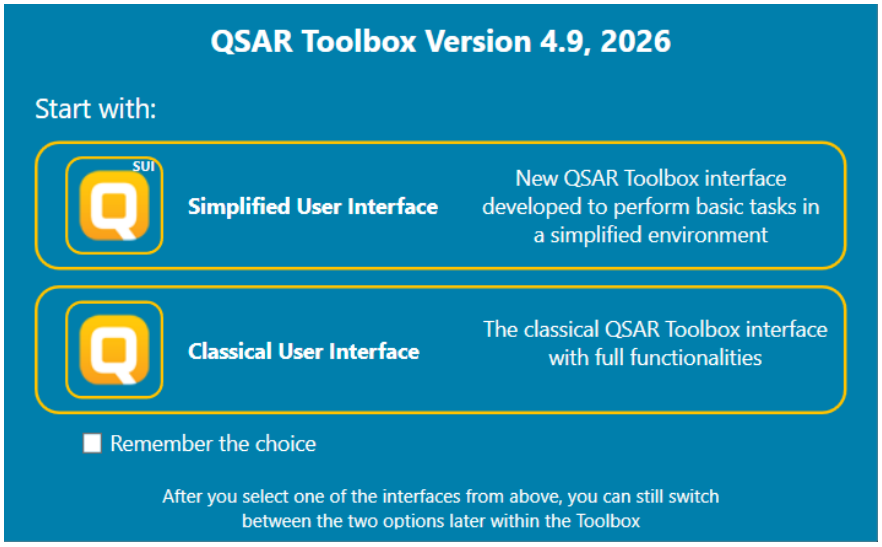
QSAR TOOLBOX

The OECD QSAR Toolbox for Grouping Chemicals into Categories

GETTING STARTED: QUICK REFERENCE GUIDE FOR THE CLASSICAL USER INTERFACE

Choose which user interface you want to work with: *Simplified User Interface* or *Classical User Interface*.



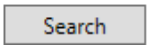
If you want to use the same user interface every time when you open the software then check ***Remember the choice*** checkbox before selecting one of the two interfaces.

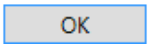
Step 1: Input - Define chemical of interest or "target chemical"

Define your target chemical by Chemical Name, CAS number, SMILES, drawing the molecule or selecting it from a list. To define a chemical by CAS number:

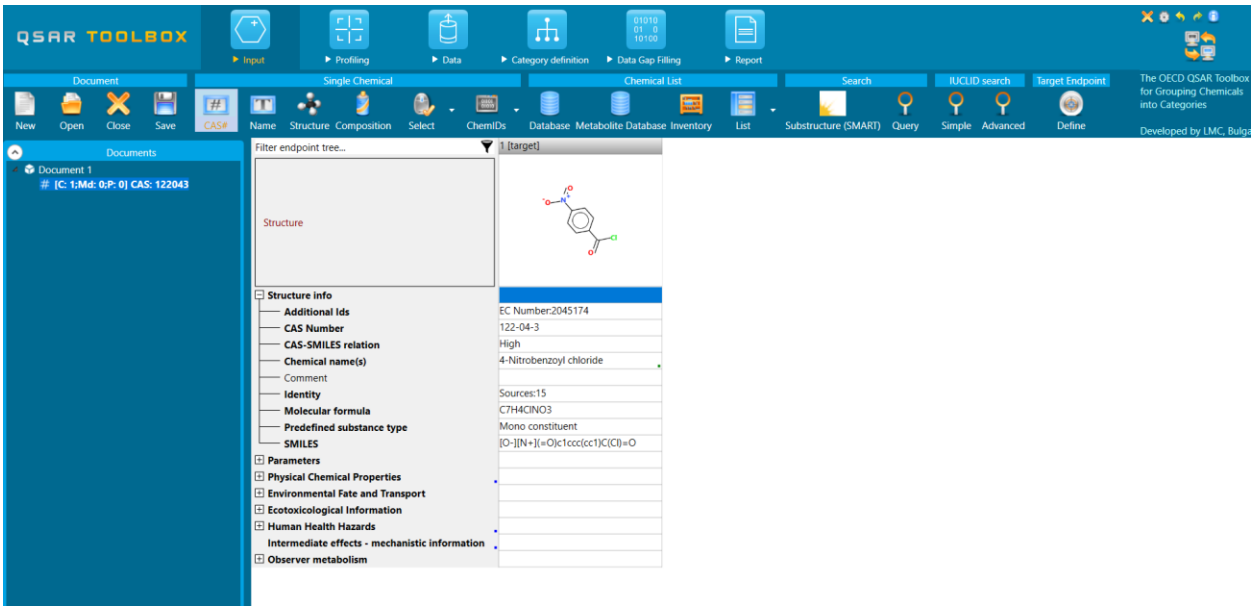
Click 

→ enter the number, and then click



→ the program displays the structure → 

The structure is displayed on the data matrix.

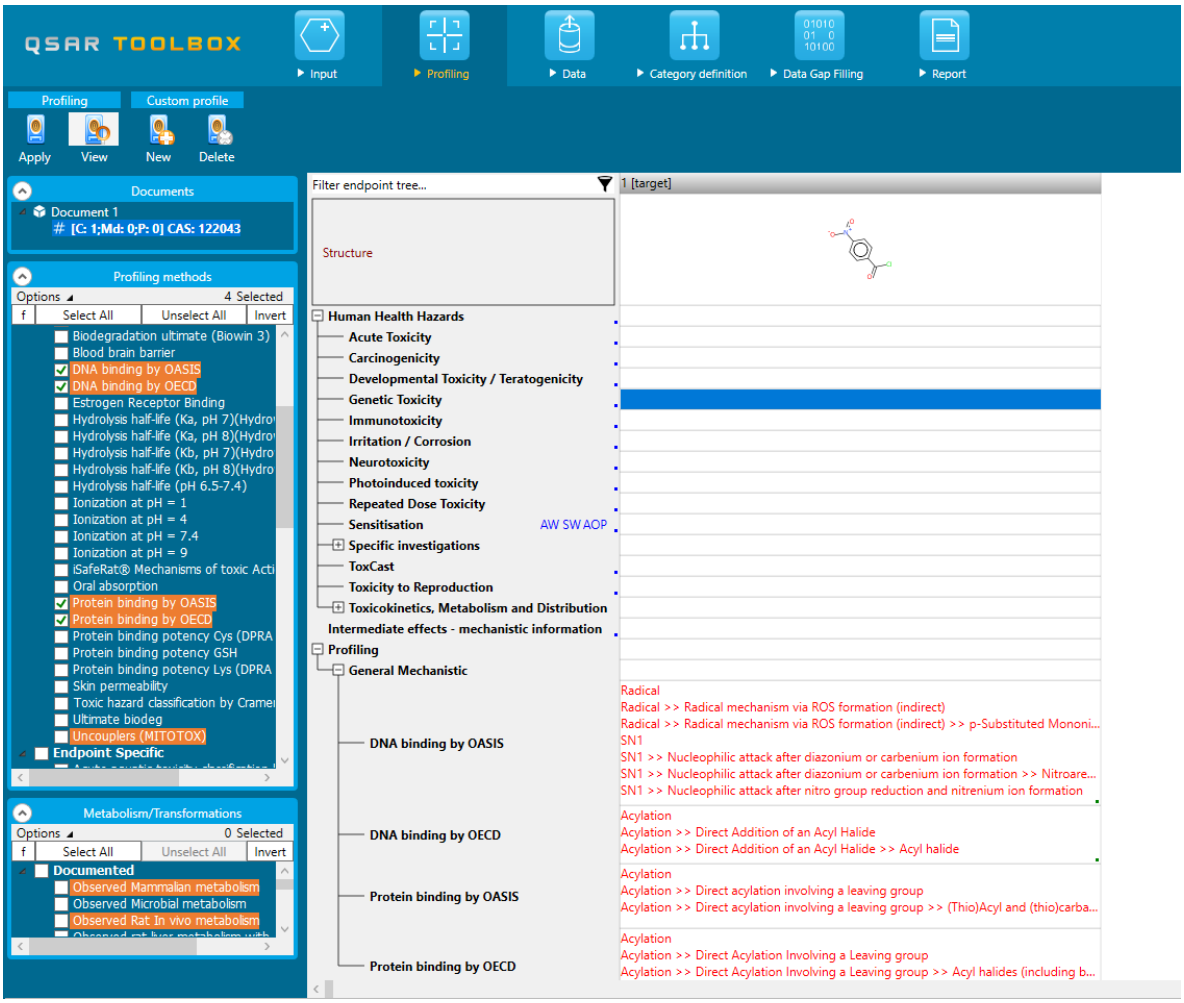


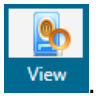
To define the target endpoint, which will be used for the predictions click 

Step 2: Profiling - Retrieve information based on the identity of the substance or its structure

Select profilers by ticking the corresponding boxes → 

. The program establishes a "profile" of the chemical based on its structure.



To obtain the general background information on any profiler, right click on it and select **About**. To obtain the scientific information used to build the profiler, select it and click 

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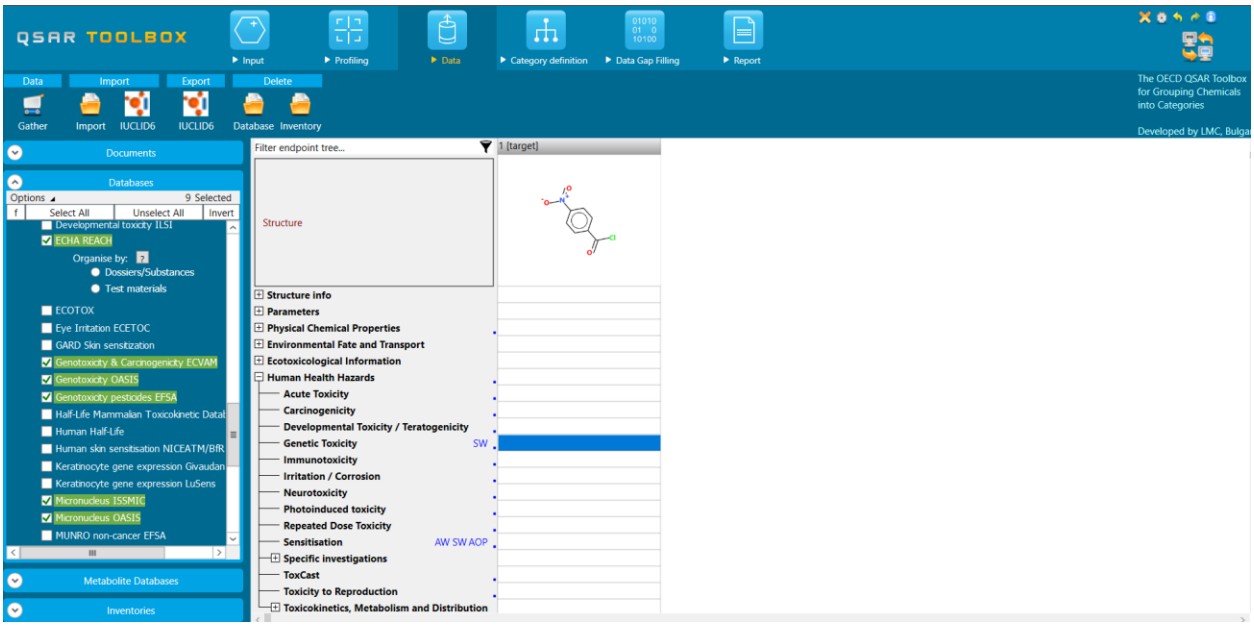
The highlighted profiles correspond to the selected endpoint in the data matrix or to the previously defined endpoint if any.

Step 3: Endpoint - Retrieve experimental results from the resident databases

Select databases by ticking ☑ the corresponding databases → Gather. The retrieved information is displayed according to four subsections in the endpoint tree:

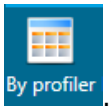


To open the data tree: left-click on the nodes. To access detailed information on the experimental results: double-click on the result in the matrix.

The highlighted databases correspond to the selected endpoint in the data matrix or to the previously defined endpoint if any.

Step 4: Category definition - Identify chemicals which could form a category with the "target" chemical

Select one of the grouping methods available in the **Categorization section**.

To identify the analogues of the target based on the profile of your target chemical → 

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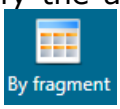
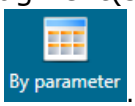
To identify the analogues of the target based on the fragment(s) identified in the target → 

or by a specific 2D or 3D parameters → 

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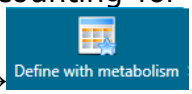
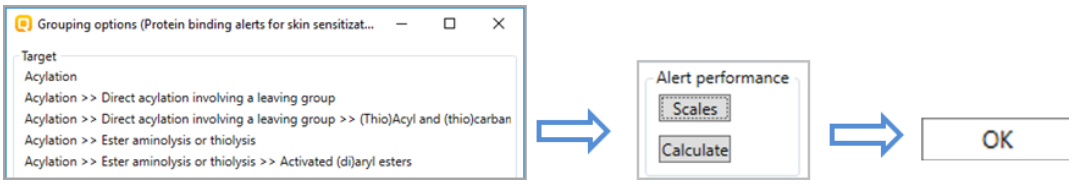
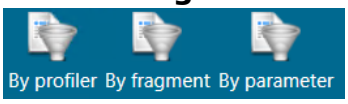
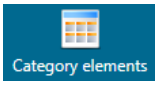
To identify the analogues of the target accounting for metabolic activation of the chemicals based on specific criteria select → 

To check how much relevant to a target endpoint an alert is, once search ***by profiler*/*with metabolism*** is selected then calculate the Alert performance:



Select of the criteria available within the **Subcategorization section** to refine a chemical category on the data matrix → 

To identify the subgroups within an existing category that are determined by the definitions of the currently selected profiling method → 

To assess the consistency of the defined category → 

The category consistency is endpoint specific. Four layers of information are considered important: Physicochemical similarity; Structural similarity and Mechanistic similarity and ADME similarity.

The highlighted profiles correspond to the selected endpoint in the data matrix or to the previously defined endpoint if any.

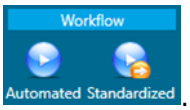
Step 5: Data gap filling - Predict missing data by read-across, trend analysis, QSAR models or automated/standardized workflows

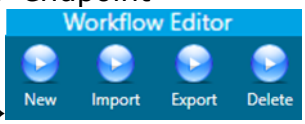
Select data gap filling by clicking in the corresponding cell in the data matrix, and then select one of the data gap filling methods:

- Read-across: for "qualitative" endpoints (skin sensitization or mutagenicity e.g. positive, negative, equivocal) or for "quantitative endpoints" (e.g., 96h-LC50 for fish) if only very few analogues with experimental results are identified. → 

- Trend analysis: for "quantitative" endpoints if many analogues with experimental results are identified. → 

- (Q)SAR models: if no analogue with experimental results is identified or to build a weight of evidence case. → 

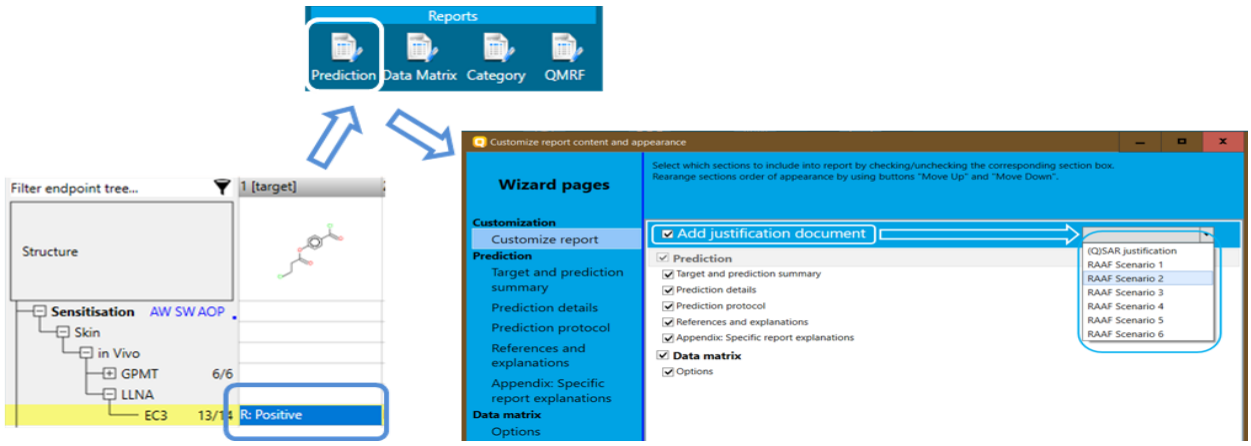
- Standardized and Automated workflows: once started, they follow the implemented logic and finish with prediction. They include read-across or trend analysis method depending on the endpoint → 

. To create or import/export your own workflows → 

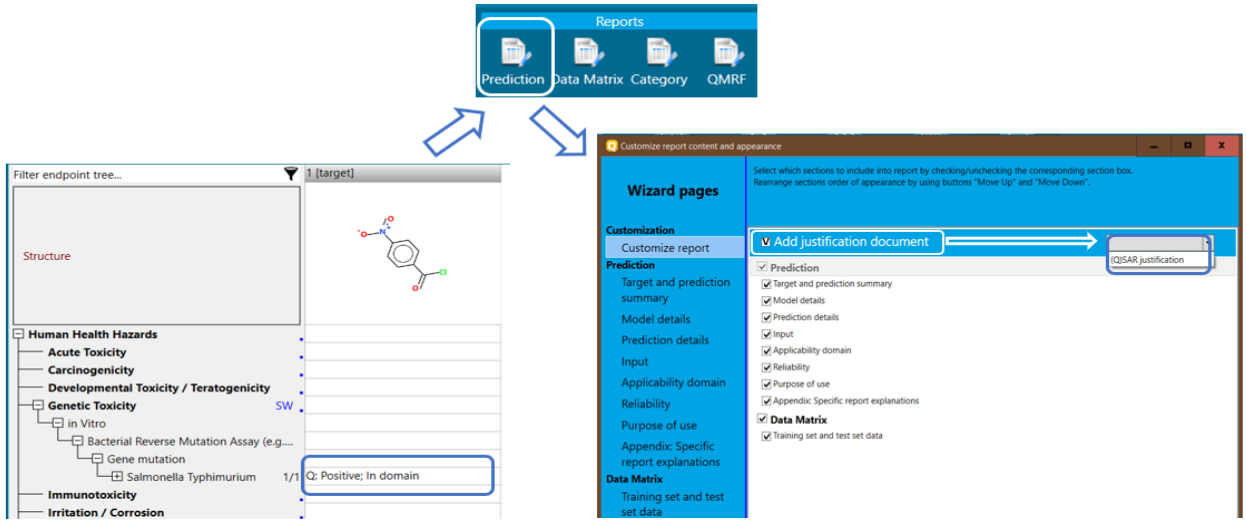
Step 6: Report – Obtain a detailed report for your prediction or category

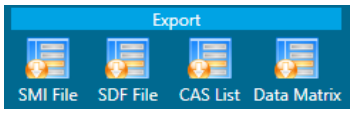
Prediction is needed to generate a *Prediction* report.

Read across Assessment Elements could be included in a separate justification document in case of regulatory interest, by selection of a ***RAAF scenario.***



For predictions from a (Q)SAR model, the **(Q)SAR justification** document including (Q)SAR assessment elements, can be selected.



Four export types are also available in Toolbox v.4.9 → 

The Export allows exporting of various information from the current data matrix.

Each of the above illustrated functionalities is explained in details in the F1 help file available with installation (press F1).