



## DETAILED HYDROCARBON ANALYSIS

Clarity Extension

ENG

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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:

**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, some sections are written in format other than normal text. These sections are formatted as follows:

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**Note:** Notifies the reader of relevant information.

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

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**█ 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 it is purchased as **p/n A33** (contains official **ASTM D6730**). Additional **ASTM D6730 DANI Optimized Method with/without Cryo** are available at DANI company exclusively. 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 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°/min.
- First hold temperature 50°C.
- First hold time 0 min.
- Second program rate 1.5°/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°/min.
- First hold temperature 60°C.
- First hold time 20 min.
- Second program rate 2°/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 develop a customized method, which can be used to calculate the DHA parameters of your chromatograms. For a description on how to create the custom norm, see the chapter "**How to create a custom norm**" on pg 25.

## 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** Instrument type of **GC**.

To switch an **Instrument** to the *DHA MODE*, select the **GC-DHA** option from the **Instrument Type Setting** dialog.

**Instrument Type Setting** dialog is invoked by clicking on the  button in the **System Configuration** dialog.

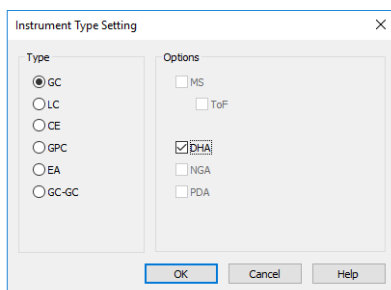



Fig 1: Switching to the DHA MODE



## 4 Description of the DHA Extension

After installation, the new functions of the **DHA Extension** will be available. Only features changed or added to the **Clarity** standard mode are listed and described here.

### 4.1 Chromatogram window

A new DHA tab is available in the [Chromatogram window](#) (opened by clicking the  icon). Also, there is a *DHA* menu at the top of the window.

#### 4.1.1 DHA

The *DHA* tab is divided into two panes:

- Left pane: includes the [DHA Results](#) and the [DHA Group Results](#) tabs.
- Right Pane: includes the [DHA Settings](#).

## 4.1.2 DHA Settings

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

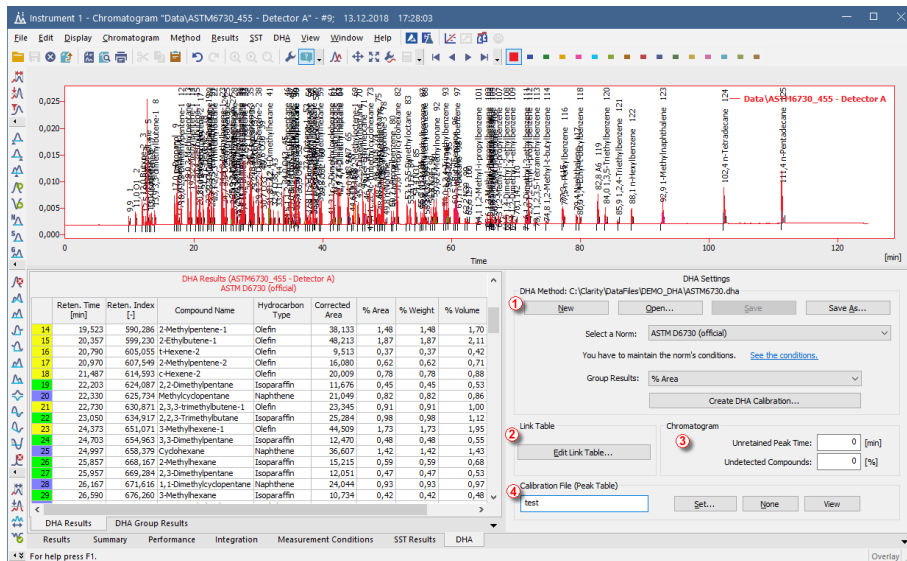


Fig 2: Chromatogram window - DHA - DHA Settings

### DHA Method ①

Currently opened *DHA Method*. All settings in the *DHA Method* are saved in the \*.DHA file and it is independent of the method opened on the **Instrument**. Last opened *DHA Method* used in the **Chromatogram** window is saved in the project file (for more details see also chapter Project).

#### New

Creates new a *DHA Method* with default settings.

#### Open

Displays the **Open DHA Method** dialog where you can open the one 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 depends on the **p/n** of the **DHA Extension** you have purchased. See the chapter "**Specification**" on pg 2.

In case you select a norm you didn't purchased, an error dialog is displayed:

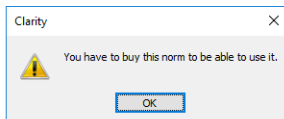


Fig 3: Error when selecting a non-available norm

### 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 on 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-Parrafins** standard sample. **Clarity** will perform an interpolation through the points from the **n-Parrafins** standard and automatically calculates *Retention Times* for all other peaks from the *Retention Indexes* in the norm.

### Link Table

The *Compound Names* for the DHA Results and the Group Results are retrieved from the *Calibration Table*, it does not matter whether the **Calibration** is saved in the linked calibration file or saved in the *Chromatogram*. You can find how to set the *Calibration* in the chapter "Calibration" in the **Clarity Reference Guide**. In the **Calibration**, you must set the detection of the peak in one signal only; otherwise you will see warnings in the [DHA Results](#).

In such situations, when *Compound Names* in norms have different names than the ones you have saved in your calibrations 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 9.

### Edit Link Table...

Opens the [Link Table](#) dialog, where you can edit the links between *Compound Names* in the 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:** An *Unretained Peak Time* is used only if the *Retention Indexes use Log. Interpolation with Unretained Peak* option in the [Calibration Options](#). Note that when this option is unchecked, then the retention indexes are calculated using **linear interpolation**. When it is checked, then **logarithmic interpolation with unretained peak** time is used.

### Undetected Compounds

The 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 using the formula  $100 - (\text{Undetected Compounds}) [\%]$ .

## 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 in norms as often as you need, without any changes in the norms table.

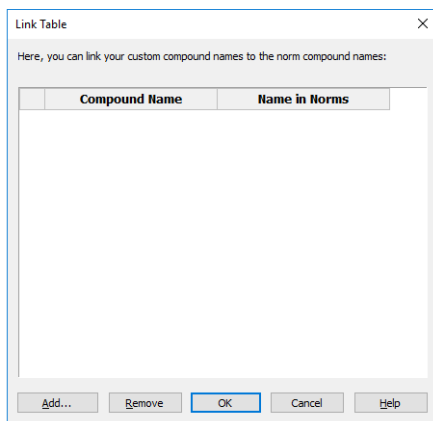


Fig 4: Link Table dialog

#### 1<sup>st</sup> column in the table

Order number in the *Link Table*.

#### Compound Name

It is the compound name (in the **Calibration**) you want to link with the Name in the Norm and thus include in the **Result Table** and **Group Result Table**.

#### Name in Norms

The Compound Names occurs in the 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 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 case when you want to link a compound name from the [DHA Results](#) to a compound name in the norm. This will include the compound in the DHA calculations.

Fig 5: Add Link dialog

#### Compound Name

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

#### Name in Norms

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

### 4.1.2.2 Create DHA Calibration

	Paraffin	Ret. Time [min]
C1	Methane	
C2	Ethane	
C3	Propane	
C4	n-Butane	
C5	n-Pentane	12,803
C6	n-Hexane	20,430
C7	n-Heptane	28,863
C8	n-Octane	38,673
C9	n-Nonane	49,657
C10	n-Decane	61,087
C11	n-Undecane	72,323
C12	n-Dodecane	83,057
C13	n-Tridecane	93,147
C14	n-Tetradecane	102,747
C15	n-Pentadecane	111,750

Fig 6: Create DHA Calibration dialog

This dialog is displayed when you click the [Create DHA Calibration...](#) button in the [DHA Settings](#). The desired table contains the list of detected

*n-Paraffins* from the measured known sample and it allows you to manually adjust the retention times of particular compounds.

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

The minimum number of *n-Paraffins* in your known sample is 5 and the maximum is 11. If this condition is not met, an error dialog is displayed:

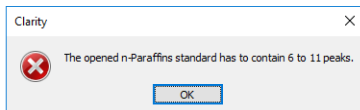


Fig 7: The opened *n-Paraffins* standard has to contain 6 to 11 peaks.

### 4.1.3 DHA Results

The *DHA Results* section on the DHA Extension contains information about the detected compounds and calculated results.

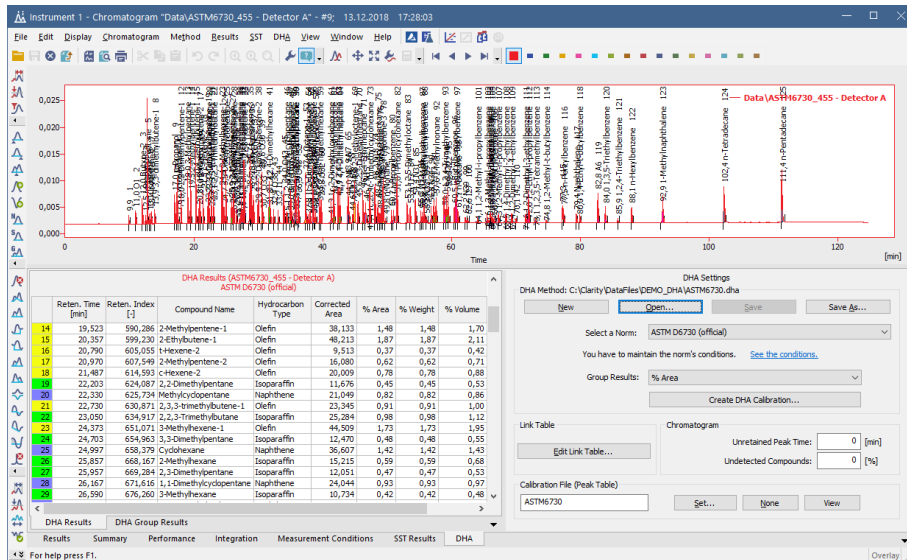


Fig 8: Chromatogram window - DHA - Result Table

#### DHA Results

Above the table you can see information about the signal from which the data was calculated and also the selected norm. To have valid data, you must create the calibration first using the [Create DHA Calibration](#) and also the created DHA Calibration uses the same norm as you have selected for displaying the Results. Otherwise you see one of the following warnings:

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

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

- **Norm selected for DHA Method (norm name) and DHA Calibration (norm name) do not match**

When displaying the *DHA Results*, you have to select the same norm as you selected when you created the *DHA Calibration*.

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



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

- **Unretained Peak Time in Chromatogram (number) and DHA Calibration (number) do not match**

You have a linked *DHA Calibration* which was generated with different *Unretained Peak Time* than the one in the current *DHA Method*. 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 for you when the *Unretained Peak Time* is set to non-zero value.

- **DHA 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 (DHA.CSV file 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. It is based on the corrected area value, which is calculated from the chromatogram peak area multiplied by the relative response factor – that means it is based on the compound amount in fact.

### **% Weight**

% Weight of a specific compound in the measured chromatogram. It 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. Calculation is (% *Weight*)/(Relative Density).

**Status**

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

### 4.1.4 DHA Group Results

In the *DHA Group Results* tab you can find the table which contains calculated results according to hydrocarbon types. The results are automatically recalculated each time you open or change the chromatogram or select different norm (or its parameters).

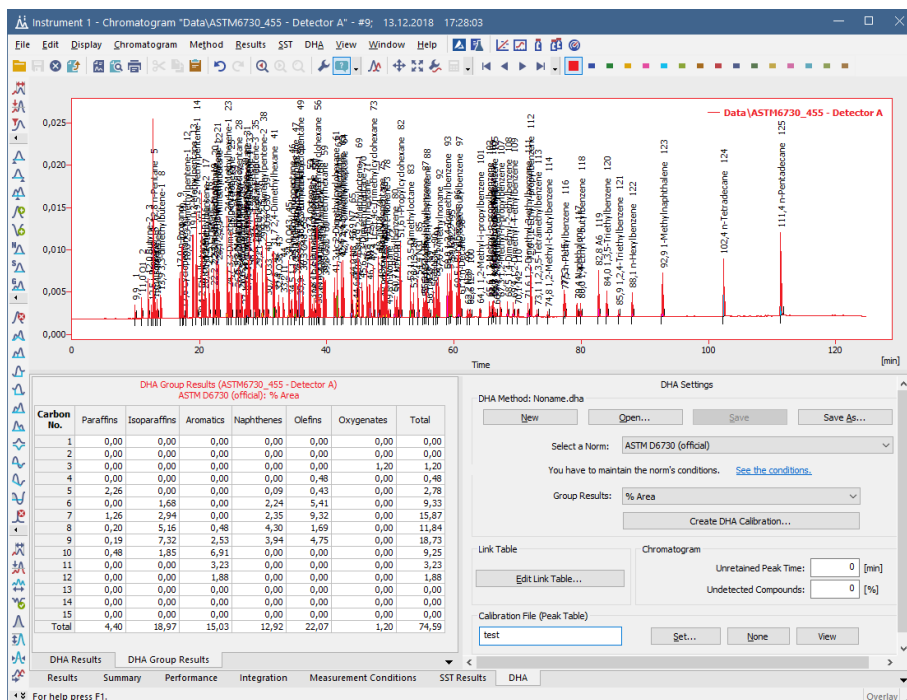


Fig 9: Chromatogram window - DHA Group Results

#### DHA Group Result Table

This table displays the results in a special pivot table. The units of the result 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 following warnings:

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

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

- **Norm selected for DHA Method (norm name) and DHA Calibration (norm name) do not match**

When displaying the *DHA Results*, you have to select the same norm as you selected when you created the *DHA Calibration*.

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

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

- **Unretained Peak Time in Chromatogram (number) and DHA Calibration (number) do not match**

You have a linked *DHA Calibration* which was generated with different *Unretained Peak Time* than the one in the current *DHA Method*. 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 for you when the *Unretained Peak Time* is set to non-zero value.

- **DHA Calibration is not linked**

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

## 4.2 Report Setup

In the [Report Setup Instrument](#) dialog, tab *DHA* you can set the printing options for the data in the **DHA Extension**.

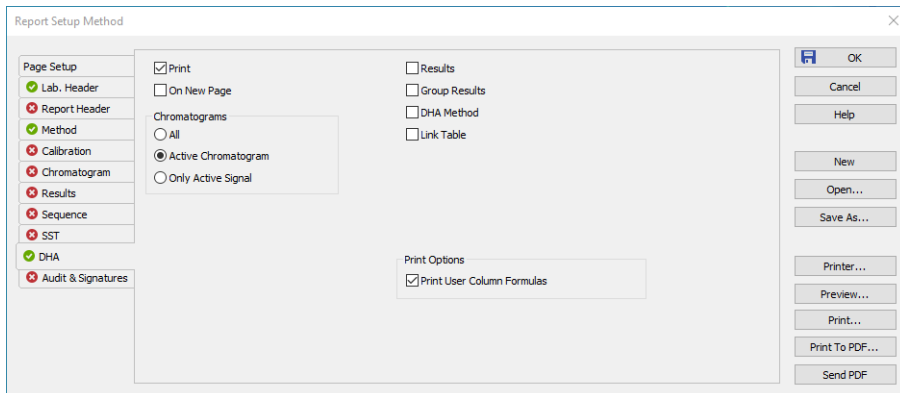



Fig 10: Report Setup Instrument dialog

### Print

Enable/disable the printing of the **DHA**. 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 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 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 also chapter Export Data in the **ClarityReference Guide**.

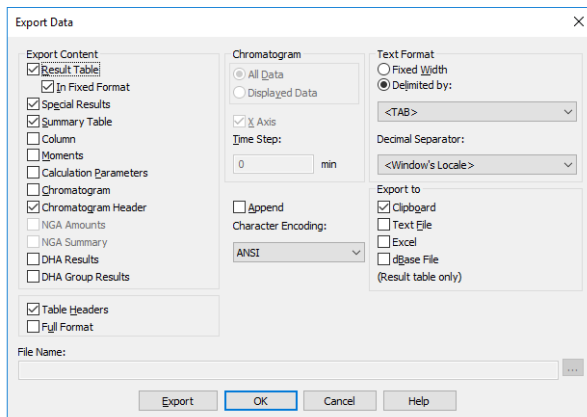


Fig 11: Export Data dialog

# 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** in the *Instrument Type Setting* dialog, for example on the *Instrument 1*.

For more details see also chapter Installation.

### Step 2

After saving and closing the **System Configuration** window, open the appropriate **Instrument**. Now open the DHA demo project: Click the *File - Project...* and in the desired window click the *Open...* button to open the project. Select the **DEMO\_DHA** in the 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 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 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 new a *DHA Calibration*. The current settings are saved in a special *.DHA* file which allows you to use the **DHA settings** on multiple **Chromatograms**. Clicking the *Open...* button and browse to 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 **Chromatogram** which is *ACTIVE* will be automatically recalculated even if you select different norms or parameters.

For more details see the chapter **DHA Settings** on pg 6.

### Step 5

In the *DHA Settings* pane, select the norm, for example the *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, 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 the **Step 5**.

**Step 7**

In the *Result Table* sub-tab of the *DHA* tab you can see the calculated results of identified compounds of 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* which 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 Chromatogram with the name in the norm.

# 6 How to work with the DHA Extension

## 6.1 How to measure DHA Data for first time

### Step 1

See the chapter "**Specification**" on pg 2. for an overview on specifications of supported DHA norms. For perfect and valid results, it is necessary to prepare your instrument and method according to the specification of 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 chapter Installation.

### Step 3

After saving and closing the [System Configuration](#) window, open the appropriate **Instrument** and select a project or create new one using the menu command *File - Project...* and in the desired window click the *New* button.

### Step 4

Now you have to create the **DHA Calibration** according to the selected norm and your instrument. **DHA Calibration** is a **Calibration** which contains special 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** if you want to have a very precise interpolation of the calculated **Retention indexes**. To create the full calibration with the all **n-Paraffins**, it is necessary to measure two standards (first for **C1-C4** and then for **C5-C15**). As minimum, you have to use **C5-C11**, however extrapolation 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 **C1-C4 n-Paraffins**, fill out their **Retention times** manually you find in the previously measured chromatogram.

Save the created **DHA Calibration**. Note that in this **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 you will use for measuring the unknown data.

If you want to automatically link the **DHA Calibration** to your measured chromatograms, select the one created in the **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 see the chapter "**How to print or export results from the DHA Extension**" on pg 24.

## 6.2 How to print or export results from the DHA Extension

Ensure that 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 20.

### 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* check box you enable other controls on that pane. By selecting the different options you can configure what information are printed.

Settings from the [Report Setup](#) are then used in the print output and preview which is 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 the *Open...* and select the *DHA\_RESULTS.STY* file.

For more details see also chapter Report Setup.

### Export

Open the *Setting - Export Data...* menu in the [Instrument](#) window. Set the *DHA Result Table* and *DHA Group Table* check boxes if you want 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 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 contains the *RICustom* column which will contains Retention indexes you will measure during developing your norm.

Follow as described below:

### Step 1

Open the DHA.CSV file in a spreadsheet application, for example the **MS Excel**. The file uses *dots* as decimal separators. If your local settings of **MS Excel** or **Windows** uses *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 the dots as decimal separator.

### Step 2

Measure the known **n-Parrafin**s samples and create the **DHA Calibration** from them using the **Custom norm**. It is best to measure all the possible **n-Parrafin**s if you want to have a very precise interpolation of the calculated *Retention indexes*. To create the full **Calibration** with the all **n-Parrafin**s, it is necessary to measure two standards (first for **C1-C4** and then for **C5-C15**). As minimum, you have to use **C5-C11**, however extrapolation 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 **C1-C4 n-Parrafin**s, fill out their *Retention times* manually you find in the previously measured chromatogram.

Save the created **DHA Calibration**. Note that in this **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-Parrafin**s.

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-Parrafin**s.

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

**Step 4**

The next step is the measuring of the compounds and calculating the **Retention indexes** for your custom norm. Now you can 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-Parrafin**s 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 detailed description the chapter "**How to work with the DHA Extension**" on pg **22**. The difference is in the **DHA Settings** where you select *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.