

Using Dragon DHA© with Clarity

The **Dragon DHA**® may be used with **Clarity** software to process the acquired chromatograms according to DHA extension. The acquired chromatograms are exported as **AIA (*.cdf)** files and automatically opened in Dragon DHA© for processing.

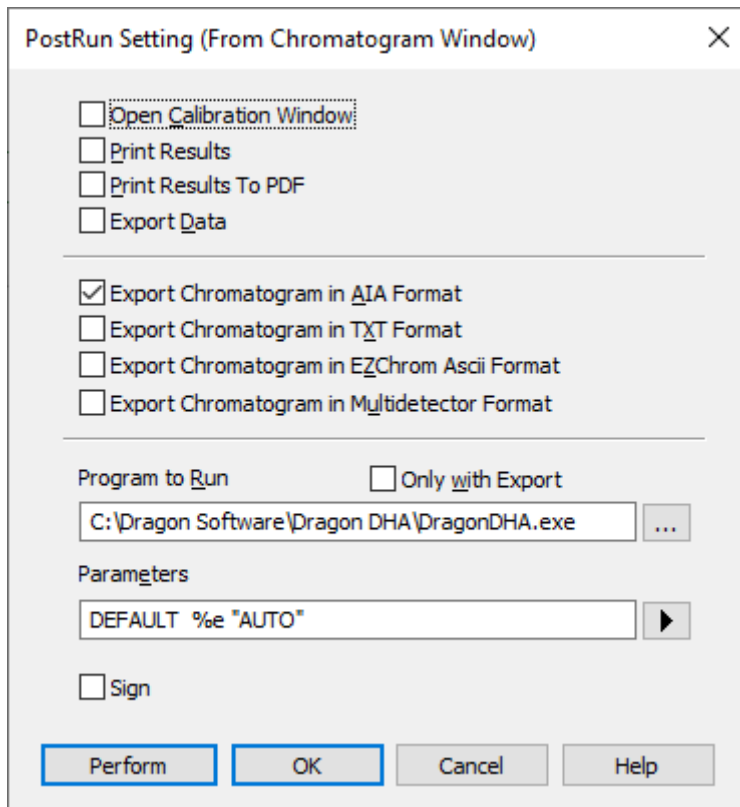
Dragon DHA© website: <https://envantage.com/dragon-software/dha-software/>

Expected workflow

- Acquire chromatograms in Clarity
- Adjust integration parameters (if necessary) of peaks
- Export (either via PostRun or manually) the chromatogram to AIA (*.cdf)
- Open the exported chromatogram in Dragon DHA© - evaluate and print results

PostRun Settings in Clarity

The below PostRun Settings can be used to automate the workflow: via Single Analysis, Sequence or as in the example below Chromatogram window.



The parameters required for Dragon DHA© are **reference** (*.dha set in the Dragon DHA software), **sample file** (*.cdf which will be exported from Clarity) and optional *AUTO* parameter for immediate processing.

When the *DEFAULT* parameter is used as first parameter, default reference file (*.dha) as specified in the Dragon DHA© Options will be used.

Note that for each processed chromatogram a new instance of Dragon DHA will be opened, the user will need to close it after processing the chromatogram.

Dragon DHA© Options

To further ease the collaboration between Clarity and Dragon DHA©, it may be necessary to set the *Default Area Reject* to 0. Thus avoiding the rejection of some peaks that were already integrated in Clarity.

The reference files (*.dha) may need to be adapted fit your specific chromatography conditions – see the Dragon DHA© help.

DHA - Set Options

General | View | Folders | File Names | User Applications | Report Options | ID Defaults | Major Peaks

Default Area Reject: 0.0000 Default Index Resolution: 0.50

Internal Standard Info

Internal Standard Name: NONE

Internal Std Amount: 0

Sample Weight: 0.0000

Sample Density: 1.0000

Normalize Peaks to 100% if Calculated Yield is: 98.00 Percent or Above

Normalize Results to: 100.0000 Percent Report Temp Values in Celsius

Auto Calculate on Open Sample File

Default Reference File: C:\Dragon Software\Dragon DHA\References\D6730_PC

Auto Load Reference File at Program Start

Always Use Identified N-Paraffins as Primary References

Always Disregard Olefins

Always Disregard Oxygenates

Always Disregard Aromatics

Exclude BP Distribution Calculations

Set Default Response Factor for Unknowns: 1.00

Set Default Density for Unknowns: 0.00

Set Default Mol % for Unknowns: 0.00

Start Analysis and Normalization at: 0.00

End Analysis and Normalization at: 0.00

Reject Components With Less Than 0.0500 Wt %

Normalize All Peaks to 100% if Total Unknown Weight is Less than 17.0000 Percent

RVP Offset Value: 1.0000

TIP: If the export of the chromatogram in **AIA** format is going to be done frequently with the same options, the icon for *Perform PostRun* can be added into the toolbar. Right mouse click in the toolbar area and choose *Customize* option. In the *Customize* dialog, find the *Perform Postrun...* command in the *File* category and drag it into the desired place on the toolbar. The export action will then be carried by clicking the icon in the toolbar – without the need to open and set any parameters in the *PostRun* Setting dialog.

