DataApex
Clarity™
CHROMATOGRAPHY SOFTWARE

# EA EXTENSION

Clarity Extension ENG

Code/Rev.: M053/100B
Date: 2025-10-22

DataApex Ltd.
Petrzilkova 2583/13
158 00 Prague 5
Czech Republic

Phone: +420 251 013 400
clarity@dataapex.com
www.dataapex.com

Author: DR

# Contents

To facilitate the orientation in the **EA Extension** 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 EA - Elemental Analysis

The **Clarity EA** is an optional **Extension** for the **Clarity Chromatography Station**. It is intended for data acquisition and evaluation from **Elemental Analyzers** using the technique of combustion/gas chromatography. Any of the **Clarity EA** Instruments can be switched to standard mode for standard chromatography processing, so the user can use both Elemental Analyzer and chromatograph attached to the same software.

**EA Extension** is also compatible with **Clarity Offline** software.

# 2 Specification

The **EA Extension** is an optional, fully integrated part of **Clarity** software. It can be ordered as a part of new datastation or as an Extension to existing datastation (p/n A30).

# 3 Installation

The EA Extension is activated by entering an appropriate user code during the installation of **Clarity** or later using the *Help - User Code…* command from the *Clarity* main window.

To enable the EA Extension on an *Instrument*, you have to set the corresponding instrument type. To set the instrument type, click the ... button in the *System Configuration* dialog.

In the invoked *Instrument Type Setting* dialog, select the EA option.

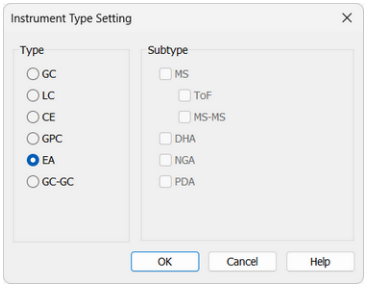



*Fig. 1: Switching to the EA mode*

# 4 Key Features

The **EA Extension** brings the following features to the **Clarity** station:

- **Sequence mode only** - since the Elemental analyzers are commonly used for large series of samples, the single analysis mode is not supported to simplify the operation.
- **Standard Table** - the composition of standards used for calibration is stored in an editable **Standard Table** and is automatically transferred to the sequence when the standard is selected.
- **Calibration** - the calibration is created automatically for each new sequence and has the same name as the sequence.
- **Calibration curves** - the calibration curves for the individual elements determined are constructed for amounts calculated from the entered *Sample Amount* and composition of the standard defined in the **Standard Table**.
- **One method in sequence** - to simplify the operation only one method can be used in one sequence.
- **Carbon Ratio** - the column providing the ratio of the respective element to the carbon is present in the **Result Table** and **Summary Table**.
- **Balances** - selected types of analytical balances can be configured to the Instrument, enabling direct transfer of sample amount to the **Sequence Table**.

The following standard **Clarity** features will also help the user to make the best of the **EA** analysis in **Clarity**:

- **User calculations** - the user can define custom calculations in the **Result Table** and **Summary Table**. You can create your own columns from the original ones and use individual mathematical functions.
- **Reports** - user selectable report sections, WYSIWYG formatting of Graphs and Tables.
- **Batch** - automatic batch processing, display, export or print of any number of chromatograms.
- **Summary Result Table** - displays and prints selected results from all simultaneously displayed chromatograms.

*Note:* In calibration, options not relevant to the EA extension (e.g., Weighting Method, or option to calculate by ISTD or STDADD) were removed.

## 4.1 Basic principles and terms

- **Elemental Analysis** (**EA**) is an analytical technique used for determination of elemental composition of various samples. The contents of common elements (C, H, N, O, S) are determined by various methods.
- One of the methods of the **Elemental Analysis** is **combustion** of the sample and separation of the products by **gas chromatography** techniques.
- Dedicated instruments called **Elemental Analyzers** are commercially available.
- **Analytical Balance** are widely used with Elemental Analyzers. **Clarity** with **EA** Extension can automatically transfer the weight from the balance to the **Sequence Table**.

We have changed titles of some text fields to better fit for the EA analyses. For more details, see the Method Setup topic.

# 5 EA Extension Description

Only the features that have been changed or added specifically for the **Clarity** EA instrument are listed and described here. For standard features, please refer to the *Reference Guide*.

Most of the changes affect the Instrument window (the *Single Analysis* and *Sequence* windows have been replaced by a single *Sequence* window adapted to EA Extension requirements), the Sequence window itself and the Chromatogram Result Table (with additional calculation columns).

Also, in the Calibration of the EA instrument, peak names must exactly match the component names in the Standard Table. These must be Nitrogen, Carbon, Hydrogen, and Sulphur - without any translations or localized versions - to ensure proper matching.

## 5.1 Instrument window

In the **EA Mode** the *Instrument* window has different appearance.

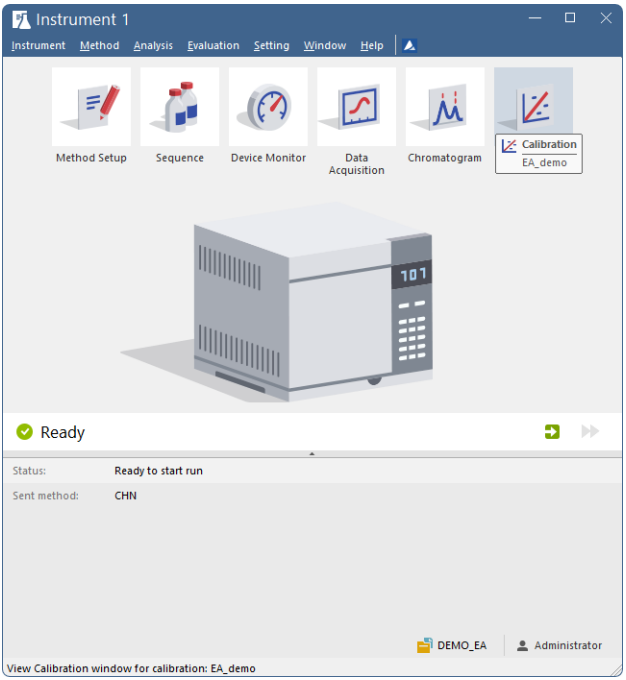



*Fig. 2: EA Instrument window*

The *Single Analysis* and *Sequence* icons in the **Scheme of Data Processing** have been replaced by a single *EA Sequence* icon.

## 5.2 Method Setup

Method Setup is amended to better fit the EA analyses.

### Measurement tab

Some of the information fields on the *Method Setup - Measurement* and also corresponding *Chromatogram - Measurement Conditions* tabs were renamed to better match the **EA** terminology.

*Tab. 1: Renamed existing informational fields:*

| Default mode | EA mode |
|---|---|
| Column | GC Column |
| Mobile Phase | Oven Temperature |
| Pressure | Left Furnace Temperature |
| Temperature | Right Furnace Temperature |

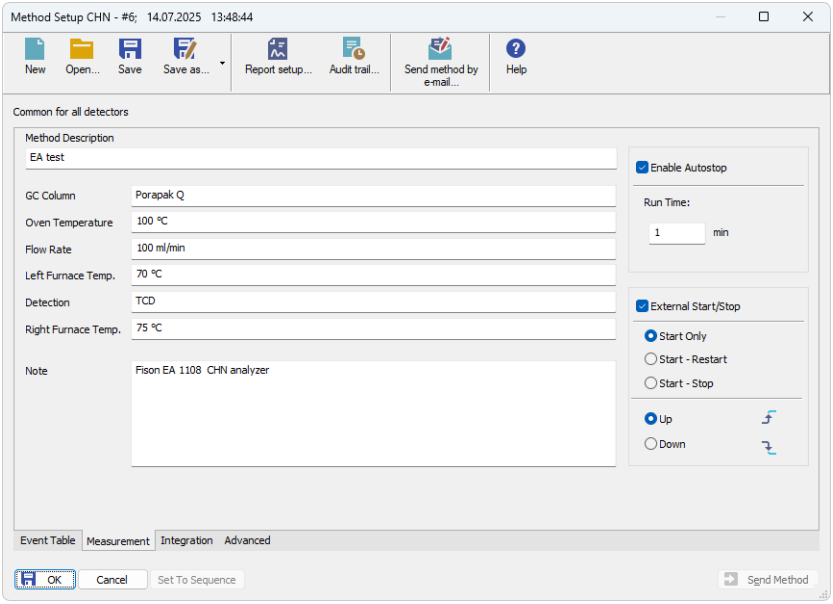



*Fig. 3: Method Setup - Measurement*

When using the EA instrument synchronized via *Colibrick*, it is usually necessary to adjust both the method and the digital output settings (depending on the used EA device) to ensure correct triggering. The method should be set to start on the *External Start* signal with the expected level set to *Up*.

The *Initial State* of the corresponding digital output line should be set to *Low* in the Digital Outputs dialog, that can be opened from the Clarity main window via *System* –

*Digital Outputs*. These two settings must be aligned to correctly generate the rising edge required to start the analysis.

### Calculation tab

***Calculation*** tab has been removed from the ***Method Setup*** dialog (and from the ***Instrument*** window menu), the calibration to be applied to the measured chromatograms is created in the sequence and it is defined by the sequence name instead.

## 5.3 Sequence window

***Sequence*** window now contains new columns of the elemental compound percentages in standards, i.e. *Nitrogen*, *Carbon*, *Hydrogen*, *Sulphur*, *Oxygen*.

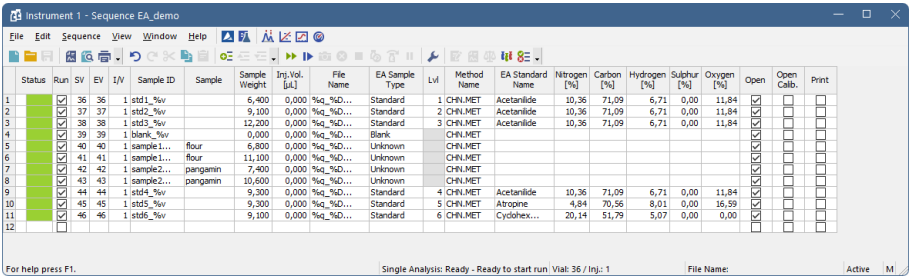



*Fig. 4: Sequence window*

### Sample Weight

Replaces the *Sampe Amount* column in **Clarity** standard mode. The Weight measured on the Balance is automatically inputed here alternatively the field can be modified manually. This value is propagated to the *Chromatogram* and its *Summary Table*.

### EA Sample Type

Replaces the *Sample Type* column in **Clarity** standard mode. It works basically the same, only Standard has some special conditions. The available entries are:

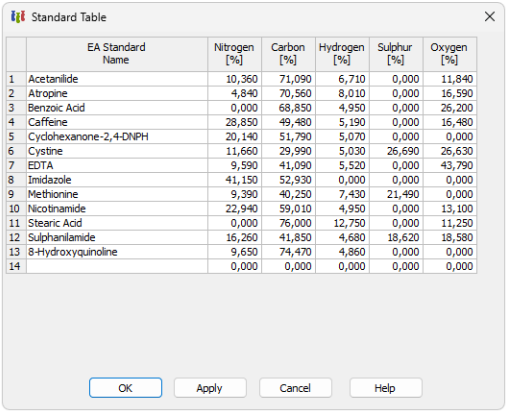
| Sample Type | Description |
|---|---|
| **Unknown** | For unknown samples. |
| **Standard** | For calibration standards. *Sample Amount*, Level (*Lvl.*) and *EA Standard Name* fields must be filled in. The composition columns will be filled automatically from the **Standard Table**. |
| **Blank** | For blank samples. The response determined will be used on Level 21 of the calibration with amount *0*, which will be counted to the calibration. |
| **Bypass** | Allows for performing an analysis in the *ACTIVE* sequence with controlled autosampler without actually injecting a sample. This is useful for running the column-cleaning or equilibrium-setting sample, etc. |

**Method Name**

Contains the method name for the current method. This method is automatically set for all rows in the sequence and can't be changed during the running sequence as the column is disabled.

*Note:* To change the method while the sequence is running, stop the sequence, change the method in any not measured row and resume the sequence. Only a user with the access right to *Select Method* can select another method.

## 5.3.1 Standard Table




| | EA Standard Name | Nitrogen [%] | Carbon [%] | Hydrogen [%] | Sulphur [%] | Oxygen [%] |
|---|---|---|---|---|---|---|
| 1 | Acetanilide | 10,360 | 71,090 | 6,710 | 0,000 | 11,840 |
| 2 | Atropine | 4,840 | 70,560 | 8,010 | 0,000 | 16,590 |
| 3 | Benzoic Acid | 0,000 | 68,850 | 4,950 | 0,000 | 26,200 |
| 4 | Caffeine | 28,850 | 49,480 | 5,190 | 0,000 | 16,480 |
| 5 | Cyclohexanone-2,4-DNPH | 20,140 | 51,790 | 5,070 | 0,000 | 0,000 |
| 6 | Cystine | 11,660 | 29,990 | 5,030 | 26,690 | 26,630 |
| 7 | EDTA | 9,590 | 41,090 | 5,520 | 0,000 | 43,790 |
| 8 | Imidazole | 41,150 | 52,930 | 0,000 | 0,000 | 0,000 |
| 9 | Methionine | 9,390 | 40,250 | 7,430 | 21,490 | 0,000 |
| 10 | Nicotinamide | 22,940 | 59,010 | 4,950 | 0,000 | 13,100 |
| 11 | Stearic Acid | 0,000 | 76,000 | 12,750 | 0,000 | 11,250 |
| 12 | Sulphanilamide | 16,260 | 41,850 | 4,680 | 18,620 | 18,580 |
| 13 | 8-Hydroxyquinoline | 9,650 | 74,470 | 4,860 | 0,000 | 0,000 |
| 14 | | 0,000 | 0,000 | 0,000 | 0,000 | 0,000 |

*Fig. 5: Standard Table*

The *Standard Table* dialog can be invoked using the *Sequence - Edit Standard Table* command or pressing the icon from the Sequence window switched to the **EA** mode.

Predefined values are listed for commonly used standards. The table can be edited to add other standards or to delete the unused ones.

## 5.3.2 Get Weight

**Clarity** with the **EA Extension** can control selected models of balance. The particular Balance Control Module must be configured to the corresponding Instrument in the *System Configuration* dialog.

To open the *Get Weight* dialog invoke the *Sequence - Balance* command or use the icon from the Sequence window. It measures the weight of the samples and automatically fills in the Sample Weight column in the Sequence.

The numbers behind the "Get Weight" inscription in the dialog header show the number of the sample to be weighted and the total number of samples selected for weighting.

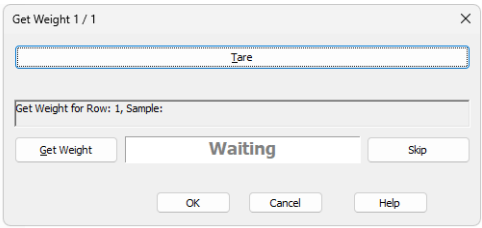



*Fig. 6: Get Weight*

**Tare**
Subtracts the weight of an empty container.

**Identification bar**
Displays information from the **Sequence Table** indicating current sample.

**Get Weight**
Transfers the weight from the analytical balance directly into the *Sample Amount* field of the **Sequence Table**.

**Status Panel**
Displays current status of the analytical balance. Possible states are:

*Waiting* - Standard state, balance are currently doing nothing or the *Tare* button have been pressed and taring operation is in process.

*Waiting for value* - The balance is measuring the weight of the sample.

*Waiting for calibrate* - Balance is calibrating itself.

**Skip**
Skips current row in the **Sequence Table**.

## 5.4 Chromatogram window in EA Extension

The Result Table in the **EA Extension** *Chromatogram* window has two additional columns performing EA calculations. These columns are:

**Carbon Amount Ratio**
Displays the ratio of the carbon amount to the given row's element amount.

Carbon Amount Ratio = Carbon Amount / Element (C,H,N,...) Amount

**Carbon Response Ratio**
Displays the ratio of the given row's element response to the carbon peak response, be it *Area* or *Height*. The column is hidden in the default desktop.

Carbon Response Ratio = Element (C,H,N,... ) Response / Carbon Response

The *Sample Weight* value, which is defined per chromatogram and typically comes from the sequence (where it may have been measured using controlled analytical balances), is displayed in the *Common for All Signals* section of the *Results* tab and also appears as a column in the *Summary Table*, showing the value for each open chromatogram.

# 6 Clarity EA operation

The typical operation procedure for **Clarity** in **EA** mode is described in this chapter in logical order. Only topics related to **EA** mode are discussed here, refer to the **Clarity User Guide** for detailed description of operations in standard mode.

## 6.1 Sequence

- Use the *File - New* command or the  icon in the *Sequence* window to create a new sequence.
- Name the sequence in the *Save As* dialog.
- The new sequence is created as a copy of the *EATemplate.seq* file stored in the *COMMON* subdirectory of the **Clarity** folder (C:\CLARITY\DATAFILES\COMMON by default). If this file is missing, default program parameters will be used.

*Note:* You can store the common part of your sequence (most commonly the sequence options and the initial standards with first sample row) to this file.

- Set the method to sequence by using one of the following:
  - After clicking in the cell in the *Method Name* column the  icon will appear. Using it invokes the dialog where the method can be selected.
  - The method can be directly input by typing the method's name in the cell in the *Method Name* column.
- Add new rows to the **Sequence Table** by clicking the checkbox in the *Run* column on the last empty line or editing any of its fields.
- Fill in the standards and samples to be measured.
- Measure the Sample Weight of the samples. Use Get Weight dialog in the case you are using configured Balance.
- Run the prepared sequence (using the *Run Sequence* command (or  icon) from the *Sequence* window) to process the samples.

It is recommended to create a new sequence for each set of measurements (daily work, series of samples), instead of reseting the measured one.

All the samples in the sequence refer to a single calibration file.

## 6.2 Calibration setup

For each new sequence a calibration file with identical name (*.CAL) is created in the calibration subfolder (CALIB by default) of the current project.

This calibration will be based on the calibration template EATEMPLATE.CAL file stored in the **Clarity** COMMON folder (C:\CLARITY\DATAFILES\COMMON by default). Display and edit the calibration in the *Calibration* window. Refer to the **Clarity Reference Guide** for detailed description of the *Calibration* window.

The retention times need to be set according to your actual standard - they will differ according to the instrument type and conditions used. The *Identification Windows*

should be set wide enough to accommodate the differences in retention times for different element amounts.

The dominant peak (usually carbon) type can be set to *Refer*, the identification windows for other peaks will be shifted accordingly.

*Linear Curve Fit Type* will usually be used with *Area* as *Response Base*.

## 6.3 Results presentation

For results presentation it is advantageous to:

- Set the **Overlay Mode** by the *File - Overlay Mode* command or icon ① in the *Chromatogram* window.
- Open all desired chromatograms using the *File - Open* command (or icon) ② . You may hold **Ctrl** key to select multiple files.
- Switch to the *Summary* ③ tab.
- Customize the **Summary Table** to display the desired information in a suitable layout. This can be done by right clicking the table and selecting the *Summary Options...* ④ or *Setup Columns...* ⑤ commands.

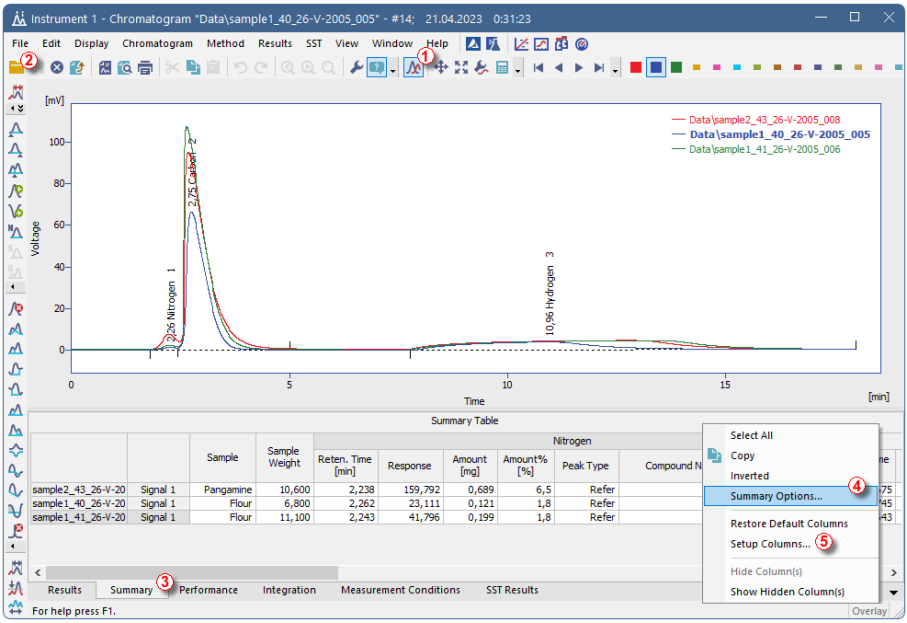



*Fig. 7: Chromatogram - Summary*

You can select which information will be printed in the report using the *Report Setup* dialog.

The **Summary Table** can be also exported in *.TXT format (*File - Export - Export Summary Table* command in the ***Chromatogram*** window) and the data thus easily transferred to other programs for further evaluation.

## 6.4 Reprocessing the results

If there were some problems encountered during the sequence acquisition, the whole sequence or selected chromatograms can be reprocessed to correct those problems. Commonly encountered problems are incorrect integration or identification of the peaks, interferences or ghost peaks in the chromatograms or errors entered in the *Sample Weight* column.

To reprocess the Results, go to the Batch dialog. For more tips how to use Batch, refer to the ***Batch*** chapter in User Guide.