Clarity (Lite)

3.0 vs 2.8

ENG

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Sections of the manual connected only to the **Clarity Full** version are marked with the Full version icon.

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Contents

To facilitate the orientation in the **3.0 vs 2.8** manual and **Clarity** chromatography station, different fonts are used throughout the manual. Meanings of these fonts are:

Instrument (blue text) marks the name of the window, to which the text refers.

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 (when you already are in the topic describing the window).

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

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

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

Note:	Notifies the reader of possibly interesting information.
Caution:	Warns the user of possibly dangerous or very important information.

Marks the problem statement or trouble question.

Description: Presents any closer information on the problem, describes its causes etc.

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

1 Preamble

Clarity version **3.0** is focused on the frequently asked improvements and options. More then one hundred new features were made in the **User Interface** options, **Calibration**, **Sequence**, **Reports**, **Import/Export** and **Event Table**. Also the list of **Control Modules** is extended and some improvements are implemented in **Extensions** like exporting pictures of graph in **PDA** extension, etc.

2 General

2.1 User Accounts Full version

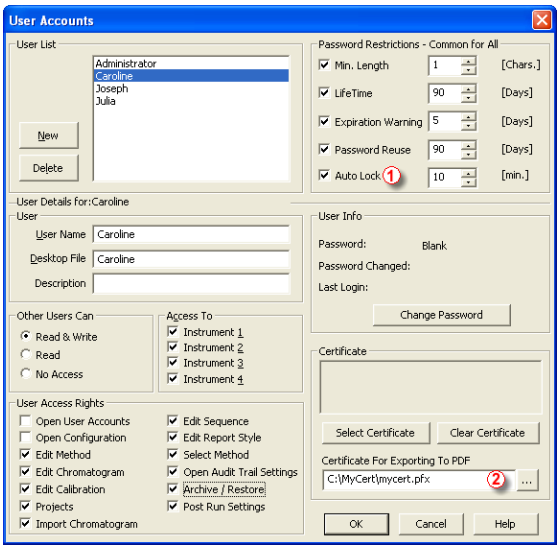

Fig. 1: User Accounts dialog

AutoLock ①

The **Instrument** will be locked after a time of computer operator inactivity. Only the current user or **Clarity** user with the *Open User Accounts* privilege could unlock it by entering his/her password. Operation is recorded in **Audit Trail**.

Electronic signature for PDF reports ②

A **PKCS#12** private key certificate file can be defined for the user. PDF documents created from **Clarity** will be then signed automatically with this certificate. As password entry is required for each print, this is not suitable for automated prints from **PostRun**.

2.2 Configuration Full version

Instrument Method Sending options

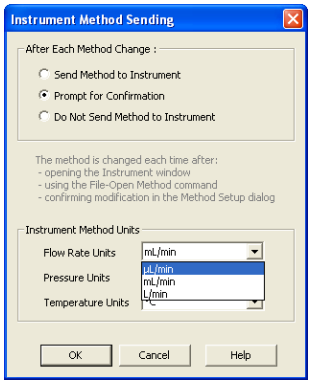

Fig. 2: Instrument Method Sending dialog

L/min has been added to options for *Flow Rate Units* in **LC Gradient**.

Thermostat

Device type **Thermostat** is now allowed on **GC Instrument** type.

2.3 Instrument

Project Selection

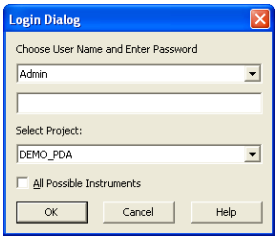

Fig. 3: Login Dialog

The project could now be selected in the Login Dialog. Last used project is offered.

Instrument

The *New* (*Method*, *Sequence*, *Calibration*) commands now open the Save As dialog to force the user to name the new file before using it.

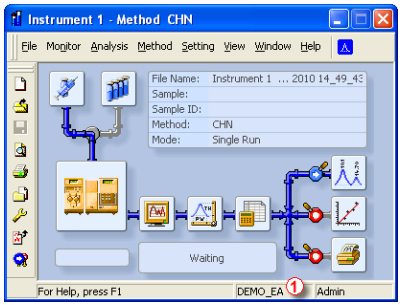

Fig. 4: Instrument window

The Project Setup dialog could now be also invoked by clicking the *Project Name* in the status bar ①.

2.4 User Options

General tab

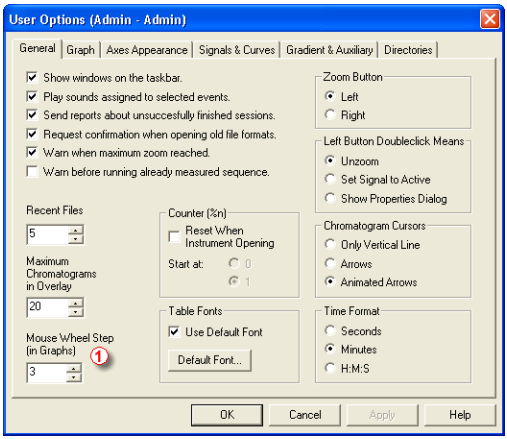

Fig. 5: Mouse Wheel Step option in the User Options dialog

Mouse Wheel Step (in Graphs) ①

Sets the mouse wheel sensitivity on zooming the graphs.

Graph tab

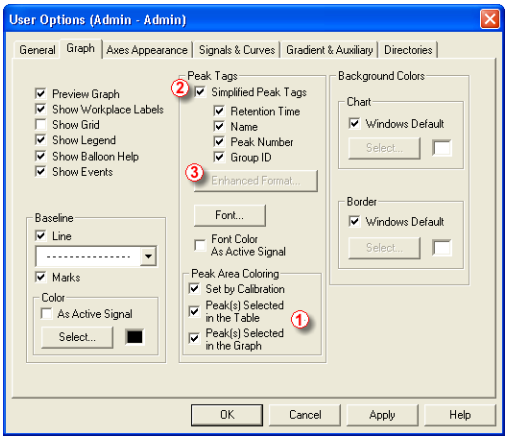

Fig. 6: New options in the Graph tab of the User Options dialog

Peak(s) Selected in the Graph ①

Clicking inside the peak area or selecting several peaks will fill them with the signal color and also mark them in the corresponding *Result Table* lines.

Peak Tags

The peaks could now be labeled with practically all parameters available in the *Result Table*:

Simplified Peaks Tags ②

Enables or disables checkboxes concerning simplified peaks tags.

Enhanced Format… ③

Displays the Peak Tags Format dialog which allows to set custom format of peak tags. Available only if the *Simplified Peaks Tag* checkbox is unchecked.

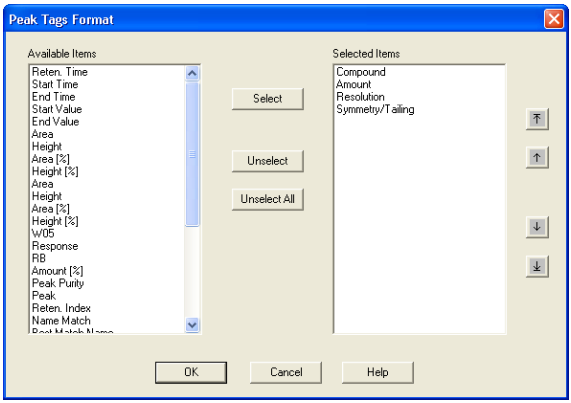

Fig. 7: Peak Tags Format dialog

Those settings are active only if the *Use User Options* option is selected in the respective graph (Chromatogram or Calibration) properties.

Directories tab

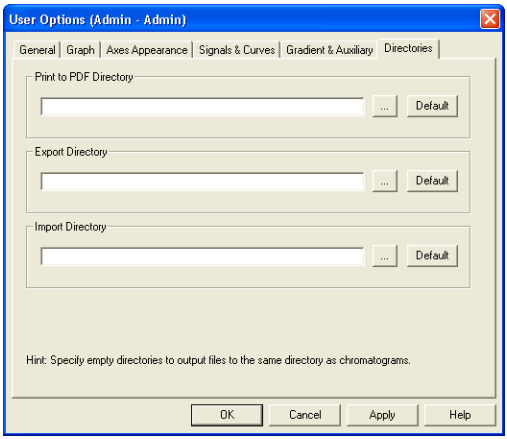

Fig. 8: Directories in the User Options dialog

Sets the directories that will be used for the automatically created *.PDF files and exported files and where **Clarity** will look for files to import. If the fields are left empty, **Clarity** will use the subdirectory where the exported chromatogram is saved and the *Analysis subdirectory* (DATA by default) of the current project for imports.

2.5 File Name variables

New variables are available in *Sample*, *Sample ID* and *File Name* fields in *Sequence* table.

- *%P* Name of the project
- *%J* Name of the method (without .MET suffix)
- *%s* Name of the sequence (without .SEQ suffix)

Those variables could be used in the Method Setup, Calculation and Calibration cloning, the *%P* and *%J* are available also in the Single Analysis window. *Sample*. The *Sample ID* and *File Name* fields in *Sequence* table.

2.6 Fill Series in tables

Using the command *Fill Series…* in the popup menu of the *Sequence*, *Calibration* and *Gradient* table it is possible to fill values in selected range with defined step. This command is also available in the *Edit* menu of Sequence and Calibration windows.

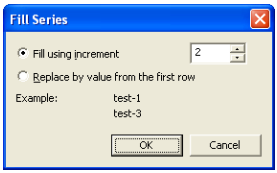

Fig. 9: Fill Series dialog

As you can see in the **Fig. 9** on pg **7**., by using this function it is possible to fill the selected range of cells with values *test-1*, *test-3*, *test-5*, etc. The number at the end of the first selected cell is automatically detected and incremented when the *Fill using increment* option is selected. For more information about this function, see the **Reference Guide**.

2.7 PostRun and Batch Options

New options are available in the PostRun Setting, Analysis Batch dialogs and Sequence table.

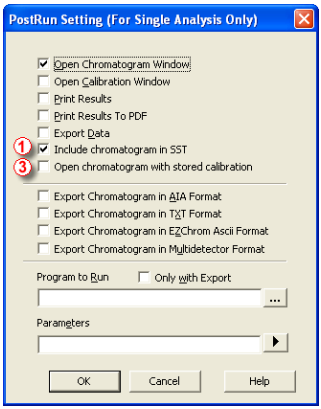

Fig. 10: PostRun Setting dialog

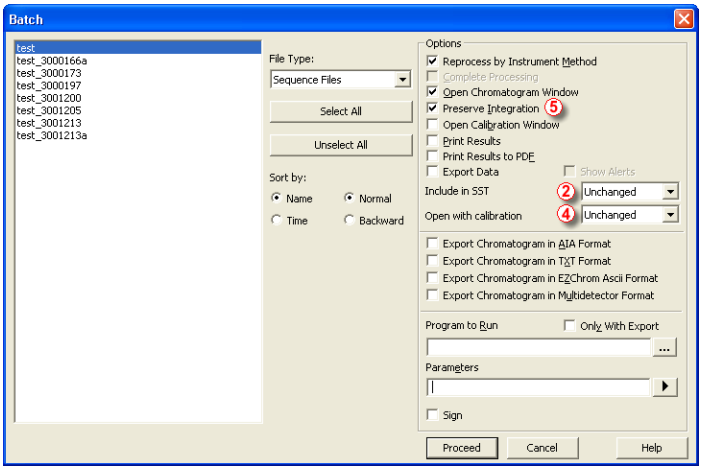

Fig. 11: Batch dialog

Include chromatogram in SST

Selects whether the batch-processed chromatograms will be included in **SST** ① calculations. In the Batch dialog, the option is called *Include in SST* and available options are *Exclude*, *Include* and *Unchanged* ②.

Open chromatogram with stored calibration

Selects the type of calibration connected to the chromatogram after the reprocess ③. In the Batch dialog, this option is called *Open with*

Calibration and available options are *Linked*, *Stored* or *Unchanged* ④.

Those attributes are set by Sequence table and stored within the chromatogram, thus the *Unchanged* option uses the value stored in *Chromatogram*, while the others will change them also in the *Chromatogram*.

Preserve integration

New option *Preserve Integration* ⑤ is available for *Reprocess by Instrument Method* or *Complete Processing* options. When active, the integration table in chromatogram will not be updated from the method used for reprocess, so the original integration will be preserved including the hand made modifications in the *Chromatogram*. This option is available only in the Batch dialog.

2.8 Export Data

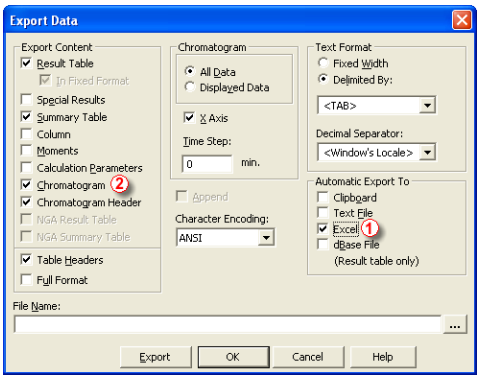

Fig. 12: Excel option in the Export Data dialog

Export in MS Excel format

The data could be now exported to formatted MS Excel file ①. The headers are automatically included for the tables. Each selected item in *Export* content is on separate sheet in the Excel file. In case the *Chromatogram* option is checked ②, graph is created from the exported data (no baseline, integration marks and peak tags).

2.9 Registration

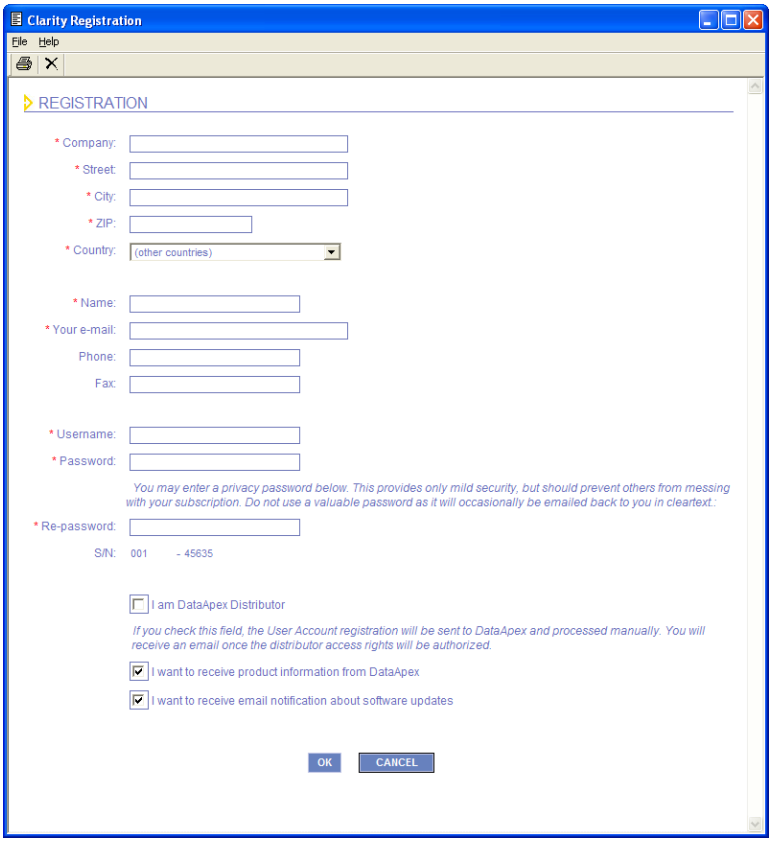

Fig. 13: Clarity Registration

New web based registration form is used. In case the computer is not connected to the Internet, the form could be filled, printed and sent by post or fax.

By registering **Clarity** you get access to direct updates for your chromatography station and also the e-mail support is faster.

3 Method Setup

3.1 Event Table tab

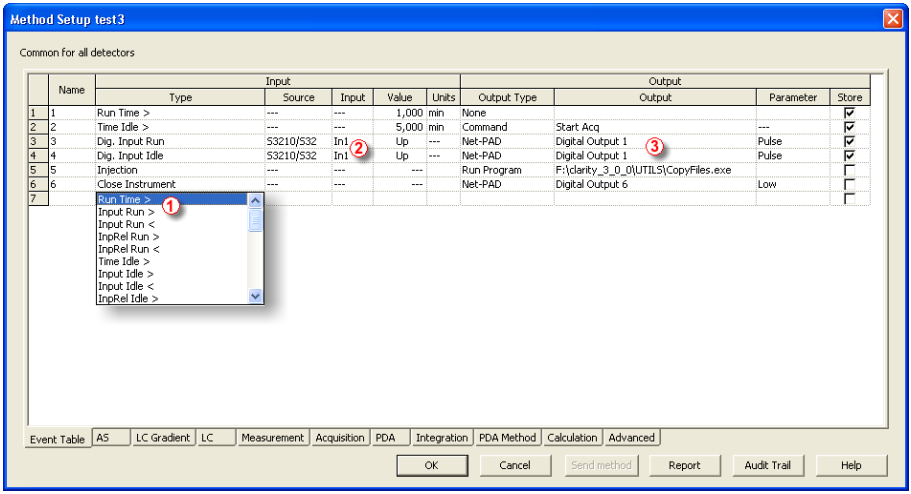

Fig. 14: New options in the Type, Input and Output columns in the Event Table

The event table is now active also outside the acquisition during the idle time. The input events are distinguished by the *RUN* and *IDLE* nominations ①. In case the event should be invoked both in *RUN* and *IDLE* stage, it must be entered twice (for each stage separately).
Please check the **Help** or **Reference Guide** for detailed description.
The *Input* ② and *Output* ③ columns are now displayed with assigned names (instead of numbers).
The Method Setup dialog is now resizable to allow displaying of longer texts and all columns.

Caution: As a consequence, methods from previous versions may show invalid *Time Table* – it is necessary to reassign the corresponding inputs and outputs.

3.2 Calculation tab

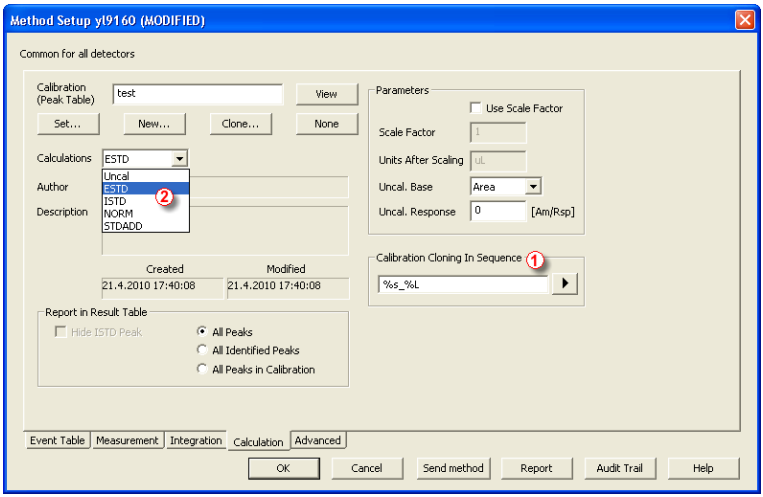

Fig. 15: Calculation tab of the Method Setup

Calibration Cloning in Sequence

Sets the name for cloned calibration files ① used in the **Standard Addition** calibration method and during the **Safe Calibration** usage and **Calibration Bracketing**. The field enables the use of any text, however it is essential to use *%variables* (added using the button) appropriate to the calibration method.

It is advantageous to use the *Sample ID* (*%q*) as a part of the variable for the **Standard Addition** measurements, where all lines belonging to one sample (Unknown, possible Blank, all Standards on other levels of the same sample) share the same *Sample ID* in the Sequence window.

For the **Calibration Bracketing**, the use of the Date and Time (in any format) or Line number as a part of the **Calibration Cloning** In Sequence field may be advantageous.

For safe calibration usage (option *Clone on first recalibration* in the Sequence Options dialog), the use of *Date* (*%D*) variable as a part of the cloned calibration name is advantageous.

New calculation modes available ②

- *STDADD* - Standard Addition.
- *NORM* - Normalized calculation

See the **Reference Guide** for detailed description.

3.3 Advanced tab

Subtraction

Subtraction chromatogram data are now stored in the *.PRM file (it is no more simply linked to it). The changes occurring with the subtraction chromatogram thus do not influence the measured chromatogram from which the background is subtracted. The subtraction, however, does not hold its history - only last subtracted chromatogram's data is saved when it is changed, previous subtraction chromatogram is discarded.

4 Chromatogram

4.1 Result Table

User Columns

Compound in Special Values

A new item **Compound** is available within the *Special Values* list ①.

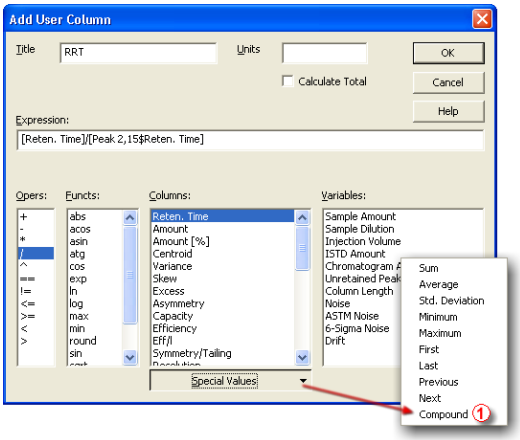

Fig. 16: Adding Special Value to User Column

Clicking the *Special Values* button and selecting the *Compound* command will invoke the dialog window showing list of compounds in the current chromatogram.

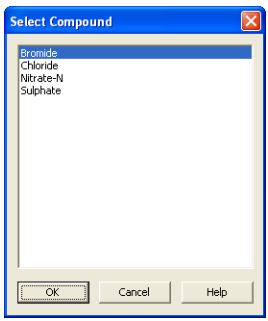

Fig. 17: Select Compound

The respective value could then be used in compound specific calculations like is the *Relative Retention Time* or *Amount Ratios* to a specific compound.

Peak Type column

Additional information is shown in the *Peak Type* column.

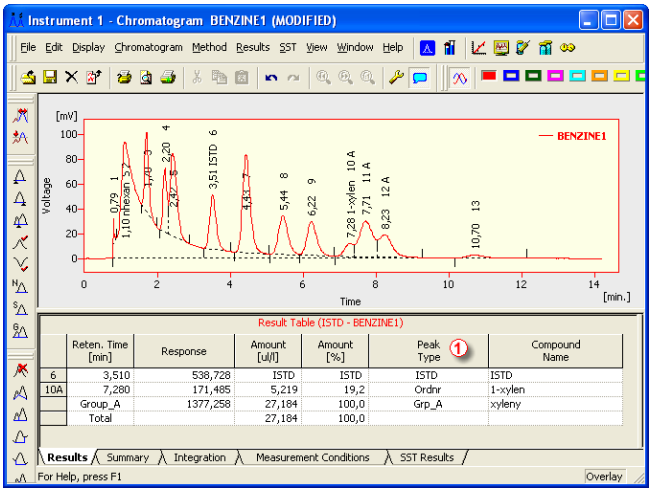

Fig. 18: Peak Type column in Chromatogram window

Tab 1: Additional information is shown in the Peak Type column:

Value	Description
Ordnr / *Ref* / *ISTD* / *RISTD* / *GRP*	Peak type.
Error	Value could not be calculated.
Error (Curve Check)	Calibration curve does not met preset criteria.
<LOD or <LOQ	Value lower then set limits.
(Forced)	Identification forced by integration table.
(by name)	Another compound calibration data used.
(CF)	Correction factor in calibration applied .

4.2 Integration

Force Peak Name

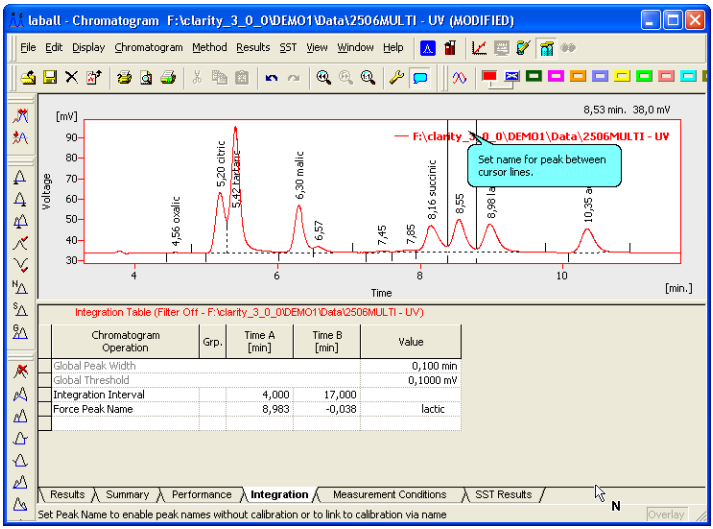

Fig. 19: Force Peak Name function

New command *Force Peak Name…* is available in the Chromatogram window by clicking on the *Chromatogram* - *Peak* menu or the corresponding icon on the *Peak* toolbar. After selecting the peak in chromatogram, window offering selection of existing peaks in the chromatogram appears. A new name could be filled in or selected. If you select a peak from the list instead of manual filling, the peak will change its name and also the corresponding integration will be used.

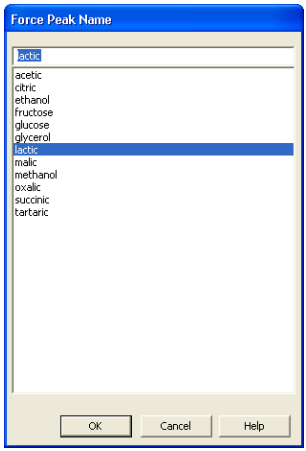

Fig. 20: Force Peak Name dialog

The purpose of this function is:

1. To name peaks in *Chromatogram* without the necessity to create *Calibration* file. Such named peaks could be used in the user column calculations – typically for purity determination, where the *RRT* and *%Area* relative to the main component need to be calculated.
2. Correct peak identification in some exceptional chromatograms (typically in aminoacid analysis even the peak order may change within series of samples) without the necessity to amend the expected retention times and identification windows in the calibration file.

4.3 Import chromatogram

New options enable simplified import of multiple files in the same format.

Import AIA files

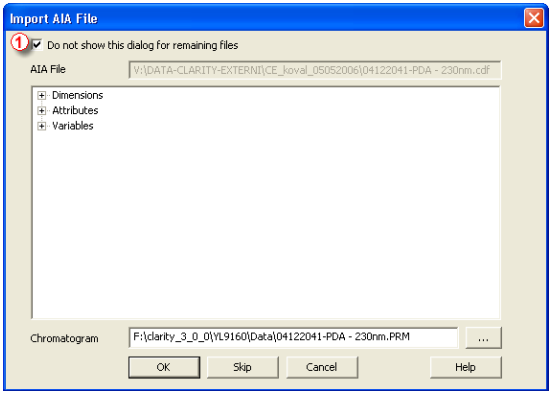

Fig. 21: Import of AIA files

For AIA files, the *Do not show this dialog for remaining files* ① will suppress it for simultaneously imported files.

Import text files

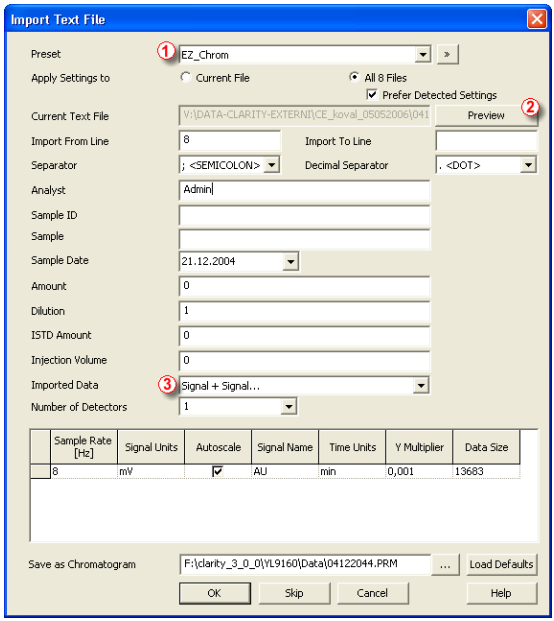

Fig. 22: Importing text files

Preset ①

When the same type of files are imported frequently, it can be useful to save import settings for further use. In drop-down box a user can select from previously saved presets, by clicking » button right to list the presets management menu will open. The menu contains commands for saving current setting (*Create from the Current Settings*), *Rename* or *Remove* presets. Presets are stored as part of *Clarity Desktop* settings.

Preview ②

This button will open the current file in simple text viewer. This can help user to identify exact meaning of particular columns when it's not clear from the file suffix.

Imported data ③

Time + *Signal* + *Time* + *Signal* - Every chromatographic curve is saved in a pair of columns, in which the first one represents a time and the second one a signal.

Signal + *Time* + *Signal* + *Time* - Every chromatographic curve is saved in a pair of columns, in which the first one represents a signal and the second one a time.

Signal only - Every chromatographic curve is saved in one column, where the values represent the signal only. The time basis is obtained from the *Sample Rate* field.
Time + Signal + Signal - Time base is contained in first column, every next column represents a signal of one detector.

Import CSV files

File type *.CSV are supported in *Import Chromatogram* and *Import Sequence* functions.

4.4 Mathematical Operations

Invert

New function to invert polarity of already measured chromatogram ①.

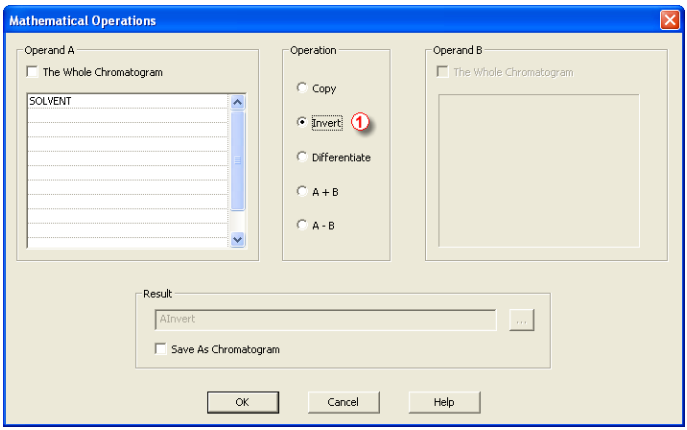

Fig. 23: Invert function in the Mathematical Operations dialog

4.5 Miscellaneous

- *Open Chromatogram Sequentially* command is active also in *Overlay Mode*.
- CTRL + *Arrows* keys will move the chromatogram in the graph (when zoomed in).
- The Audit Trail (cleared in previous versions during *Save As*) is preserved.
- File Open dialog includes *Overlay Mode* checkbox to toggle the *Overlay mode* on/off directly from this dialog.
- Graph Properties: *Show Data Points* checkbox to indicate data points in Chromatogram.
- Possibility to make chromatogram active by double clicking the respective row in *Summary* or *SST* table.

- Possibility to highlight peaks and corresponding row in tables by clicking inside the peak area in the chromatogram.
- Last subtraction chromatogram will be stored in chromatogram history.

5 Calibration

New columns in the *Compounds* table. To display them use the Setup columns… command in the pop-up menu of the table.

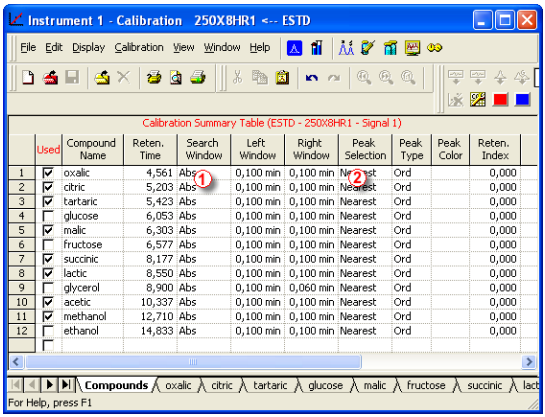

Fig. 24: Search Window and Peak Selection columns in the Compounds table

New columns *Search Window* and *Peak Selection* enable more flexibility in compounds identification.

Search Window ①

Defines whether the *Left Window* and *Right Window* content will be inserted in *Abs* (absolute - set in minutes) or *Rel* (relative - set in percents of the *Reten. Time*) values.

Peak selection ②

Defines the way the correct peak is matched with the Retention time when several peaks are present in the same identification window. The options available are Nearest (closest possible to the selected retention time - default for standard peaks), *First*, *Last* and *Biggest* (default for *Reference* peaks).

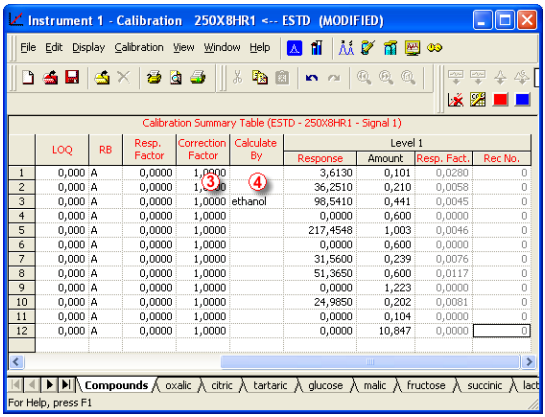

Fig. 25: Correction Factor and Calculated By columns in the Compounds Table

New columns *Correction Factor* and *Calculate By* enable to use another compound response or calibration curve for quantification

Correction Factor ③

Allows for the correction of amount due to the lower recovery, etc. The *Amount* value is multiplied by the *Correction Factor* to calculate the final *Amount*. The use is indicated in the *Peak Type* column in the *Result* table in the Chromatogram window, see the **Reference Guide**.

Calculate By ④

Clicking the field of this column on a given row opens the Calculate By dialog, which allows to set a compound whose *Response* will be used for the *Amount* calculation for a given compound. Use is indicated in the *Peak Type* column in the *Result* table in the Chromatogram window, see the **Reference Guide**.

Those *Calibration Curve* parameters are now available directly from the *Compounds - Calibration table* as columns (display them by using the *Setup Columns…* in the pop-up menu of the table).

- Curve Fit Type
- Origin
- Ending Point
- Weighting Method
- Linearisation X
- Linearization Y
- Lin Response
- Lin Amount

5.1 Calibration Options

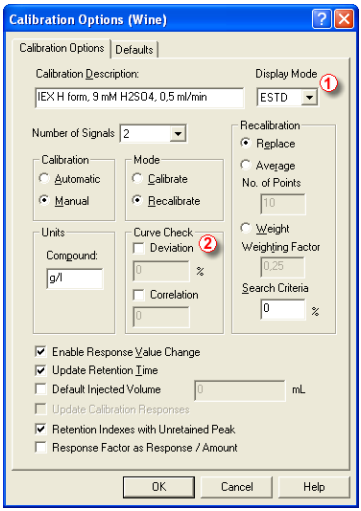

Fig. 26: Calibration Options

Display Mode

New items *NORM* and *STDADD*. For more details see the chapter **Standard Addition Calculation** on pg **29**. and the chapter **"Normalization Calculation"** on pg **30**.

Curve Check

The parameters of calibration curve could be checked against the set limits.

Deviation

In *%* as displayed in the *Deviation* column in the Calibration and *Compound* table.

Correlation

The correlation factor displayed under the calibration curve equation with values between *0* and *1*.

Failure to comply is indicated in the *Result Table - Peak Type* column by Error (Curve Check).

Response Factor as Response/Amount

Option to display the *Response Factor* as Response/Amount (inverted value to the default Amount/Response).

In calculations the Amount/Response value is used in both cases, the checkbox only influences the display of the *Response Factor* in the Calibration or *Result Table*. Useful in case the Response Factor is a small

number and the valid digits could not be properly displayed due to the decimals limitation.
The used option is indicated in the column header tooltip.

Miscellaneous

- *Open Standard as Chromatogram* command will open the standard in the Chromatogram window.
- *Link Calibration to Standard* command in the *File* menu. Links currently opened chromatogram of standard to calibration file in which this standard is used. This will enable showing the names of peaks, as they were coined in the calibration file.
- Bubble hint in the graph of calibration standard for *Add Peak* function.

5.2 Calibration Options - Defaults

Identification Windows.

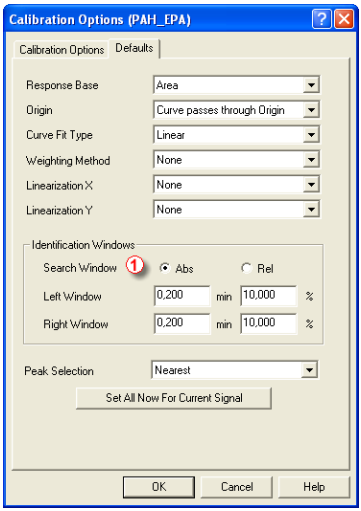

Fig. 27: Identification windows in the Calibration Options dialog

A user can select between absolute (*Abs*) and relative (*Rel*) values and set values for both of them independently. ①.

Curve Fit Type

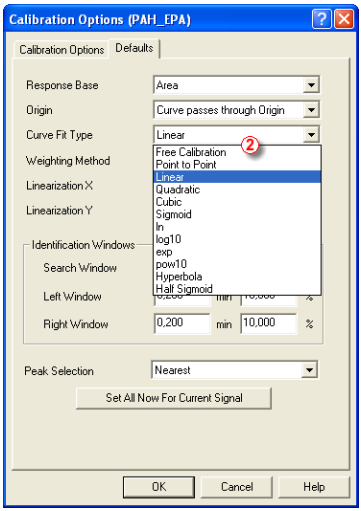

Fig. 28: Curve Fit Type in the Calibration Options dialog

New Curve Fit types ②:

- ln
- log10
- exp
- pow10
- Hyperbola
- Half Sigmoid

For more details see chapter **Calibration** in **Reference Guide**.

Linearization X & Linearization Y

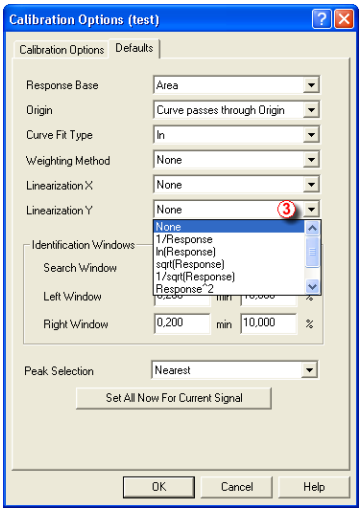

Fig. 29: Linearization X and Linearization Y in the Calibration Options dialog

Sets the axis linearization for the calibration curve calculation ②. The function and its possible options are described in the chapter **Calibration** in the **Reference Guide**.

5.3 Graph Properties

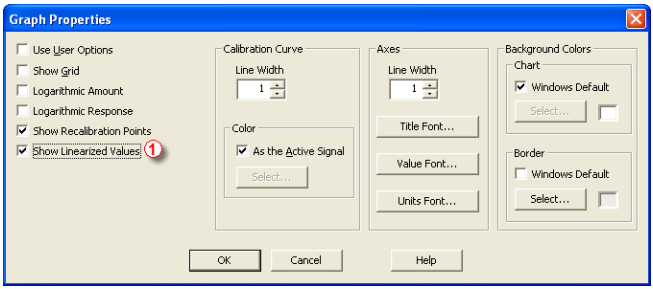

Fig. 30: Graph Properties dialog

The checkbox *Show Linearized Values* ① toggles the display of original and linearized values in the calibration curve graph. The choice is indicated in the Axis description.

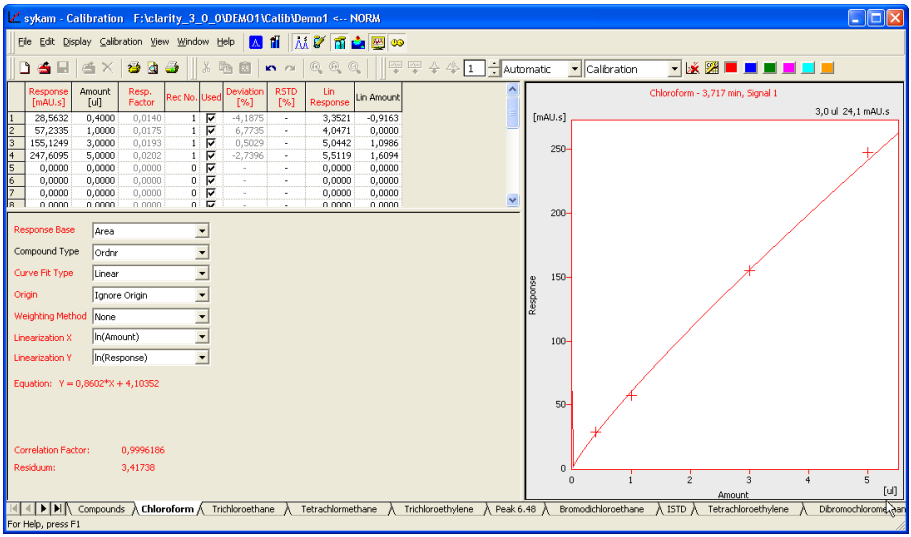

Fig. 31: Calibration window without linearized values

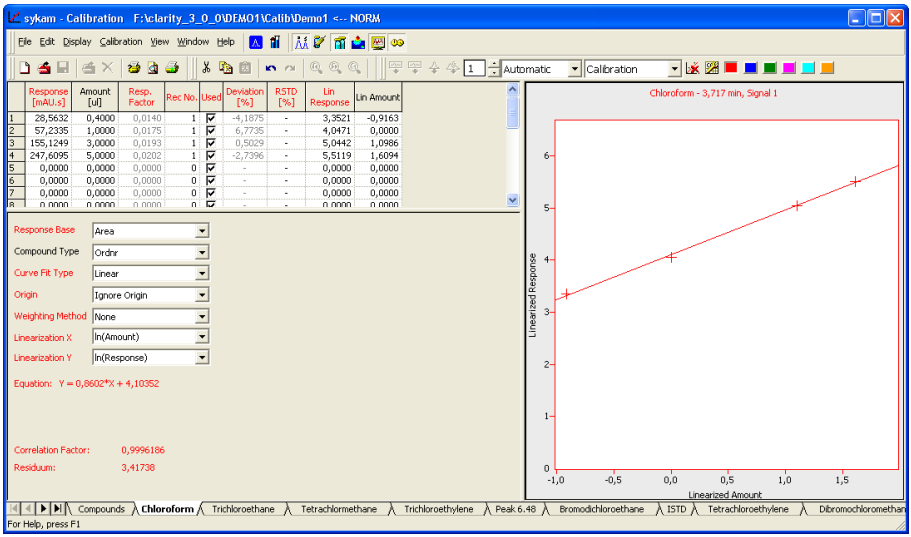

Fig. 32: Calibration window with linearized values

The linearized values are displayed in the *Lin Response* and *Lin Amount* columns on the compound tab.

5.4 Standard Addition Calculation

New **Standard Addition** calculations has been added. The following order of measurements is used: *Blank* (optional), *Unknown* , *Unknown with Standard Addition1*, *Unknown with Standard Addition2*, etc.
First calibration level in *Calibration Table* is used for *Unknown*, the other levels are shifted accordingly. Calibration curve is constructed using the Standard Additions concentrations (assuming Unknown concentration = 0) and the Unknown concentration is determined as an intercept of this curve with the zero response line.
In case a *Blank* is used, its response will shift the zero line used for determination of the intercept.

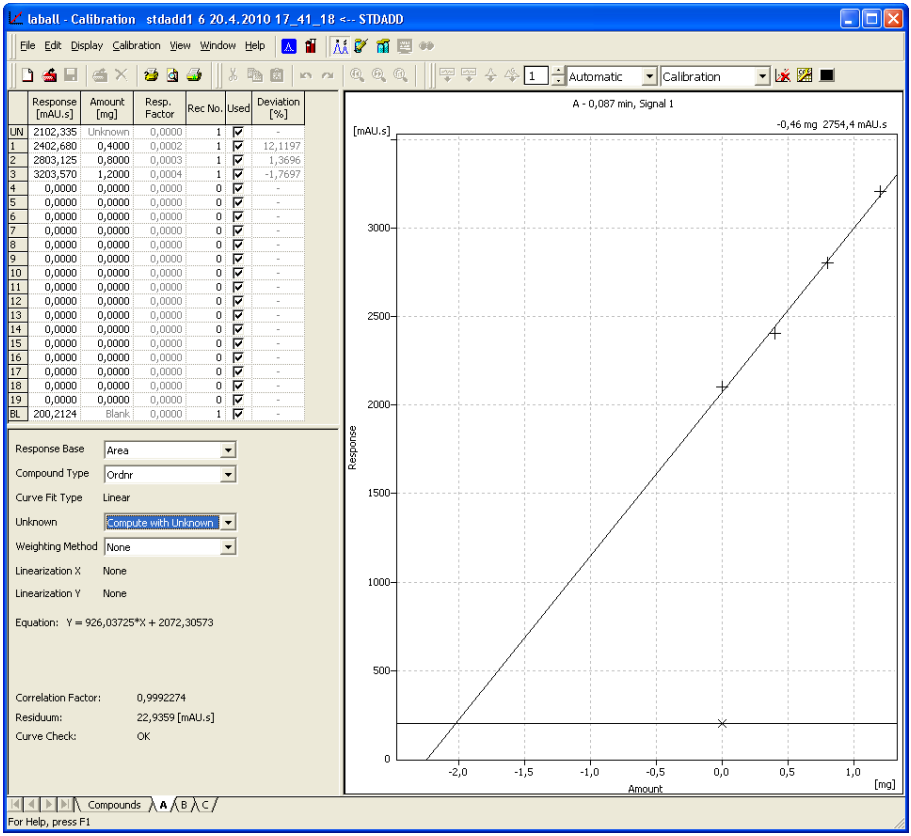

Fig. 33: Standard Addition

Unknown
Specifies the method for including the unknown sample into the calibration curve calculation in the Standard Addition mode. This value is individual for each signal.

Without Unknown Sample
The Unknown sample is not used in calibration curve calculation.

Compute with Unknown
Considers the Unknown sample to be one of the calibration points with *Amount=0*.

Curve passes through Unknown
Always passes the calibration curve through the Unknown sample for *Amount=0*.

Blank
In standard addition calculation the response for blank (Calibration *Level 21* is used to shift the zero response level used to calculate the *Unknown* concentration.

5.5 Normalization Calculation

New **NORM** calculation has been added. This calculation type performs the calculations identically to the **ESTD** calculations according to the actual calibrations settings. The desired *Norm%* results are displayed in the *Amount%* column, the calculation checks the condition that all identified peaks are calibrated and all peaks in calibration were identified in the chromatogram. No results and warning message in *Result Table* header are given in opposite case. It means that *Peak Type* would be *ERROR* and *Amount%* zero.

5.6 Calibration Curve Export

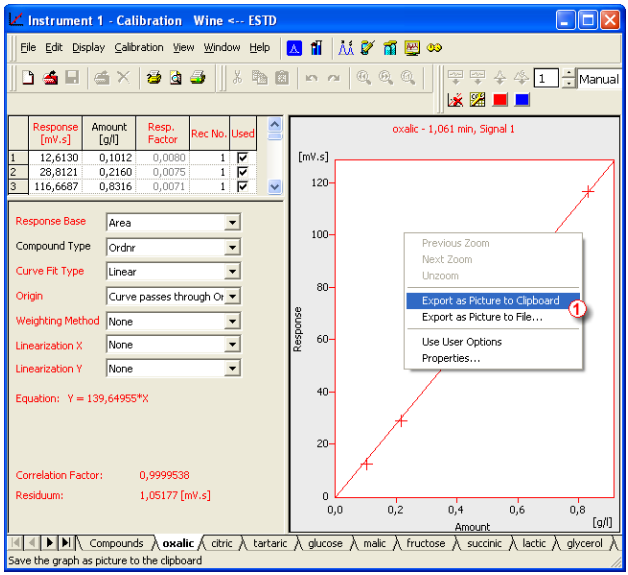

Fig. 34: Exporting the calibration curve

Using the menu *File - Export* or popup menu of the calibration curve area ① it is possible to perform new export functions.

Export as Picture to Clipboard

This command will copy the calibration curve to Windows clipboard. It allows user to quickly utilize picture in another program using the *Paste* command.

Export Calibration Curve as Picture…

This command will open the Save As… dialog, which will save the calibration standard curve into **Enhanced Metafile** format supported by Microsoft Windows and Microsoft Office.

6 Sequence

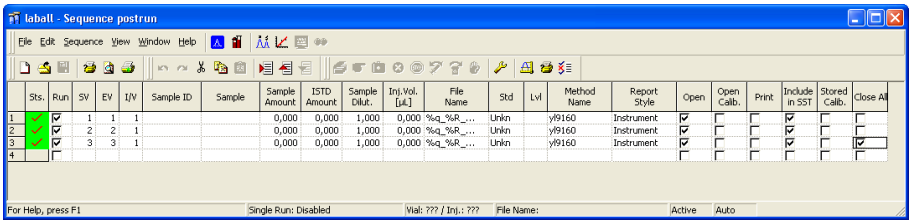

Fig. 35: Sequence window

Sample ID

This field is now limited to *64* characters (was limited to 20).

File name variables

New variables are available in *Sample*, *Sample ID* and *FileName* columns.

- *%P* Name of the project
- *%J* Name of the method (without path and .MET suffix)
- *%s* Name of the sequence (without .path and .SEQ suffix)

Std

Specifies/Sets the type of the sample being measured instead if the previously used *YES*/*NO*. The possible options are:

Unknown

Denotes an unknown sample.

Standard

Specifies the calibration standard. Samples marked as *Standard* must have the calibration level filled in the *Lvl* column. Chromatograms created on the sequence rows marked as calibration standards will be stored in the calibration subdirectory (CALIB by default) instead of the analysis subdirectory (DATA by default).

Bypass

This *Std* type allows for performing an analysis in the *ACTIVE* sequence with controlled autosampler without actually injecting a sample. This may be useful for system clean-up, etc.

Blank

In fact a calibration standard with no amount of added sample. The *Blank* is thus one point of a calibration curve (with the *Amount* of *0*, used on calibration *Level 21*).

Post run columns

New PostRun columns has been added. To display them, use the *Setup Columns…* in the pop-up menu of the *Sequence* table.

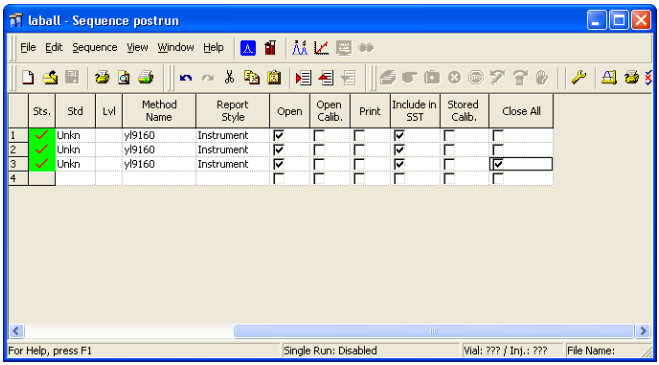

Fig. 36: New PostRun columns

Include in SST

This checkbox allows user to set whether the particular chromatogram will be included in the SST calculations or not.

Close All

This checkbox allows user to close all currently opened chromatograms. Those options enable to create a specific summary reports during sequence run. Opening of the chromatogram measured in the same line of sequence is not influenced by this setting, it follows setting of Open checkbox only.

Stored Calib.

This checkbox causes the chromatogram will be opened with the stored version of the calibration file, as opposed to the linked calibration when not checked. As the use of linked calibration is preferable, should be used exceptionally.

6.1 Sequence Options

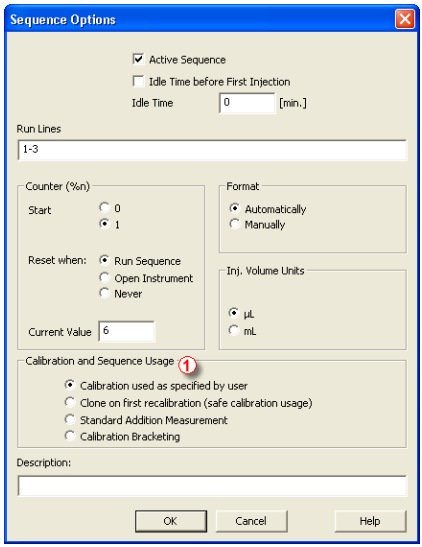

Fig. 37: Sequence Options

Calibration and Sequence Usage

Selects the mode of the calibration and sequence usage. With exception of the first option, suitable calibration file *Cloning* in Method Setup - Calculation should be set, see pg **12**.

Calibration used as specified by user

Sets the sequence and calibration to the standard **Clarity** use (the only way available to version **2.8**). The calibration set in the Method Setup - Calculation dialog is used for calibration and recalibration, no calibration cloning is performed.

Clone on first recalibration (safe calibration usage)

Sets the sequence and calibration to the safe calibration usage mode. The calibration will be cloned at each start of the sequence and at each start of a new sequence. Setting this options *ON* prevents from situations when new measured standards with different responses may devaluate already measured standards because all chromatograms are linked to the created calibration.

Standard Addition Measurement

Sets the sequence and calibration to the Standard Addition mode use. As each unknown sample will use one calibration file, calibration will be cloned from the original calibration file whenever an unknown

sample or blank follows the calibration standard. All responses are cleared from a newly cloned calibration. For more information, see the **Reference Guide**.

Calibration Bracketing

Sets the sequence and calibration to the *Calibration Bracketing* mode use. As every unknown sample series is demarcated by calibration standards and as such uses a single calibration file, calibration will be cloned from the previous calibration clone whenever an unknown sample or blank follows the calibration standard. The unknown samples are calculated against the standards immediately preceding and following them. All responses are cleared from a newly cloned calibration and preserves just the last recalibration responses.

7 Report

Order of the report sections could be modified in the Report Setup dialog.

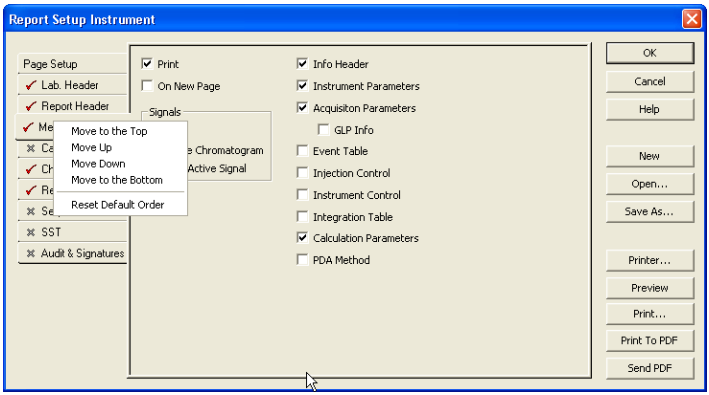

Fig. 38: Popup menu of tabs in the Report Setup

The report is printed in order respective to tabs order on the left. By right click on the tab you can move the tab up or down. The order of *Page Setup* and *Audit & Signatures* can't be changed since they don't represent the print section.

Electronic signature for PDF

Electronic signature for PDF reports (used for GLP). For more details see the chapter **General** on pg **2**.

8 Control Modules Full version

New Control Modules has been added.

Agilent 1200

- Testing.
- Only the **G1315D Diode Array Detector** is currently supported. It has to be controlled by one separate LAN communication line using the **1200** Control Module and the rest of the **1100**/**1200** system by other LAN or GP-IB communication line using the **1100** Control Module on the same **Clarity Instrument** .

Agilent 7890

- Testing.

Sedere ELSD LT80/LT85

- Testing.

Esa Coulochem II

- Testing.

Currently not supported:

- Scan Mode.
- RS 232 (only the USB communication is supported).
- Not possible to control more than one detector at once.
- *Rate* and *Range* are shared in *DC* and *Pulse* Mode due to restriction in **Clarity SDK**.
- *Time Table* is not yet implemented.

8.1 LC Control

- Method Setup - *LC Gradient*: new option *Initial - Standby* in the *Idle State* group enables to set different flows at sending the method and after finishing the analysis. Grayed out for modules not supporting this option.
- Method Setup - *Valves* new *Set Home position on Close instrument* checkbox.

8.2 FC Control

The Fraction Collector (FC GP driver)

- New checkbox *Collect All* in the Method Setup - *FC* - Vial Numbers dialog for FC without diverter value.

- New option *Delay Volume 2* in the Method Setup - *FC* - Fraction Table dialog enables to compensate for volume between valve and collection point.

9 Extensions Full version

9.1 GPC

- **Calibration broad on narrow** - changes of *K* and *Alpha* values will be recorded in the Chromatogram Audit Trail.

9.2 PDA

Export Picture

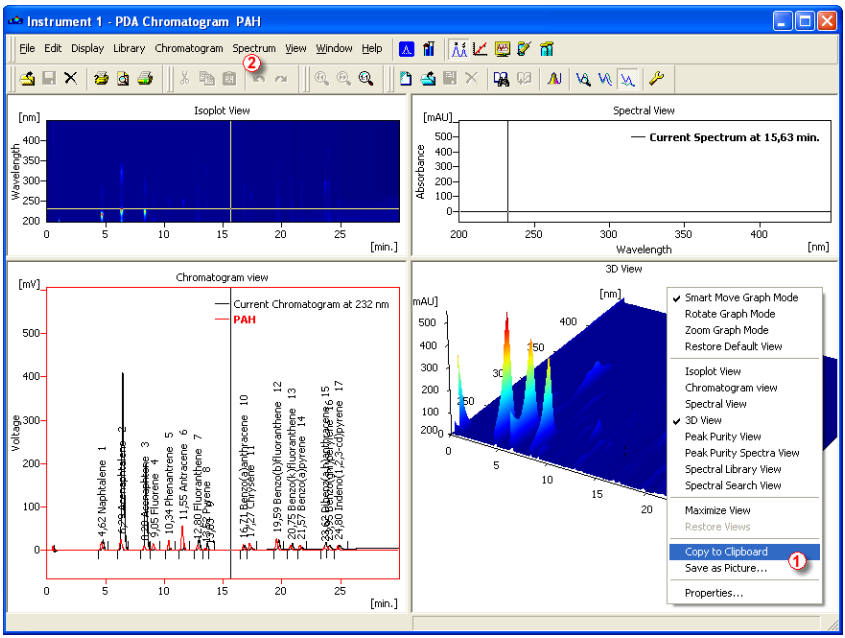

Fig. 39: Export picture in PDA Window

Copy to Clipboard
Available from context menu in the Graph Panes in PDA View window ①.

Save as Picture...
Available from context menu in the Graph Panes in PDA View window ①.

Spectral Library

Add All Identified Peaks
Using the menu *Spectrum - Add All Identified Peaks* ② will add spectra of all identified peaks in chromatogram to a Spectral Library.

Confirmation window will appear:

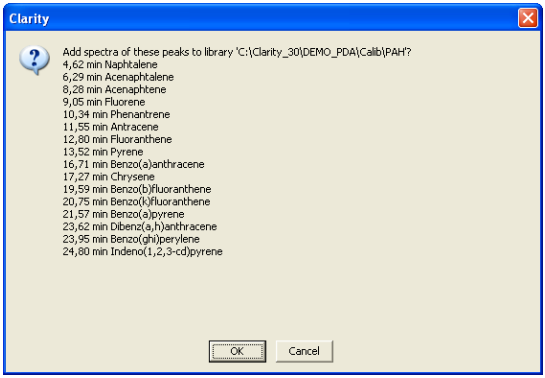

Fig. 40: Question before all identified peaks are added to the library

Spectrum Overwriting

Warning Window will appear upon attempt to add duplicate spectrum name in library.

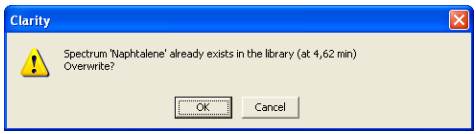

Fig. 41: Warning before duplicate spectrum is added to the spectrum library

10 Other

CopyFiles

Standalone utility "CopyFiles" to copy selected file types to specified directory (available in the UTILS subdirectory of **Clarity** installation folder).

By using this utility in the PostRun Setting dialog it is possible, for example, to additionally copy files such as PDF documents to another network destination. If the network directory is not currently accessible, the **Clarity** will still works without any exception.