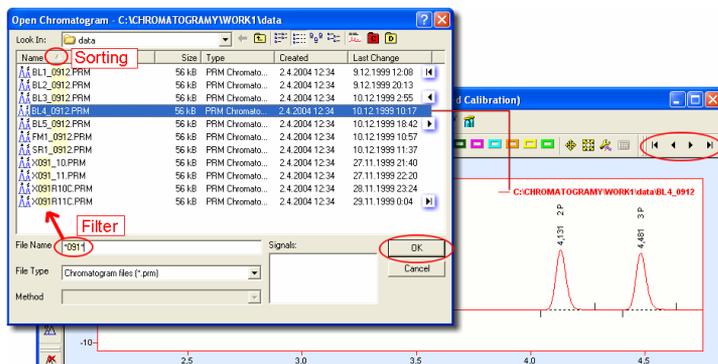
To apply sorting and filtering do the following:
- Check that the **Overlay** mode is **OFF**.
- Use the **File - 📖 Open Chromatogram** command and navigate to the folder from which you want to open chromatograms.

- Specify the <u>filters</u> by writing partial name in the **File Name** field and **Sorting** to limit the set to desired chromatograms only.

Note: *It is possible to use the wildchars (*** ?**) like in the example displayed in the image (*O91*).*

- Click the desired column header to set ascending/descending <u>sorting</u> according to that column.
- Select a chromatogram from the defined set and open it using the **OK** button.
- In the **Chromatogram** window use the commands from **File - Open Chromatogram Sequentially** menu or icons ⏮ ◀ ▶ ⏭ to browse through the chromatograms from the defined set.

  The **Open Chromatogram Sequentially** function will always open the whole chromatogram (all of its signals).

Automatic FFT filter

The **FFT** **FFT Filter On** command from the **Chromatogram** window applies the **FFT Filter** (*Fast Fourier Transformation*) for signal smoothing to a selected interval.

The **FFT** **FFT Filter Off** command suspends the **FFT Filter** (*Fast Fourier Transformation*) for signal smoothing on selected interval.

Text Imports

Improved and extended text import of chromatograms

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Balloon Tool Tips

Interactive chromatogram modifications were extended by a more detailed **Status Line** and by optional 💬 **Balloon Tool Tips** on the cursor.
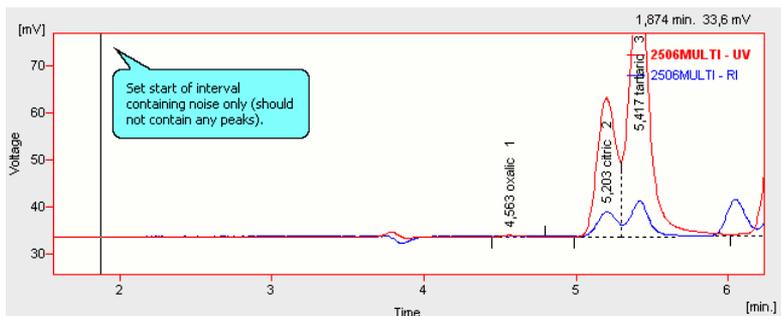
Note: *This function is available only in **MS Windows 2000** and later.*

Opening of Chromatograms

If the external calibration file cannot be found while opening the chromatogram, stored calibration will be offered instead

Detector Names

It is now possible to set the **detector names** also in single detector chromatograms using the **Chromatogram - Set Signal Names** command in the **Chromatogram** window.

Calibration

LOD, LOQ

The possibility to set the *Limits of Detection* (**LOD**) and *Limits of Quantification* (**LOQ**) in the **Calibration** window.

The exceeding of the limits will be displayed in the **Result table** (**Chromatogram – Results**). The exceeded limit will be indicated by the "< *LOD*" or "< *LOQ*" inscription in the **Peak Type** column.

Retention (Kovats) indexes

New **Reten. Index** column in the **Calibration Summary Table** in the **Calibration - Compounds** window enables to set the retention indexes.

Note: *In the implicit layout the **Reten. Index** is not visible. Use the **Edit - Setup Columns** command to display it.*

Calibration Template

The default parameters for new calibrations can be set by the TEMPLATE.CAL template file stored in the **Clarity's** COMMON directory (C:\CLARITY\COMMON\ by default).

When **Clarity** is running in **GPC** or **EA** mode corresponding files e.g. EATEMPLATE.CAL can be used.

If the template files do not exist, the new calibrations will be based on values internally preset in **Clarity**.

Floating Averages

The template calibration can be used to set for example the recalibration to work with the *floating averages*.

To do that:

- In the **Calibration** window use the **File – Open** command and navigate to the C:\CLARITY\COMMON directory and open the TEMPLATE.CAL calibration file.
- Open the **Calibration Options** dialog using the **Calibration – Options** command and set the desired **No. of Points** for the averaging.

Possibility to erase responses

Clone and **Save As Calibration** commands have been extended by the option to erase all responses. So that the new file contains for example definitions of peak starts, identification windows and amounts for future recalibrations, but not the responses.

Sequence

PostRun functions for each row

The sequence has been extended by the possibility to select **PostRun** functions for each row separately.

The columns **Open**, **Open Calib.**, **Print**, **Print to PDF**, **Export Data**, **Export AIA**, **Export TXT**, **Export EZChrom**, **Export Multidetector**, **Run Program**, **Program to Run** correspond to the analogous items in the **PostRun Setting** dialog.

When the sequence is running the indication of the **PostRun** switches in the **Instrument** window will be locked to the state set on the currently running row.

Note: *In the implicit layout only the **Open, Open Calib.** and **Print** columns are visible, the rest of the columns are hidden. Use the **Edit - Setup Columns** command to display the desired columns.*

All the **PostRun** switches can be modified before applying the **Complete Processing** from the **Batch** dialog. All other settings of the **Sequence Table** will be <u>locked</u>.

Sequence Template

The default parameters for new sequences can be set by the TEMPLATE.SEQ template file stored in the **Clarity's** COMMON directory (C:\CLARITY\COMMON\ by default).

When **Clarity** is running in **GPC**, **PDA** or **EA** mode corresponding files e.g. EATEMPLATE.SEQ can be used.

If the template files do not exist, the new sequences will be based on values internally preset in **Clarity**.

Stop actual analysis

The 🛑 **Stop** command ([Ctrl] + [T] shortcut) normally halts the running of a sequence. Currently running acquisition will be completed.

If the 🛑 **Stop** is used **second time**, it will <u>stop</u> also the <u>acquisition in progress</u>. Data from the partially finished acquisition <u>will be saved</u> (unlike after the ❌ **Abort** command). If there is a running control program it will keep running.

Note: *To stop also the control program use the* ❌ *Abort command.*

Optimized sequence

The <u>speed</u> of the sequence table and improved <u>pre-run check</u> provide more comfort to the working with the sequence table.

Instrument   ✓Full version

Sending method to controlled instrument   ✓Full version

Directly controlled instruments have an option to send the control method to the device automatically/upon prompt.

The 🔽 button in the **System Configuration** dialog invokes the **Instrument Method Sending** dialog.

It sets whether the LC/GC/AS method has to be sent to the instrument (device) at each change of the template method.

After Each Method Change

The method change occurs when:

- Opening the **Instrument** window (it automatically loads template method)
- Loading new template method to the **Instrument** window using the **File – Open** command
- Changing the currently opened template method (i.e. after editing the **Method Setup** dialog).

Send Method to Instrument - The LC/GC/AS method will be sent to the instrument (device) automatically without prompt.

Note: *This used to be the default for **LC Control**.*

Prompt for Confirmation – At each method change Clarity will display the **Send Method Confirmation** dialog in which the sending of the method may be confirmed or suppressed.
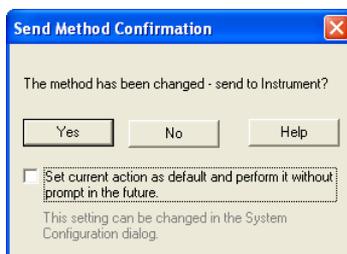
Do Not Send Method to Instrument – Clarity will not send LC/GC/AS method to instrument (device) on every change.

Note: *This used to be the default for **GC Control**.*

The setting is <u>individual</u> for each **Clarity Instrument**.

The setting is <u>common</u> to all instruments (GC/LC/AS devices) attached to the same **Clarity Instrument**.

Regardless on the setting the LC/GC/AS method <u>will be sent</u>:

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- Before each injection from the <u>running</u> **Active Sequence** according to the **Sequence Table**.
- **Manually** using the **Send Method** button from the **Single Analysis** dialog.

Switching Instrument to GPC Mode   ✓ Full version

To enable **GPC Mode** on a **Clarity Instrument** it must be first set in the **Instrument Type** section of the **System Configuration** dialog.

Note: *GPC is an Add-On module, that has to be purchased.*

In the **Instrument** window the **GPC Mode** can be switched On/Off using the **Setting – GPC Mode** command.

Report Setup

Direct printing to PDF format

- All reports can be printed to PDF document using the **File – Print to PDF** command located in the menu of all major **Clarity** windows.
- The printed PDF file can be automatically enclosed as an attachment of an email using the **File – Send printed PDF by Email** command located in the menu of all major **Clarity** windows.

Improved Reports

- Thanks to new options in the **Report Setup - Report Header** dialog reports can print filenames with full path or without the path (only for files within the project.

- Reports can print extensive **GLP information**: version of **Clarity**, name of the PC, User, etc.)
- ✓ **Full version**
  Printing of the **SST Table** extended by the option to print **Active Signal** only or **All Signals**.

Other

- The **Digital Output Control** dialog now displays the state of the relay contact visually
- The zooming on CTRL + Mouse wheel now conforms to **MS Windows** standards
- The **Open Chromatogram** dialog has been extended by information about applied *electronic signatures* and *PDA data*.
- The **User Columns** are now available also in the **GPC Result Table**.

Add On Modules   ✓ **Full version**

New and improved **Add On** modules.

PDA module   ✓ **Full version**

PDA module is an integrated add-on module for acquisition, display and evaluation of "3D" chromatograms from **PDA** (**DAD**) detectors.

Note: *Detailed information can be found in a separate **PDA Module** manual*

Clarity EA   ✓ **Full version**

Modified version of **Clarity** for measuring and evaluating of **Elemental Analyses**.

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Note: *Detailed information can be found in a separate **EA Module** manual*

Agilent 1100 ✓Full version

Control module for direct control of **Agilent 1100** HPLC set using the **HPIB** or **LAN** interfaces.

Note: *Detailed information can be found in a separate **Agilent 1100 Module** manual*

Agilent 6890N ✓Full version

Current control module for **Agilent 6890 GC** has been significantly extended by the support of **LAN** communication.

Note: *Detailed information can be found in a separate **Agilent 6890 Module** manual*

Net-PAD ✓Full version

External **LAN A/D** converter with **Ethernet** interface and **TCP/IP** protocol.

Note: *Detailed information can be found in a separate **NetPAD** manual*