
Clarity

Clarity vs CSW32

ENG

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Multiple detector Arrangement

1 Measuring with up to four four-detector chromatographs simultaneously

The **Clarity** station allows signals to be measured from up to four detectors simultaneously and saved in a single chromatogram. The channel orientation of **CSW** stations has been substituted by instrument orientation, and what used to be called channel windows are now in the **Clarity** station represented by whole chromatographs (instruments), and hence we call them now instrument windows. One instrument represents one time base.

2 Working with the method

Measurements and evaluations, same as with the **CSW** station, are determined by the template method file opened in the **Instrument** window. The method is divided into several parts, which correspond to different tabs. Some tabs are common for all detectors (**Measurement Conditions**, **Calculations**, **GC/LC/AS Control**), parameters of others (**Acquisition** and **Integration**) can be set for each detector separately.

3 Saving signals

Signals measured by all detectors are saved in a single file – chromatogram. When opening the file, you can choose whether all signals are to be displayed or only selected ones.

4 Displaying and evaluating signals

- In the window **Chromatogram**, each signal is displayed as a separate chromatogram. In the toolbar **Overlay**, the belonging of the signals to a single chromatogram is indicated by a connecting line underneath the colour symbols of each signal. The **Open**, **Save**, **Close** and other commands of course work with all signals of the same chromatogram simultaneously.
- Name of each signal consists of the chromatogram name and the detector name at the time



of measurement. The names of all signals are displayed in the **Chromatogram** menu and in the legend located in the top right corner of the graph. Name of the active signal is displayed in the header of the **Chromatogram** window and also in the header of **Result** and **Integration** tables.

- The Result table always applies to the active signal. The same applies to the integration table, and hence all operations from the **Chromatogram** menu (adjustments of the baseline, peaks, etc.) are made only with the active signal.
- On the other hand, calculation parameters including the calibration file and parameters on the **Chromatogram - Measurement Conditions - Instrument** tab apply to all signals of the active chromatogram.
- If you need to display the results of all signals of a single chromatogram simultaneously, use the summary table –**Summary** tab.

5 Calibration and multiple detectors

The **Clarity** station's multiple detector arrangement leads to a multiple detector version of calibration files. Each chromatogram is linked to only one calibration file, which might contain a set of independent calibration curves for each signal.

- The list of substances in the main calibration table in **Calibration - Compounds** window is common for all signals. Same applies to retention time, identification windows and compound type.
- Other parameters, particularly **Response** and **Amount**, are signal-specific. These parameters are distinguished by different colours, always corresponding to the active signal colour.
- You can set the active signal using the **Calibration - Set Signal** command, or by clicking on the relevant colour square in the main toolbar.
- The active signal is also set automatically in accordance with the active signal of the displayed calibration standard, or with the chromatogram's active signal in the **Chromatogram** window which uses this calibration.
- The active signal's name is displayed in the calibration table header.



- The number of displayed signals is determined by the saved status or by the number of signals of the displayed calibration standard.
- Commands for creating calibrations (**Add All**, **Add Existing**, etc.) transfer only values of active signals.
- Automatic calibration in the sequence transfers values of all signals.

6 Other file formats

The transition to multiple detector arrangement and the **21CFR Part 11** conditions called for a change of all file formats. However, the **Clarity** station of course maintains compatibility with the formats of all previous **CSW** stations. When opening an older format file, the system will remind you, and when you save it, it will be automatically converted to the new format. If you for whatever the reason wish to maintain the original format, or if you want to convert a file into an older format, you can do so by using the **Save As** instead of the **Save** command, and select the relevant format in the **File Type** item.

Caution! *Be aware that older formats do not allow most of the new features and parameters of the **Clarity** station to be saved.*

7 Configuring the station

With the transition to multiple detector arrangement, the method of configuring the station has changed. It is done in the **System Configuration** dialog.

- First using the command **Add**, add to the list on the left-hand side all devices available which you intend to use. Then simply drag the relevant device or its part from the left-hand list to the selected instrument's tab.
- Unlike with the **CSW** station, you can for each instrument choose its own icon, assign to it any available digital input and output port to synchronise it with the chromatogram or autosampler, and also name all connected detectors.



Tools to Support 21CFR Part 11

8 Electronic signature

One of the key new features of the **Clarity** station is the implementation of electronic signature.

- Current version of the chromatogram can be signed, using the **File - Sign** command in the **Chromatogram** window.
- You can sign the chromatogram either as an active user, making use of the internal user name and password administration system, or by using a certificate issued by one of the certification authorities.
- You cannot sign when:
 - One of the saved versions of the chromatogram is open
 - If you have not opened an account.
- Every signature requires a username and password to be entered.
- For each signature you can specify the reason. You can either select it from preset reasons, or type in your own.
- Tool for signing electronically a series of chromatograms has been implemented – the **Batch** command has been extended by a new section **Sign**.
- Using the **File - Verify** command, you can simply and in an easy-to-see way display all signatures of the active chromatogram, and for each of them display details as to who, when, how and why signed the chromatogram.
- All signatures of the currently opened chromatogram version can be easily printed out. The **Report Setup** dialog has been extended by a **Audit and Signatures** tab, where in section Signature you select whether the table containing all signatures of the current version is to be printed after the chromatogram and the method, or after the result table, or at the end of the whole report.



9 Enhanced user accounts and access rights system

In accordance with the **GLP** and, in particular, the **21CFR Part 11** requirements, the user accounts and access rights system is now concentrated in the **User Accounts** and **User Details** dialogs.

- Passwords being entered are not visible; the user without access to the **User Accounts** can simply change his password in the **User Details** dialog.
- For each user can be set up a minimum password length, maximum validity time, minimum time after which the password can be used again, and a certificate can be assigned to him for a qualified electronic signature.

10 Enhanced login procedure

- If user accounts have been set, it is not necessary when logging in to the instrument to type in the username, it can be selected from an available list.
- In repetitive logins, the station will automatically offer the last user logged in.

11 Saving method history in chromatograms

- To assure full traceability of the conditions under which all results were obtained, the **Clarity** station automatically logs the current method status including calibration file at the moment of printing or exporting the chromatogram. The status is of course also saved when using the **Save** command.
- Hence the major difference compared to the **CSW** station is that, although the current calculation of results still takes place by reference to an external calibration file, the chromatogram in addition stores all saved calibration curves, thus preventing their accidental or intentional modification.
- In the **Open Chromatogram** dialog, item **Method**, you can select any of the saved chromatogram histories. Items **Recent (Linked Calibration)** and **Recent (Stored Calibration)** will open the chromatogram with the last saved method. The item **Recent (Stored Calibration)** will use calibration curves saved in the chromatogram



instead of the current ones in the calibration file to which the chromatogram is linked up.

12 Enhanced Log - Audit Trail

Requirements for full conclusiveness and traceability called for changes in the station's activity logging system. In addition to the main daily logs and logs of each chromatogram, the station now also logs calibrations and sequences. Every log is secured against unauthorised modifications by internal coding.

- All logs except the station log are an integral part of corresponding files.
- Last but not the least, extended has also been the quantity and detail of all logged operations.
- The command used to display the station log has been renamed from **Log** to **(Station) Audit Trail**, and the chromatogram log from **Log Table** to **Chromatogram Audit Trail**.

Summary Results Table

- For easy display, printing and exporting selected parameters from all displayed chromatograms in a single table, the **Chromatogram** window has been extended by a **Summary** tab to display a table of summary results.
- The table displays results for calibrated peaks only.
- Rows correspond to individual chromatograms and their signals.
- Columns show selected parameters for each identified substance.

13 Option to interchange rows and columns

Using the **Inverted** command from a local menu, rows and columns can be easily interchanged.

14 Option to change display order of substances and parameters

Using the **Summary Options - Parameter Header** command, you can determine whether all parameters of the first substance will be displayed first, or the first parameter of all substances.



15 Export from Summary Table

Using the **File - Export Summary Table** command, you can export the currently displayed summary table. The table will be exported in a text form, including all row and column headers. Values are separated by tabulator.

16 Displaying sequence results

Using the **File - Open Chromatogram from Sequence** command, you can display the results of all chromatograms measured in a defined sequence. A prerequisite for the display is a switched on **Overlay** mode and a non-zero sequence status (blue fields in column **Sts.** in the sequence table).

Data Acquisition

17 Snapshot

- Using the function **Snapshot** no longer increases the count of the **%n** sample counter.
- After repeated use of the **Snapshot** function, you will no longer be warned that the existing file will be overwritten.
- The **Snapshot** command is now available also from the **Data Acquisition** window.

18 Option to reverse the signal's polarity

Part of the setting of individual A/D converter channels is an option to reverse an input signal's polarity. Thanks to this feature you don't have to reconnect cables when some of the measured peaks have a reversed orientation.

19 Option Bipolar

Option to measure also negative signals – the option **Bipolar** has been moved from the method file (tab **Acquisition**) to the setting of a relevant channel of the A/D converter in the **System Configuration** dialog (part of the CSW.CFG configuration file, common for the whole station).



20 Default assignment of digital outputs for active sequence

- New installations use new default assignment of digital outputs as illustrated below:

Instrument	Clarity	CSW	Clarity and CSW
1.	OUT1	OUT 1	IN 1
2.	OUT2	OUT 3	IN 2
3.	OUT3	OUT 5	IN 3
4.	OUT4	OUT 7	IN 4

- When upgrading from a **CSW** station, the default assignment is preserved.
- You can change the setting easily in the **System Configuration** dialog whenever you want.

21 Data Acquisition icon and command

All main windows have been extended by **Data Acquisition** icon and command in the menu **Window**.

Integration

22 Integration parameters part of integration table

- All integration parameters originally located in the tab **Integration** (**Peak Width**, **Threshold**, **Rejection**, **Separation Parameters**, etc.) are now part of the integration table. Apart from tendency to unify the access to all integration parameters, the main reason for this change was that the majority of these parameters have been changed to interval parameters. This means that it is possible to define a time period of their validity and, even more importantly, select different values for different parts of the chromatogram.
- You will appreciate this advantage particularly in parameters **Peak Width** and **Threshold**. Since these parameters are essential for basic integration, the integration table always contains default values of these parameters, applicable to the whole chromatogram.



23 Filtration of redundant rows

The integration table has been extended by an option to filter off redundant rows. For example after a series of adjustments of the start of a single peak, it is unnecessary to display the entire history. Using the **Filter** command from the **Edit** menu or from a local menu of the integration table, you can either display or hide these redundant rows.

24 Integration Start - Integration Interval

- The new option to define an interval for all parameters lead to replacing the parameter **Integration Start** with **Integration Interval**. As the name suggests, it is now possible to define not only the start of integration, but the whole interval, even repeatedly.
- Important – **Integration Interval** is not a reverse function of the already previously existing command **Integration Lock**. Although their logic is reversed, by using the former you permit the interval, while with the latter you disallow it. However, there is a significant difference, because while when using the **Integration Interval** command you define where the integration algorithm is to be applied, when using **Baseline - Lock** you merely exclude already integrated peaks. A practical consequence of this is that the **Baseline - Lock** command does not significantly alter the shape of the baseline.

25 Interactive entry of selected parameters

- The menu **Chromatogram** was extended by a submenu **Integration**, comprising commands for interactive entry of selected parameters by means of interval lines. These are commands **Peak Width**, **Threshold**, **Integration Interval**, **Area**, **Height** and **Half Width**.
- After being called up (same as with the **Baseline** submenu commands), interval lines are gradually displayed, by which you delimit the interval within which you wish to modify the selected parameter. Then a dialog window will open,



prompting you to confirm the selected interval and to enter the value of the selected parameter.

26 Repetition of the last used integration command

- If, before using a command from the **Chromatogram** menu or one of the icons of the **Baseline**, **Peak** toolbars, you hold depressed the **CTRL** button, you can use this command repeatedly without having to select it again.
- You can cancel the repeat feature at any time by pressing the **Esc** button.
- The repeat feature is very useful when making manual adjustments, such as shifting starts/ends of peaks, or manual integration using the **Add Positive**/ **Add Negative** commands.

27 Function FFT

The **FFT** filter in the **Chromatogram** window has been taken out.

Displaying Chromatograms

28 Extended automatic scaling options in Chromatogram window

The introduction of multiple detector chromatograms called for the extension of originally automatic scaling.

- In the **CSW** station, all chromatograms had a common scale determined by maximum and minimum values from all displayed chromatograms.
- The **Clarity** station brings the following new options situated in the **Graph Properties - Signals** dialog:
 - **Scale to Active Signal** – the range of the voltage axis is determined by the active signal.
 - **Scale to All Signals** – the range of the voltage axis is determined by minimum and maximum values of all signals.
 - **Scale Signals Separately** – the range of the voltage axis is determined individually by the range of each signal.



- The above scaling using the **Scale to** item can in all cases be applied to:
 - The whole signal - **Maximum Value**
 - Values of the largest peak - **Largest Peak**
 - Values of the second largest peak - **2nd Largest Peak**
 - Values of the third largest peak - **3rd Largest Peak**
- If no negative peak has been detected, the minimum value is determined by the lowest value of the baseline. If negative peaks are detected, then all four above variants apply for determining the minimum value.

29 Chromatogram legend

- In the top right corner of the **Chromatogram** window is as standard displayed a legend of the displayed chromatograms. Each signal is represented by a line with a name and a corresponding colour. The name is composed of the chromatogram's name followed in the case of multiple detector chromatograms by a hyphen and the signal's (detector's) name.
- Similarly extended by the legend of currently displayed detectors has also been the **Data Acquisition** dialog.
- The legend in both windows can be easily hidden using the **Properties - Graph Legend** command from the local menu.

30 Selecting active signal

- The options of selecting an active signal have been extended by a double-click on its name in the **Chromatogram** window legend.
- Selection of the time axis units has again been extended (it was already part of **CSW17**) by the item **Fixed**. It allows any user units to be selected for the chromatogram's time axis.

31 User-selected colours for eight basic signals

Thanks to the modified **Graph Properties** dialog, the **Clarity** station allows colours of the first eight



displayed signals to be pre-selected without the need to first download the signals.

32 Mouse functional wheel

In the **Chromatogram**, **Data Acquisition** and **Calibration** windows, it is now possible to use the mouse wheel to speed up working with the graph.

Wheel only	Scrolling the chromatogram up/down
SHIFT + wheel	Scrolling the chromatogram left/right
CTRL + wheel	Enlarging/reducing the chromatogram

33 Displaying control methods

The tab **Measurement Conditions** has been extended by a new tab, **Instruments**, containing the method used to measure the active chromatogram.

34 Displaying Event Table

The tab **Measurement Conditions** has been extended by a new tab, **Detectors**, containing the description of the measurement converter setting and the content of the used **Event Table**.

Calibrated Calculations

35 Calculation of percentage representation

In the **CSW** station, when the corrected percentage quantity in column **Amount [%]** in the results table exceeded **200%**, question marks were displayed instead of the percentage. Now the percentage representation of individual substances is always displayed.

36 Using the Free calculation

The **Free** calculation (using the **Global Response Factor** rather than read offs from the calibration curve) is in the **Clarity** station used only when it has been explicitly selected in the tab of the relevant substance in the calibration file. Previously it was used automatically whenever reading off the calibration curve was not possible.



37 Changing calculation type

- If the requested type of calculation (**ESTD** or **ISTD**) cannot be used, the reason for it is displayed in the results table header.
- If the requested type of calculation cannot be used, an uncalibrated calculation – **Uncal** – will always be used, not the nearest possible calculation type as it used to be in the **CSW** station.

38 Values in row Total

- In the row **Total** of the results table is shown a sum of only those peaks, which are displayed in the table (cases when the **All Identified Peaks** or **All Peaks from Calibration** filter has been applied).
- The **CSW** station always displayed sums of all detected peaks.

39 Reductions of the ISTD types of calculation

- Three types of **ISTD** calculations have been simplified to automatic application of **ISTD2** or **ISTD3**.
 - The **ISTD3** calculation is used when the quantity of internal standard has been specified in the chromatogram and the calibration file.
 - The **ISTD2** calculation is used when the quantity of internal standard has not been specified in either place.
 - When the quantity of internal standard has been specified in one place only, no calculation according to the **ISTD** method is performed and the reason for this is displayed in the results table header.

40 Units in item Amount

The item **Amount** on the **Result** tab has been extended by a display of current units from the calibration file.

Calibration File

41 Calibration and Multiple detectors

For changes in calibration as a result of the **Clarity** station's multiple detector arrangement, refer to Section 5 on page 7.

42 Automatic calculation of Resp. Factor column no longer supported

- Automatic calculation of the **Resp. Factor** column in the main calibration table on **Compounds** tab in the calibration file is no longer supported.
- In the **CSW** station a rule applied that if you did not enter the **Resp. Fact.** value yourself, the system automatically used an arithmetic mean of **Local Response Factor** from all calibrated levels. In the new system, if you don't enter the **Resp.Factor** value yourself, it remains being equal to zero.
- Values from the **Resp. Factor** column are used when the option to interpose the **Free** substance has been used, instead of actually reading them off the calibration curve.

43 Other recalibration calculations

- The number of recalibrations is now reset to zero after manual entry of a zero response. In the **CSW** station, the counter was never reset to zero.
- The number of recalibrations is set to one after manual entry of a different response value. In the **CSW** station the value was set to one only when the recalibration type had been changed to **Replace**.
- The number of recalibrations is now displayed also on the tab of each substance.

44 Sigmoid interposal

Sigmoid interposing of the calibration curve has been implemented – suitable for **ECD** detectors.



45 Current units in substance calibration table headers

In the header of calibration tables of individual compounds are now displayed current units of response and quantity in accordance with the calibration file setting.

46 Default number of displayed decimal places

The default number of decimal places displayed in columns **Amount** and **Response** is now four. Of course you can change it to a different number using the **Setup Columns** command from a local menu of each table.

47 Weighing of calibration points

For every substance you can now select a weighing factor for each calibration point. On each tab of individual compounds you will find an item called **Weighting Method**, in which you can choose the importance of the point as being indirectly proportional to the quantity and response, or the square thereof.

Responses can be reset to zero using the **Calibration - Clear All Responses** command (suitable for **Clone**).

Sequence

48 Command Insert New Line

- The **Sequence** window has been extended by a new command and a new icon for inserting a new line above the one selected.
- The new line is pre-filled in with default values.

49 Line swapping

- The sequence table allows selected lines to be swapped using the *drag & drop* function: Select the required lines, press the left mouse button above one of the field in the first column (containing the line numbers), drag the lines to the required location and release the mouse button.
- You can reverse the drag operation easily using the **Edit - Undo** command.

**50 Enhanced status line of the sequence window.**

The sequence status line has been rearranged and extended by the display of a current analysis time.

51 Command Snapshot now functional also for Sequence

The **Sequence** window has been extended by a new **Snapshot** icon and command.

52 Running sequences from Data Acquisition window

The **Data Acquisition** window has been extended by an icon and command for directly opening/running sequences

53 Modified function Paused

An active sequence can now be suspended also when in the **WAITING** status.

54 Blocking sequence runs

Neither a sequence nor a single run can be started unless a direct functional control has been configured.

55 Sequence reports

Unless a print style is specified in column **Report Style** of the sequence table, no report will be produced. In the **CSW** station, this column was incorrectly ignored and a report was always produced, using the print style defined in the **Instrument** window.

Printing

56 Printing only valid substances and levels

- Printing of calibration files has been extended by an option to print only valid substances and levels (**Levels - Valid** and **Substances - Valid** selections) in the **Report Setup - Calibration** dialog.
- Valid compounds are compounds that have the **Used** field on the **Compound** tab checked and have at least one calibration point entered.



- Valid levels are levels which have the **Used** field on the substance's tab checked and have a non-zero **Response** and **Amount**.

57 Printing table row sequence numbers

The **Clarity** station now prints also a sequence number of the right hand side column of most tables.

58 Printing date and place for signature

The new **Audit and Signatures** tab in the **Report Setup** dialog has a new item, **Gap for Date and Manual Signatures**. The item will print out at the end of the printing protocol pre-printed boxes for a date and a long-hand signature to be added.

59 Disabling printing chromatogram background

The **Print BG Color** checkbox in the **Report Setup - Chromatogram** dialog allows you to choose whether the chromatogram's background and surrounding areas colours should be printed or not.

60 Selecting all or only active signal to be printed

In the **Method**, **Calibration** and **Results** tabs using the **Signals - All** and **Only Active** items allows to choose whether in multiple detector chromatogram printed should be the selected sections for all signals, or only for active signals, respectively.

61 Automatic saving of print styles

Printing style modifications carried out in the **Report Setup** dialog are saved in the moment the window is closed by pressing the **OK** button. If you close the window by pressing the **Cancel** button, all modifications made on all tabs will be lost.

62 Printing chromatograms from Instrument and Batch window

In the **CSW** station, chromatograms printed from the instrument window using the **Postrun** and **Batch** functions and the **As on Screen** option, did not respect the current setting of the **Chromatogram** window.



63 Table print alignment

If different font sizes have been used in a single table, all fonts will be bottom-aligned.

64 Extended function of Report Setup and Print icons

- In all toolbars after positioning the cursor on the **Report Setup** icon, the current printing style will be displayed.
- In all toolbars after positioning the cursor on the **Print** icon the name of the current printing style and the selected printer will be displayed.

Import/Export

65 Rearranged and renamed commands and items

- **Import** and **Export Text** commands have been renamed to **Import** and **Export Chromatogram**.
- The **Export** command has been renamed to **Export Data**.
- The **Save as Picture** command has been renamed to **Export as Picture**.
- All import and export commands have been moved to a different menu level, under the **Import** and **Export** items.
- The **Data** item in the **Export Data** dialog has been renamed to **Chromatogram**.

66 New dialog window Export Chromatogram

- Allows an easy selection of output format (CDF, CHR, TXT, ASC), selection of signals to be exported, data separators, decimal symbol and the name of the resultant file.
- A new option has been added, allowing all signals including those in single-detector formats (CDF, TXT) to be exported. In such case more files will be created simultaneously, differing from each other by the detector name.



SST Module

67 Modified calculation types

- Calculations in accordance with the *Statistical Moments* and *Height in 10%* standards are no longer available.
- A new calculation in accordance with the **JP** (*Japanese Pharmacopoeia*) standard has been introduced.

Working With Files

68 Working with a single file on more instruments

- The possibility to open single chromatogram or calibration file simultaneously on more instruments has been discontinued.
- On multiple stations this option has been preserved. The file can be edited only at the station which opened the file as first, on the remaining stations the file will be available in read only mode.

69 Enhanced feature for automatic generation of chromatogram names

Only basic variables are displayed in the main list (%n - %D). Supplementary variables for time definition (%H - %Z) are now included in a submenu, and it is no longer necessary to prefix them with the variable %T.

70 Automatic file association

After successful installation, basic files of the **Clarity** station (chromatogram, method, calibration, sequence) are associated with the station. By clicking on any file in the Windows Explorer, the file can be immediately opened on the first instrument of the **Clarity** station.

71 Command line

The **Clarity** station has available many command line parameters which can make automation of some actions for you easier.



LC Control

72 Editing gradient table

After filling a line in, you can now easily move to the next line by simply pressing **Enter**.

73 Setup of gradient components in the Chromatogram window

- The number of components in the **Graph Properties - Gradient** dialog has been reduced from 8 to 4.
- Gradient components have been renamed from **Component A .. H** to **Solvent 1 .. 4**.

Upgrade from CSW32 to Clarity for multidetector methods

74 Creating of multidetector method

In **CSW32** it was necessary to open independent window with method, calibration and respectively sequence for each detector. When upgrading to **Clarity** it is the best to start with the method for one of the used detectors and fill in the differing values for other detectors in the **Acquisition** and **Integration** tabs. Current detector can be selected from the listbox in the upper left corner of the **Method Setup** dialog.

75 Creating of multidetector calibration file

Upon upgrade from **CSW32** to **Clarity** it is the best to start with the calibration file for one of the used detectors. This file contains peak names, identification windows, amounts of compounds and responses of the current signal. For other utilized detectors (signals) it is necessary to re-calibrate the signals at the relevant level using the multi-detector standard chromatogram. If these signals contain not yet identified peaks, you can add them using the **Add Peak** command. In the **Used** column you can select which peaks will be applied in the particular signals.

76 Creating of multidetector chromatogram

If you want to use for the calibration the chromatogram standards from **CSW32**, you can compose the required multi-detector chromatogram using the **Chromatogram - Merge** command. Open the chromatogram for the first detector and merge second and further signals by the **Chromatogram - Merge** command. The names of the signals can be edited by the **Set Signal Names** command.

Miscellaneous

77 Unification of global and local user setups

- A hierarchical structure of user setups of graphs and tables has been consistently implemented.
- Most sections in the **Graph Properties** and **Setup Columns** dialogs contain the **Use User Settings** item that allows the appearance and behaviour of graphs and tables to be unified as defined in the **User Options** dialog (you can display the dialog using the **View - Options** command from the **Instrument** window).
- Terminology and setup tabs of all graphs and tables have been unified.

78 Calculation types on tab Column Performance

The calculation of moments from 10% peak height has been taken out.

Please note:

*The **Column Performance** tab is now as a default hidden, you can display it using the **View - Show Tables - Performance table** command in the **Chromatogram** window.*

79 Unidentified Peaks - Response Factor in ISTD calculation

- To calculate the quantity of unidentified peaks can be used, even in **ISTD** method, only **Unidentified Peaks - Response Factor**.
- The **CSW** station in such case used the **Unidentified Peaks - Response Factor** ratio and a read off from the internal standard calibration curve. As a consequence, the **Amount** item for unidenti-



fied peaks differed, depending on the calculation method used (**ESTD/ISTD**).

80 New key shortcuts

The **Clarity** station makes full use of the option to control the system by key shortcuts of the type **Ctrl+Key**. You will find most of these shortcuts described in the menu itself, after the command name.

Listed here are some of the not obvious shortcuts:

CTRL + A	Highlight all files in the dialog box to be selected
TAB	Move cursor forward between table items or fields
SHIFT + TAB	Move cursor backward between table items or fields
CTRL + mouse clicks	Highlight non-congruous files or table items (rows, columns or individual cells) to be selected – keep pressed when selecting by mouse Repeated use of the function to adjust the chromatogram
SHIFT + mouse clicks	Highlight congruous files or table items (rows, columns or individual cells) to be selected – keep pressed when selecting by mouse
ALT + TAB	Switching between open windows (even to windows of other programs) -.

81 Creating a calibration file from the Method Setup window

- The following buttons have been added to the **Method Setup - Calculation** dialog:
 - **New** to open a new, empty calibration file.
 - **Clone** to create and assign a copy of the currently assigned calibration file (suitable in combination with the **Clear All Responses** command)
 - **View** for direct display of currently assigned calibration file in the **Calibration** window.

Please note:

The **Calibration** window is displayed "under" the **Method Setup** dialog. The reason is a modality of the **Method Setup** dialog. Therefore if you wish to work in the calibration window, you must first close the **Method Setup** dialog.

**82 Icon Calculation in window Instrument**

The **Instrument** window now has icons of all major parts (tabs) of the **Method Setup** dialog.

83 Enhanced automatic update from Internet

The **Help - Check for Updates** command is now able to select, using the serial number, the correct update file, thus significantly shortening the Internet download time.

84 Rapid shutting of all instruments

If while attempting to open the system configuration, password administration, etc., some of the instruments are opened, you are reminded and you can shut them all down using the **Logout All Now** button.

85 Chromatogram window tab configuration

If you are not using all tabs displayed in the **Chromatogram** window, you can hide them using the **View - Show Tables** command.

86 Single Run/Sequence switch

It is now longer possible in the **Instrument** window to select the type of analysis by clicking on the icon “Valve” of either **Single Analysis** or **Sequence**. Nevertheless, the “Valve” symbol indicates during acquisition whether the measurements are being made using a sequential table.