How to determine non-volatile hydrocarbons according to DIN H53 (ISO 16703)?

The recommended procedure for H53 method integration in Clarity (method 1):

1. Use *Baseline – Lock* on the whole chromatogram.
2. Apply *Baseline – Allow Crossing* to the whole chromatogram with the *To Start/End* option.
3. Via *Peak – Add positive*, add the following peaks:
   - A peak with the start time just before the solvent peak (this is the initial point of the baseline) and the end time at the beginning of the first fraction.
   - The first fraction (C10) peak with the start time precisely at the end time of the previous peak and the end time at the end of the fraction.
   - In a similar manner, i.e., with non-overlapping time frames, add the other peaks for remaining fractions (optionally, C10–C20, C20–C30, and C30–C40).
4. Set *Baseline – Together* and *Baseline – Forward horizontal* over the entire chromatogram.
5. Assign peaks to respective fractions using *Force Peak Name* (exact times are filled automatically when selecting the peak from the graph).
6. Create a calibration file for the present fractions.

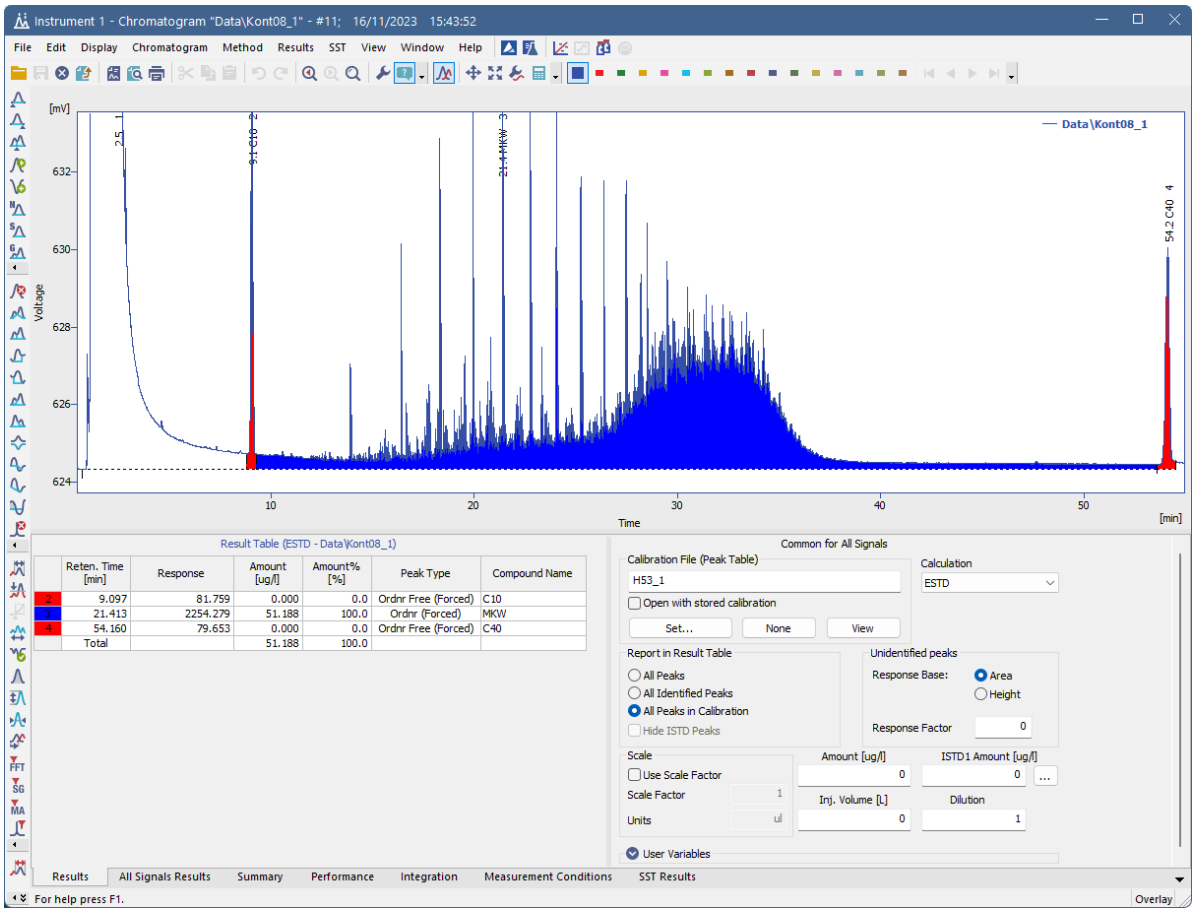
When the chromatogram is integrated appropriately, you can use the *Method - Save as Template* command from the *Chromatogram* window to save the method as a template so it can be used for further measurements. If you have already measured all the samples, you can apply the integration on all your chromatograms via *Analysis – Batch* reprocess by method.

Integration Table

Chromatogram Operation	Time A [min]	Time B [min]	Value
Global Peak Width			0.100 min
Global Threshold			0.1000
Global Filter - Bunching			2
Baseline - Lock	0.000	0.000	
Baseline - Allow Crossing	0.000	0.000	To Start/End
Peak - Add positive	0.700	8.800	
Peak - Add positive	8.800	9.300	
Peak - Add positive	9.300	53.600	
Peak - Add positive	53.600	54.500	
Baseline - Together	0.000	0.000	
Baseline - Forw. horizontal	0.000	0.000	
Peak - Force Peak Name	8.800	9.300	C10
Peak - Force Peak Name	9.300	53.600	MKW
Peak - Force Peak Name	53.600	54.500	C40

Note: If the amounts of some compounds in standards are unknown, it is necessary to set the *Curve Fit Type* to *Free Calibration* on the tabs of these compounds in the *Calibration* window.

Example of an evaluated chromatogram



An alternative procedure for H53 method integration in Clarity (method 2):

1. Use the same *Peak Width* and *Threshold* as in standard integration.
2. Apply *Baseline – Together* to the whole chromatogram.
3. Apply *Baseline – Forward Horizontal* to the whole chromatogram.
4. Mark all the peaks between C10 and C40 as a group (the group boundary lines may exceed the C10 and C40 peaks; only fully contained peaks will be included).
5. Amend the peak starts and ends by manual peak tools if necessary for the C10 and C40 (use the Peak - Both, with the A time corresponding to the respective C10 or C40 time and B time positive or negative, respectively. The times are relative, i.e., will be shifted accordingly in other chromatograms).
6. Create calibration file for C10, C40, and Group A peaks.

If the integration is not correct at this point (e.g., the integrated area for Group A between C10 and C40 peaks does not start/end precisely where the C10/C40 peaks end/start respectively, as shown in the figure below), an additional step might be added after step 3.: Apply again *Baseline – Together* to the whole chromatogram. Continue with the remaining steps.

To subtract a baseline, in the *Method Setup – Advanced* dialog, set the baseline chromatogram, and in the *Matching*, set *No Change*. The baseline file should be acquired on the stabilized system, preferably without the injection of solvent or at least with a lower volume of the solvent. Otherwise, negative artifacts will appear, interfering with the correct baseline setting in Clarity later on.

Integration Table

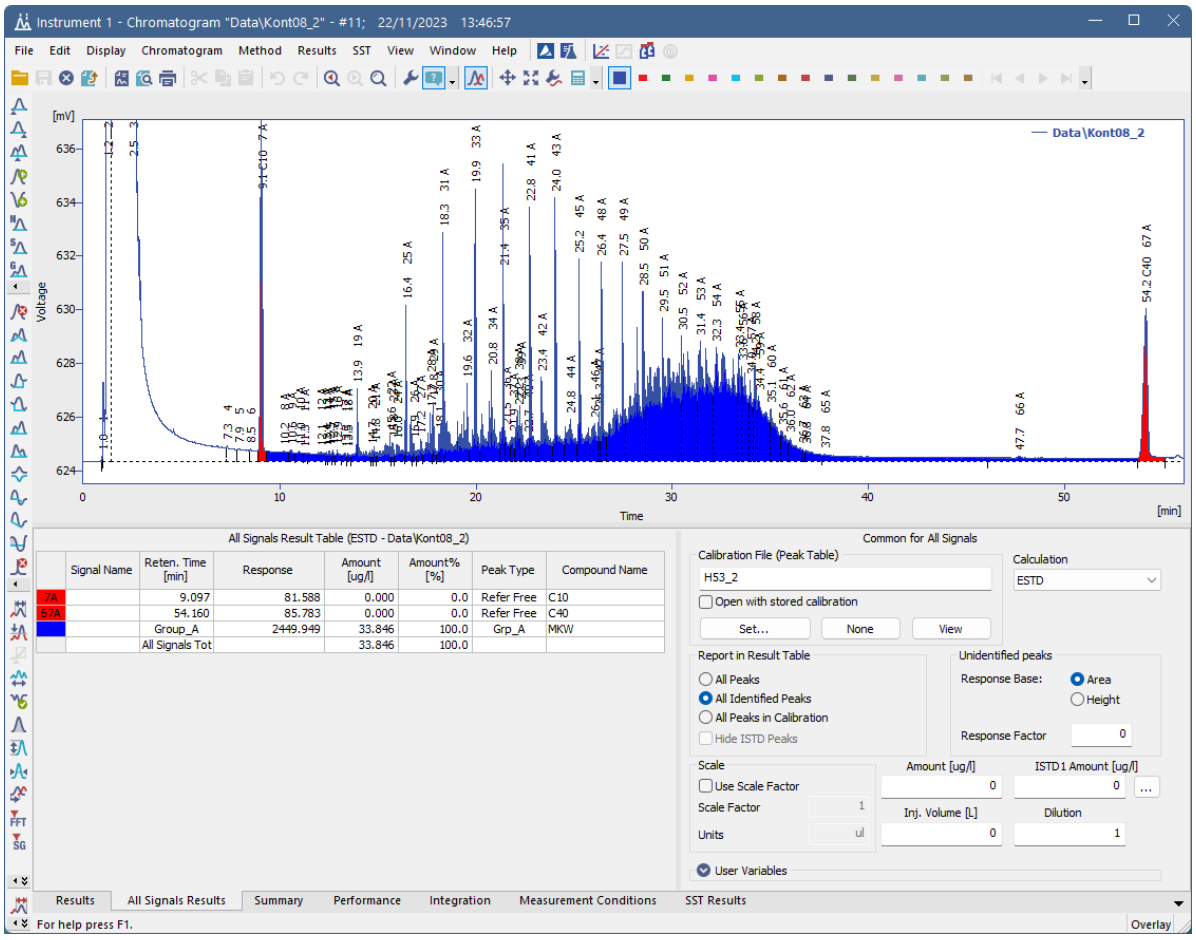
Chromatogram Operation	Time A [min]	Time B [min]	Value
Global Peak Width			0.100 min
Global Threshold			0.1000
Global Filter - Bunching			2
Group - Add group	9.061	54.490	A
Baseline - Together	0.000	0.000	
Baseline - Forw. horizontal	0.000	0.000	
Baseline - Together	0.000	0.000	
Peak - Both	12.520	-3.204	
Peak - Both	54.093	-0.454	

There is a condition that must be met:

- **The drawn baseline must not cross the chromatogram line (the negative areas arising do not have any physical meaning).**

This approach is generally less reliable and more sensitive to the choice of Integration Algorithm.

Example of an evaluated chromatogram



Sample data for Clarity

- DIN_H53.zip - zipped chromatograms, methods, and calibrations.
- Din-H53-processed.dgz - archived Clarity Project to restore with Clarity via the Archive/Restore function