DataApex
Clarity™
CHROMATOGRAPHY SOFTWARE

DETAILED HYDROCARBON ANALYSIS

Clarity Extension   ENG

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Contents

To facilitate the orientation in the **Detailed Hydrocarbon Analysis** manual and **Clarity** chromatography station, different fonts are used throughout the manual. Meanings of these fonts are:

> *Open File* (italics) describes the commands and names of fields in **Clarity**, parameters that can be entered into them or a window or dialog name.
> WORK1 (capitals) indicates the name of the file and/or directory.
> *ACTIVE* (capital italics) marks the state of the station or its part.
> [Chromatogram](#) (blue underlined) marks clickable links referring to related chapters.

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

Note: Notifies the reader of relevant information.

Caution: Warns the user of possibly dangerous or very important information.

▌**Marks the problem statement or trouble question.**

Description: Presents more detailed information on the problem, describes its causes, etc.

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

1 DHA - Detailed Hydrocarbon Analysis

The **DHA Extension** is an optional addition to the **Clarity Chromatography Station** (from version **4.0**) if purchased as **p/n A33** (by default it contains official **ASTM D6730**). Additional **ASTM D6730 DANI Optimized Method with/without Cryo** are available exclusively for the DANI company. Any **Clarity *Instrument*** can use *DHA MODE*.

The **DHA Extension** is a tool for data processing and it expands the capabilities of **Clarity Chromatography Station** by providing an interactive tool for calculations according to a selected norm and its properties. These methods are often referred to as **PONA**, **PIONA**, **O-PONA**, etc.

2 Specification

The **DHA Extension** analyses chromatogram data in compliance with the following norms:

ASTM D-6730

- Included in **p/n A33**.
- Standard test method for determination of individual components in spark ignition engine fuels by 100–metre capillary (with precolumn) high-resolution gas chromatography. See the documentation of this norm for details.

ASTM D6730 DANI Optimized Method with Cryo

- Not included in **p/n A33**, available exclusively at DANI company only.
- See details in the chapter **"ASTM D6730 DANI Optimized Method with Cryo"** on pg. **2**.

ASTM D6730 DANI Optimized Method without Cryo

- Not included in **p/n A33**, available exclusively at DANI company only.
- See details in the chapter **"ASTM D6730 DANI Optimized Method without Cryo"** on pg. **3**.

Custom Method

- Included in **p/n A33**.
- See details in the chapter **"Custom DHA Method"** on pg. **3**.

2.1 ASTM D6730 DANI Optimized Method with Cryo

Oven

- Initial temperature 5 °C.
- Initial time 10 min.
- First program rate 5 °C/min.
- First hold temperature 50 °C.
- First hold time 0 min.
- Second program rate 1.5 °C/min.
- Final temperature 200 °C.
- Final hold time 5 min.

Injector

- Temperature 250 °C.
- Split ratio 150:1.
- Sample size 0.5 uL

Detector

- FID.
- Temperature 250 °C.
- Hydrogen 30 mL/min.

- Air 300 mL/min.
- Nitrogen 30 mL/min.

Carrier gas
- Helium, pressure constant: 4.16 bar.

2.2 ASTM D6730 DANI Optimized Method without Cryo

Oven
- Initial temperature 35 °C.
- Initial time 15 min.
- First program rate 1 °C/min.
- First hold temperature 60 °C.
- First hold time 20 min.
- Second program rate 2 °C/min.
- Final temperature 200 °C.
- Final hold time 5 min.

Injector
- Temperature 250 °C.
- Split ratio 150:1.
- sample size 0.5 uL.

Detector
- FID.
- Temperature 250 °C.
- Hydrogen 30 mL/min.
- Air 300 mL/min.
- Nitrogen 30 mL/min.

Carrier gas
- Helium, pressure constant: 4.16 bar.

2.3 Custom DHA Method

In the **DHA Extension**, it is possible to set up a custom method, which can be used to calculate the DHA parameters of your chromatograms. For a description on how to create a custom norm, see the chapter **"How to create a custom norm"** on pg. **20**.

3 Installation of the DHA Extension

The **DHA Extension** is enabled by the appropriate user code, entered during the installation or later by using the *Help - User Code…* command from the *Clarity* main window.

Caution: *DHA mode* is available only on **Clarity GC** Instrument type.

To switch an *Instrument* to the *DHA MODE*, select the *GC-DHA* option from the *Instrument Type Setting* dialog, which is invoked by clicking on the ⋯ button in the *System Configuration* dialog.
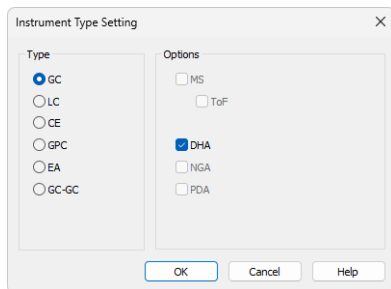
Fig. 1: Switching to the DHA MODE

4 Description of the DHA Extension

The functions of the **DHA Extension** are enabled in **Clarity** when a User Code containing **p/n A33** is entered. This manual lists and describes the features changed in or added to **Clarity** via the **DHA Extension**.

4.1 Chromatogram window

A new <u>DHA</u> tab is available in the *Chromatogram window* (opened by clicking the 🏔 icon). Furthemore, there is a new *DHA* menu at the top of the window.

4.1.1 DHA

The *DHA* tab is divided into two panes:

- Left pane: includes the <u>DHA Results</u> and the <u>DHA Group Results</u> tabs.
- Right pane: includes the <u>DHA Settings</u>.

4.1.2 DHA Settings

In this pane you can set up the **DHA Method** - choose the norm and edit its specific parameters.

Fig. 2: Chromatogram window - DHA - DHA Settings

DHA Method ①

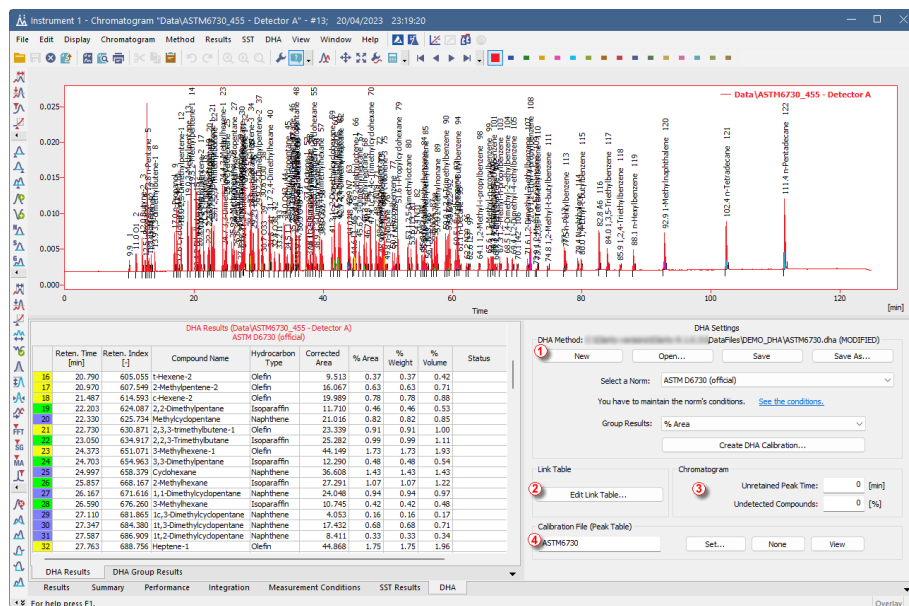Shows the currently opened *DHA Method*. All settings in the *DHA Method* are saved in the *.DHA file, which is independent on the method opened from the *Instrument* window. The last opened *DHA Method* used in the *Chromatogram* window is saved in the project file (for more details, see also the chapter Project).

> **New**
> Creates a new *DHA Method* with default settings.

> **Open**
> Displays the *Open DHA Method* dialog where you can open the *DHA Method* you want to use.

> **Save**
> Saves the settings of the current *DHA Method*.

> **Save As…**
> Opens the *Save As* dialog for saving the *DHA Method* into a new file.

> **Select a Norm**
> Select the norm you want to use for your calculations.

....

Caution: Norms available in this menu depend on the **p/n** of your purchased DHA Extension. See the chapter the chapter **"Specification"** on pg. **2**.

In the case you select a norm you have not purchased, an error dialog is displayed:
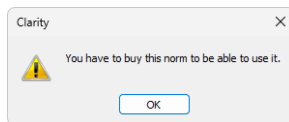
Fig. 3: Error when selecting a non-available norm

> **See the conditions**
> By clicking on the link, you can display the help containing the conditions valid to each norm.

> **Group Results**
> Select units used in the DHA Group Results.

> **Create DHA Calibration**
> By clicking this button, the Create DHA Calibration dialog is displayed. It allows you to create a DHA Calibration and display it in the *Calibration* window.

> The *DHA Calibration* is created from the opened standard chromatogram, which must contain from 6 to 11 calibrated peaks from the **n-Paraffins** standard sample. *Clarity* will perform an interpolation through the points from the **n-Paraffins** standard and automatically calculate *Retention Times* for all other peaks from the *Retention Indexes* in the norm.

Link Table ②

The *Compound Names* for the DHA Results and the Group Results are retrieved from the *Calibration Table*. In the *Calibration*, you must set the peak detection to one signal only; otherwise you will see warnings in the DHA Results.

In situations, when the *Compound Names* in norms have different names than the ones you have saved in your calibration, you can use *Link Table* for linking those *Compound Names* and ensure that all compounds are included in the selected norm calculations. For more details see the chapter **Link Table** on pg. **7**.

Edit Link Table…
Opens the Link Table dialog, where you can edit the links between compound names in calibrations and norms.

Chromatogram ③

Unretained Peak Time
This parameter defines the column dead time in minutes. This field corresponds to the same field in the Performance tab.

Caution: The *Unretained Peak Time* is used depending on the *Retention Indexes use Log. Interpolation with Unretained Peak* option in the *Calibration Options*. When this option is not checked, the retention indexes are calculated using **linear interpolation**. When it is checked, **logarithmic interpolation with unretained peak** time is used.

Undetected Compounds
This parameter defines the value in % of compounds which are undetected in the DHA Results - column *% Weight* (*% Volume* is calculated from the *% Weight* column). The weight of the particular detected compound will be calculated as: 100-(*Undetected Compounds*) [%].

Calibration File (Peak Table) ④

This field and group of buttons work identically as the buttons in the *Results* tab.

Set…
Opens the *Open Calibration* dialog for setting the linked *Calibration*.

None
No Calibration will be used.

View…
Displays the linked Calibration.

4.1.2.1 Link Table

This dialog is used for editing the *Link Table* in the **DHA Extension**. The *Link Table* is used in those cases, when you have unresolved compound names in the Result Table. For example, you are using compound names specific to your language, but in the selected norm, there is a different name for the same compound. The *Link Table* allows you to use your custom compound names from calibrations and chromatograms as often as you need, without any changes in the norms.
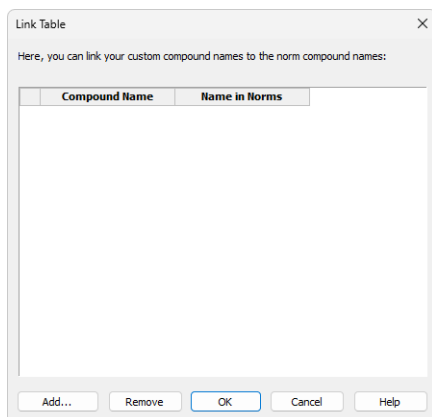
Fig. 4: Link Table dialog

1st column in the table

  Line number of compounds present in the *Link Table*.

Compound Name

  The compound name in the *Calibration* that you want to link with the name in norms, and thus to include in the Result Table and Group Result Table.

Name in Norms

  The compound name present in norms (if the name is in multiple norms, only one occurrence is displayed).

Add…

  Displays the Add Link dialog for adding a new record to the link table.

Remove

  Removes the selected record from the *Link Table*.

OK

  Saves the settings to the *Link Table* and exits.

Cancel

  Exits the dialog without saving any changes to the *Link Table*.

4.1.2.1.1 Add Link

  The *Add Link* dialog is used for adding a new item to the Link Table. It is useful in the case you want to link a compound name from the DHA Results to a compound name in a norm. This includes compounds in the DHA calculations.
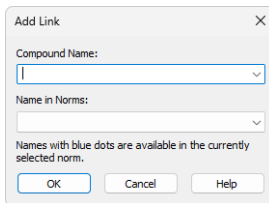
Fig. 5: Add Link dialog

Compound Name

Enter the compound name you want to link to a name from norms. Unresolved compounds in the chromatogram are suggested in the drop-down menu.

Name in Norms

Select the appropriate compound name from norms. Names from all supported norms are available in the drop-down menu. For better orientation, blue dots are displayed on the names from the norm selected in the DHA Settings.

4.1.2.2 Create DHA Calibration
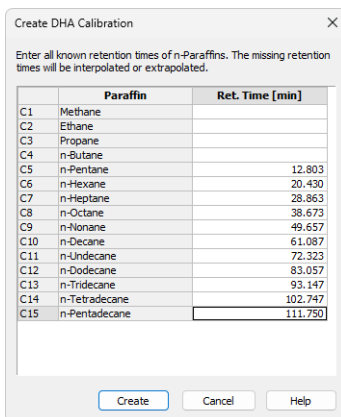
Fig. 6: Create DHA Calibration dialog

This dialog is displayed when you click the *Create DHA Calibration…* button in the DHA Settings. The table contains the list of detected *n-Paraffins* from the measured known sample. The dialog allows you to manually adjust the retention times of particular compounds.

The main purpose of this dialog is to enter the retention times of *Methane*, *Ethane*, *Propane*, and *n-Butane* which you may have measured in a different chromatogram.Starting from the n-Pentane paraffin, the retention times are automatically added.

The minimum number of n-Paraffins in your known sample is 6 and the maximum is 11. If this condition is not met, an error dialog is displayed:
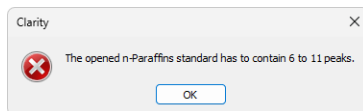
Fig. 7: The opened n-Paraffins standard has to contain 6 to 11 peaks.

4.1.3 DHA Results

The *DHA Results* section on the *DHA* tab contains information about the detected compounds and calculated results.
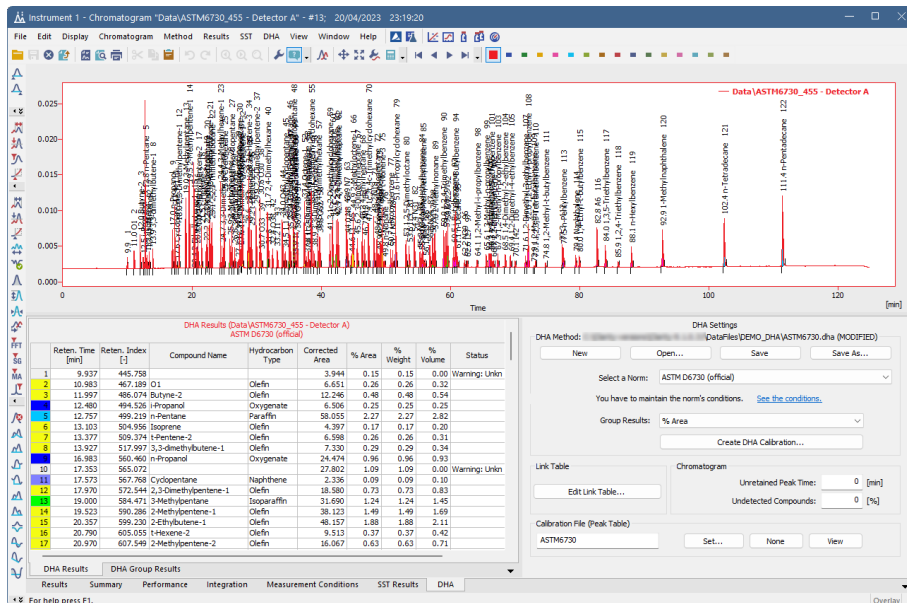
Fig. 8: Chromatogram window - DHA - DHA Results

DHA Results

Above the table, you can see information about the signal from which the results were calculated, and also the selected norm. To obtain valid data, you must create a calibration first using *Create DHA Calibration*. The calibration must use the same norm as selected for displaying the Results. Otherwise, you will see one of the following warnings:

- **Linked calibration was not generated by DHA**

  The *Calibration* you have linked to the chromatogram was not created using the **DHA Extension**. Create it using the *n-Paraffins* known sample via the Create DHA Calibration… button.

- **Norm selected for DHA Method <norm name> and DHA Calibration <norm name> do not match**

Different norms are selected in *DHA Results* and *DHA Calibration*.

- **Unretained Peak Time has to be enabled in Calibration**

  To correct this behavior, you must open the Calibration Options dialog in the linked *Calibration* and enable the *Retention Indexes use Log. Interpolation with Unretainded Peak* option.

- **Unretained Peak Time in Chromatogram <number> and DHA Calibration <number> do not match**

  Your linked *DHA Calibration* was generated with different *Unretained Peak Time* than what the current *DHA Method* contains. Correct it in the DHA Settings or create *DHA Calibration* again with the requested *Unretained Peak Time*.

- **Unretained Peak Time is non-zero**

  This is an informational message that appears when the *Unretained Peak Time* is set to a non-zero value.

- **DHA Calibration is not linked**

  Calibration is not linked. You will not see any results until you link a *DHA Calibration*.

Reten. Index
 Retention Index of a compound. It is saved in the norm table (the DHA.CSV file located in the CLARITY\DATFILES\COMMON directory).

Compound Name
 If the chromatogram contains calibrated peaks or groups, the names are shown in the *Compound Name* column. The table contains compounds from all signals in the chromatogram.

Hydrocarbon Type
 The hydrocarbon type of the compound retrieved from the selected norm.

Corrected Area
 Corrected area of a specific compound in the measured chromatogram.

% Area
 % Area of the a specific compound in the measured chromatogram. The value is based on the corrected area value, which is calculated from the chromatogram peak area multiplied by the relative response factor – meaning that it is in fact based on the compound amount.

% Weight
 % Weight of a specific compound in the measured chromatogram. The value is based on the entire sample amount. It may be corrected for the undetected compounds percentage (like water etc., determined by external methods) entered in the respective field. When this field is non zero, the *% Area* and *% Weight* values will differ accordingly.

% Volume

% Volume of a specific compound in the measured chromatogram. It is calculated as the ratio of *(% Weight)/(Relative Density)*.

Status

A Warning may appear if the compound name is not found in the selected norm. If you can match the present compound with a compound from the norm, click on the Edit Link Table… button. In the displayed window, you can link compounds from the chromatogram with compound names in the norm.

4.1.4 DHA Group Results

In the *DHA Group Results* tab, you can find results calculated according to hydrocarbon types. The results are automatically recalculated each time you open or change the chromatogram or select different norm or modify its parameters.
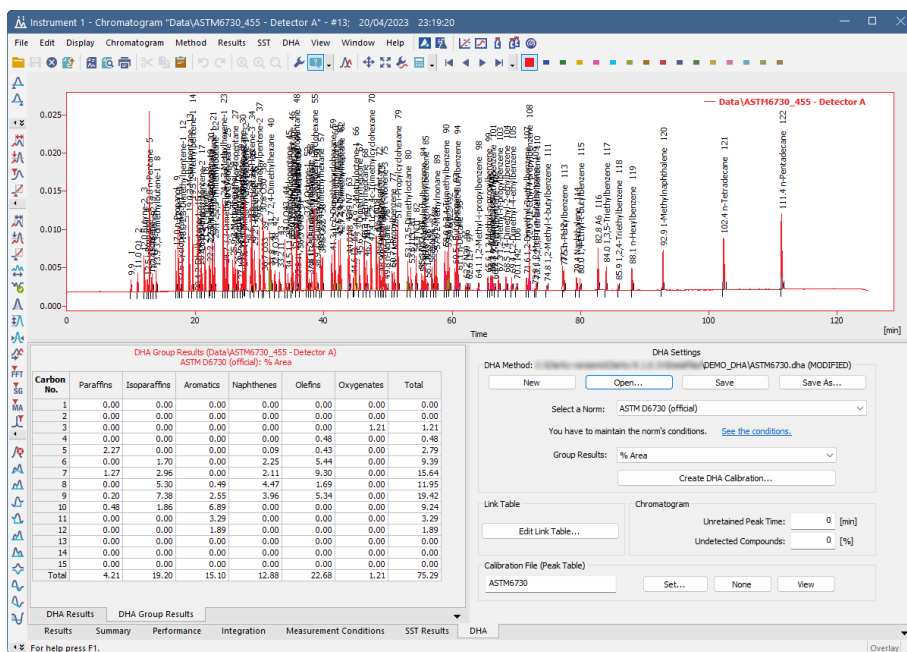
Fig. 9: Chromatogram window - DHA Group Results

DHA Group Result Table

This table displays the results in a special pivot table. The units of the results in the table depend on the units you have selected in the *DHA Settings - Norm - Group Results* combo-box. You can see the summary results per carbon number or per a group of paraffins. You may see the following warnings:

- **Linked calibration was not generated by DHA**

The *Calibration* you have linked to the chromatogram was not created using the **DHA Extension**. Create it using the *n-Paraffins* known sample via the Create DHA Calibration… button.

- **Norm selected for DHA Method <norm name> and DHA Calibration <norm name> do not match**

    Different norms are selected in *DHA Results* and *DHA Calibration*.

- **Unretained Peak Time has to be enabled in Calibration**

    To correct this behavior, you must open the Calibration Options dialog in the linked *Calibration* and enable the *Retention Indexes use Log. Interpolation with Unretainded Peak* option.

- **Unretained Peak Time in Chromatogram <number> and DHA Calibration <number> do not match**

    Your linked *DHA Calibration* was generated with different *Unretained Peak Time* than what the current *DHA Method* contains. Correct it in the DHA Settings or create *DHA Calibration* again with the requested *Unretained Peak Time*.

- **Unretained Peak Time is non-zero**

    This is an informational message that appears when the *Unretained Peak Time* is set to a non-zero value.

- **DHA Calibration is not linked**

    Calibration is not linked. You will not see any results until you link a *DHA Calibration*.

4.2 Report Setup

In the *Report Setup* dialog, tab *DHA*, you can set the printing options for the data in the **DHA Extension**.
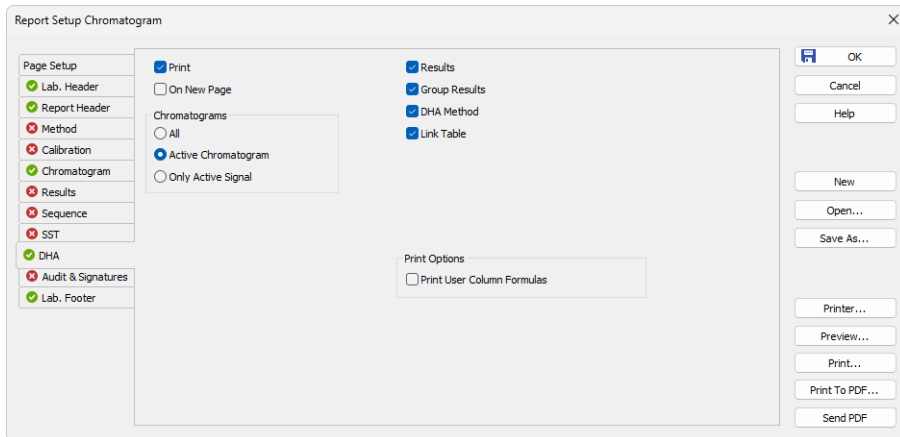
Fig. 10: Report Setup DHA dialog

Print

Enable/disable the printing of the DHA details. If checked, the symbol ⊘ will be shown before the tab name and other fields on the tab will become editable.

On New Page
If checked, the **DHA Section** is printed on a new page.

Chromatograms

> **All**
> Prints data for all chromatograms opened in the *OVERLAY MODE*.

> **Active Chromatogram**
> Prints data for the *ACTIVE Chromatogram* only.

> **Only Active Signal**
> Prints data for the *ACTIVE Signal* only.

Results
If checked, prints the *DHA - Results*.

Group Results
If checked, prints the *DHA - Group Results*.

DHA Method
If checked, prints the information about the DHA method.

Link Table
If checked, prints the Link Table.

Print Options

Defines additional options for the printed report.

Print User Column Formulas

Adds calculation formulas used in added User Columns including *User Variables* at the end of the appropriate table to be printed.

. . . .

Note: For the GLP mode, formulas are printed automatically, even if the checkbox is disabled.

4.3 Export Data

In the *Export Data* dialog, you can set whether the **DHA - Result Table** and the **DHA - Group Result Table** will be included in the exported data. For more details, see the chapter Export Data in the **Clarity Reference Guide**.
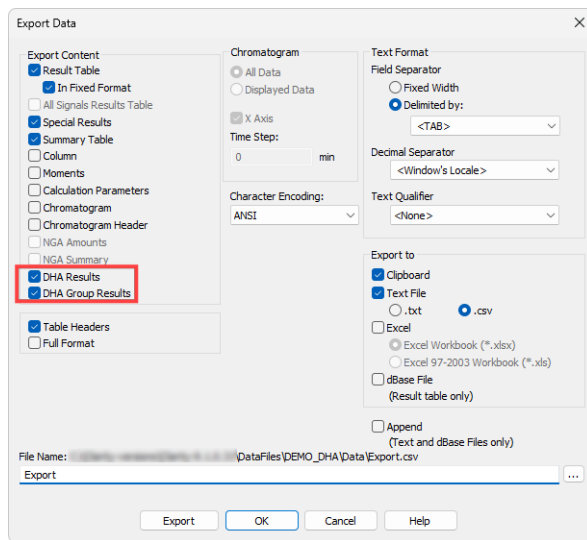

Fig. 11: Export Data dialog

5 How to try the DHA Extension

5.1 How to try the DHA demo project

In this chapter, you can find information on how to try the **DHA Extension** using the DHA demo project for the first time.

Step 1

In the *System Configuration* window (menu *Clarity - System…*), select the **DHA** option in the *Instrument Type Setting* dialog, for example on *Instrument 1*.

For more details, see also the chapter Installation.

Step 2

After saving and closing the *System Configuration* window, open the appropriate **Instrument**. Now, open the DHA demo project: in the *Login Dialog*, select **DEMO_DHA** in the *Select Project* drop-down list and click the *OK* button.

Step 3

Open the *Chromatogram* window (it can be opened by clicking on the menu *Window - Chromatogram*). In the lower part of the *Chromatogram* window, you can see the new *DHA* tab. Open the chromatogram N_ PARAFFINS_ FOR_ ASTM6730.PRM using the *File - Open Chromatogram…* menu. The file is located in the DEMO_DHA\DATA folder in your **Clarity** installation directory (by default C:\CLARITY\DATAFILES). This file is the calibrated (known) sample, including the n-Paraffins standard.

Step 4

Click the *DHA* tab, and on the right side of the pane, you will see the *DHA settings*. There you can set the norm or create a new DHA Calibration. The current settings are saved in a special .DHA file, which allows you to use the **DHA settings** on multiple **Chromatograms**. Click the *Open…* button to browse the **Clarity Installation** directory (by default C:\CLARITY\DATAFILES). In the DEMO_DHA subdirectory, select the ASTM6730.DHA file. **DHA Method** will be loaded, and the **Chromatogram** which is *ACTIVE* will be automatically recalculated when you choose different norms or parameters.

For more details see the chapter **DHA Settings** on pg. **5**.

Step 5

In the *DHA Settings* pane, select the norm, for example *ASTM D6730 (official)*. This norm will be used when creating the *DHA Calibration*. Click the *Create DHA Calibration* button, and the **Calibration** window, including the new *DHA Calibration*, will be displayed. Save the calibration file. If you link this calibration to an unknown sample (chromatogram) in the DHA Extension, you will see the calculated result of specific groups.

Step 6

Close the **Calibration** window, and in the **Chromatogram** window, open an unknown sample from the DEMO_DHA project, for example the ASTM6730_455.PRM. Click the *DHA* tab, and in the lower part of the *DHA Settings*, you will see that this

chromatogram has already linked a calibration file *ASTM6730_C5-C15-RI*. Note that this is the same function as the *Calibration File* field in the *Results* tab of the *Chromatogram* window. You can change it to the calibration created in **Step 5**.

Step 7

In the *Result Table* sub-tab of the *DHA* tab, you can see the calculated results of compounds identified in the chromatogram. Click the *Group Result Table*, where the compounds are calculated in a pivot table. It contains the sums of all compounds per group or carbon number.

If there is a compound in the *Result Table* that is not in the selected norm in the *DHA Settings*, the *Status* column displays a warning. The norm requires that all the compound names are the same as in the norm tables. If you need to link a compound name from the chromatogram with a matching compound name from the norm, click the *Edit Link Table…* and in the displayed dialog, link the compound name from the chromatogram with the name in the norm.

6 How to work with the DHA Extension

6.1 How to measure DHA Data for the first time

Step 1

See the chapter **"Specification"** on pg. **2**. for an overview of specifications of supported DHA norms. For perfect and valid results, it is necessary to prepare your instrument and method according to the specification of a particular norm. Otherwise, the data you are about to measure will be useless.

Step 2

In the *System Configuration* window (menu *Clarity - System…*), select the **DHA** in the *Instrument Type Setting* dialog, for example on the *Instrument 1*. For more details, see also the chapter Installation.

Step 3

After saving and closing the *System Configuration* window, open the appropriate **Instrument**. Now, create a new project: in the *Login Dialog*, select **<New Project>** in the *Select Project* drop-down list and click the *OK* button. In the *Create Project or Save as...* dialog, name your new project and click *OK*.

Step 4

Now, you have to create the **DHA Calibration** according to the selected norm and your instrument. **DHA Calibration** is a *Calibration* that contains parameters required for the DHA calculations. Proceed as follows:

Measure the known **n-Paraffins** samples. It is best to measure all the possible **n-Paraffins** to have an exact interpolation of the calculated **Retention indexes**. In order to create the full calibration with all **n-Paraffins**, it is necessary to measure two standards (first for **C1-C4** and then for **C5-C15**). As a minimum, you have to use **C5-C11**, however, extrapolations usually do not work.

Open the measured chromatogram with integrated **C5-C15 n-Alkanes**, and in the *DHA Settings*, select the norm you intend to use and click the *Create DHA Calibration* button. The displayed dialog automatically fills the **n-Alkanes** starting from **C5**. If you have measured the **Retention times** of **C1-C4 n-Paraffins** beforehand, fill them out manually based on the corresponding chromatogram.

Save the created **DHA Calibration**. Note that in this type of calibration, the option *Retention Indexes use Log. Interpolation with Unretained Peak* in the *Calibration Options* is automatically enabled.

Step 5

Now, you can prepare a method for measuring the unknown data.

If you want to link the **DHA Calibration** to your measured chromatograms automatically, select the one created in **Step 4** using the *Set…* button in the *Method Setup - Calculation* window below the *Calibration (Peak Table)* field.

Step 6

Measure the unknown data using the *Method* created in the previous step.

Step 6

In the *Chromatogram* window - *DHA* tab, you can find the DHA Results and DHA Group Results subtabs containing the DHA Calculations.

Finally, you can continue to the chapter **"How to print or export results from the DHA Extension"** on pg. **20**.

6.2 How to print or export results from the DHA Extension

Ensure you have selected the **DHA** *Instrument Type* in the *System Configuration* window as described in the chapter **"How to try the DHA Extension"** on pg. **17**.

Print

To print the data from the **DHA Extension**, open the Report Setup window by clicking the menu *File - Report Setup…* in the *Instrument* window or in the *Chromatogram* window.

On the left side, select the *DHA* tab. By clicking the *Print* checkbox, you enable other controls on that pane. By choosing different options, you can configure what information will be printed.

Settings from the *Report Setup* are then used in the print output and preview, accessible from the *File* menu on the *Instrument* window and the *Chromatogram* window.

You can also use the prepared DHA Report style. In the Report Setup window, click *Open…* and select the DHA_RESULTS.STY file.

For more details, see also the chapter Report Setup.

Export

Open the *Setting - Export Data…* menu in the *Instrument* window. Set the *DHA Result Table* and *DHA Group Table* checkboxes to include those tables in the exports. Settings in this window are then used in the *Single Analysis - Post Run Settings* tab.

For more details, see also the chapter Export Data.

6.3 How to create a custom norm

Besides the selected norms, the **DHA Extension** enables you to create your own norm that meets the conditions for analyzing the DHA data in your laboratory.

DHA Extension uses the DHA.CSV file located in the COMMON subdirectory of the installation directory (for example, C:\CLARITY\ DATAFILES\ COMMON\ DHA.CSV). This file contains Compounds, Retention indexes, and other information required for DHA calculations. It also includes the *RICustom* column, which contains Retention indexes you will measure while developing your norm.

Follow as described below:

Step 1

Open the DHA.CSV file in a spreadsheet application, for example **MS Excel**. The file uses a *dot* as the decimal separator. If your local settings of **MS Excel** or **Windows** use a *comma* as the decimal separator, this may corrupt the DHA.CSV

file when saving any changes. Before editing this file, change the local settings of your **Windows** to use a *dot* as the decimal separator.

Step 2

Measure the known **n-Paraffins** samples and create the **DHA Calibration** using the **Custom norm**. It is best to measure all the possible **n-Paraffins** to have an exact interpolation of the calculated *Retention indexes*. In order to create a full *Calibration* with all **n-Paraffins**, it is necessary to measure two standards (first for **C1-C4** and then for **C5-C15**). As a minimum, you have to use **C5-C11**, however, extrapolations usually do not work.

Step 3

Open the measured chromatogram with the integrated **C5-C15 n-Alkanes**, and in the *DHA Settings*, select the *Custom norm (edit DHA.csv)* and click the *Create DHA Calibration* button. The displayed dialog automatically fills the **n-Alkanes** starting from **C5**. If you have measured the **Retention times** of **C1-C4 n-Paraffins** beforehand, fill them out manually based on the corresponding chromatogram.

Save the created **DHA Calibration**. Note that in this type of calibration, the option *Retention Indexes use Log. Interpolation with Unretained Peak* in the *Calibration Options* is automatically enabled. Now, you have prepared the initial **DHA Calibration** with **n-Paraffins**.

In the *Calibration* table, display the *Reten. Index* column. You can see that the calibration has automatically filled out the **Retention indexes** for the **n-Paraffins**.

Also, check the *Reten. index* column in the *Chromatogram* window - *Result table*,

Step 4

The next step is measuring the compounds and calculating the **Retention indexes** for your custom norm. You can now measure your data, including compounds for developing the **Custom norm**. The *Retention indexes* of the measured compounds are automatically calculated by **Clarity** based on the **Retention indexes** of **n-Paraffins** in the *Calibration* and **Retention times** in the *Chromatogram*. You have to obtain the **Retention indexes** of all compounds listed in the first column of the DHA.CSV file and write them manually into the last *RICustom* column. This file will be used for generating the final **DHA Calibration**, which you will use for measuring the unknown data.

Step 5

Finally, you will create the **DHA Calibration**. Follow the detailed description in the chapter **"How to work with the DHA Extension"** on pg. **19**. The difference is in the DHA Settings, where you select the *Custom norm* and click the *Create DHA Calibration* button. The **DHA Calibration** will contain extrapolated **Retention times** calculated from the **DHA Custom norm**. Note that the DHA.CSV file is applied when opening the **Clarity** station. You need to restart **Clarity** for the modifications to take effect.