

# Clarity Lite

v.2.2

## *Clarity Lite vs CSW32*

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Phone/Fax: +420 251 613 507  
Phone/Fax: +420 251 612 067  
clarity@dataapex.com  
www.dataapex.com

© **DataApex Ltd. 2003**  
Podohradská 1  
155 00 Prague 5  
The Czech Republic

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# Multiple detector Arrangement

## 1 Measuring with up to four four-detector chromatographs simultaneously

The **Clarity Lite** 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 Lite** station represented by whole chromatographs (instruments), and hence we call them now instrument windows.

## 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**), 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 Lite** 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. The 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 called for a change of all file formats. However, the **Clarity Lite** 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 Lite** station to be saved.*

The **Clarity Lite** station is compatible with **Clarity** station. Both stations use the same data format.

## 7 Configuring the station

The Clarity Lite station uses only Plug and Play A/D converters **INT7** and **U-PAD** which enables fully automatic configuration of the station.

## 8 User accounts and access rights system

**Clarity Lite** does not provide user accounts and access rights policy. These features are included in the full version.



## 9 Saving method history in chromatograms

- To assure full traceability of the conditions under which all results were obtained, the **Clarity Lite** 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.

### ~~40 — Log — Audit Trail~~

**Clarity Lite** station (contrary of the **Clarity**) does not enable reviewing of station logs.

## 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.



- 11 Option to interchange rows and columns**
- Using the **Inverted** command from a local menu, rows and columns can be easily interchanged.
- 12 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.
- 13 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.
- 14 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

- 15 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.
- 16 Option to reverse the signal's polarity**
- Clarity Lite** station (contrary of the **Clarity**) does not provide the option of reversing the signal's polarity.



## 17 Option Bipolar

**Clarity Lite** station (contrary of the **Clarity**) does not provide the option of changing bipolar range (measurement of negative voltage) to unipolar.

## 18 Default assignment of digital outputs for active sequence

**Clarity Lite** station uses always the IN1 input for the start of acquisition and in case of active sequence the OUT1 output for enabling the injection.

## 19 Data Acquisition icon and command

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

## 20 ~~Background chromatogram in Data Acquisition window~~

The displaying of background chromatogram in the **Data Acquisition** window is not available in the **Clarity Lite** version.

## 21 ~~Automatic subtraction of chromatogram~~

The automatic subtraction of chromatogram from the **Method Setup - Measurement** dialog in is not available in the **Clarity Lite** version.

# 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.

# Displaying Chromatograms

## 27 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 Lite** 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.

## 28 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.

## 29 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.

**30 User-selected colours for eight basic signals**

Thanks to the modified **Graph Properties** dialog, the **Clarity Lite** station allows colours of the first eight displayed signals to be pre-selected without the need to first download the signals.

**31 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
<b>SHIFT</b> + wheel	Scrolling the chromatogram left/right
<b>CTRL</b> + wheel	Enlarging/reducing the chromatogram

**32 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

**33 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.

**34 Using the Free calculation**

The **Free** calculation (using the **Global Response Factor** rather than read offs from the calibration curve) is in the **Clarity Lite** 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.



### 35 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 used to be in the **CSW** station.

### 36 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.

### 37 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.

### 38 Units in item Amount

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



# Calibration File

## 39 Calibration and Multiple detectors

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

## 40 Automatic calculation of Resp. Factor column no longer supported

- Automatic calculation of the **Resp. Factor** column in the main calibration table on **Calibration - 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.

## 41 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.

## 42 Sigmoid interposal

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



### 43 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.

### 44 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.

### 45 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

### 46 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.

### 47 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.

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

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

**49 Command Snapshot now functional also for Sequence**

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

**50 Running sequences from Data Acquisition window**

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

**51 Modified function Paused**

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

**52 Blocking sequence runs**

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

**53 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

**54 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**.

#### 55 Printing table row sequence numbers

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

#### 56 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.

#### 57 Selecting all or only active signal to be printed

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

#### 58 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.

#### 59 Printing chromatograms from Instrument window

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

#### 60 Table print alignment

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



## 61 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

## 62 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.
- Item **Data** in the **Export Data** dialog has been renamed to **Chromatogram**.

## 63 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

## 64 — SST module

**Clarity Lite** station (contrary of the **Clarity**) does not provide the option to use **SST** module.



## Working With Files

### 65 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 sub-menu, and it is no longer necessary to prefix them with the variable **%T**.

### 66 Automatic file association

After successful installation, basic files of the **Clarity Lite** 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 Lite** station.

### 67 Command line

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

## LC Control

### 68 ~~GC, LC, AS Control~~

**Clarity Lite** station (contrary of the **Clarity**) does not provide the option of direct control of selected chromatographs and autosamplers.

### 69 ~~Digital acquisition~~

**Clarity Lite** station (contrary of the **Clarity**) does not provide the option of digital acquisition from selected detectors. This implies that the station must be equipped with INT7 or U-PAD A/D converter.



# Upgrade for multidetector methods

## 70 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 Lite** 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 **Method Setup - Acquisition** and **Integration** dialogs.

**Please note:** *Current detector can be selected from the listbox in the upper left corner of the **Method Setup** dialog.*

## 71 Creating of multidetector calibration file

Upon upgrade from **CSW32** to **Clarity Lite** 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 recalibrate the signals at the relevant level using the multidetector 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.

## 72 Creating of multidetector chromatogram

If you want to use for the calibration the chromatogram standards from **CSW32**, you can compose the required multidetector 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

### 73 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** checkbox, which allows the appearance and behaviour of graphs and tables to be unified as defined in the **User Options** dialog (you can display the window using the **View - Options** command from the **Instrument** window).
- Terminology and setup tabs of all graphs and tables have been unified.

### 74 Calculation types on tab Column Performance

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

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

### 75 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 item **Amount** for unidentified peaks differed, depending on the calculation method used (**ESTD/ISTD**).

### 76 New key shortcuts

The **Clarity Lite** 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:



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

## 77 Creating a calibration file from the Method window

- The following buttons have been added to the tab **Calculation**:
  - **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.*

## 78 Icon Calculation in window Instrument

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

## 79 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.



## 80 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.

## 81 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.