

# 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*.


**QSAR Toolbox Version 4.8, 2025**

Start with:

|   |                                  |   |
|---|----------------------------------|---|
|   | <b>Simplified User Interface</b> | New QSAR Toolbox interface developed to perform basic tasks in a simplified environment |
|  | <b>Classical User Interface</b>  | The classical QSAR Toolbox interface with full functionalities                          |

☐ Remember the choice

After you select one of the interfaces from above, you can still switch between the two options later within the Toolbox

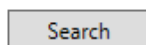
 If you want to use the same user interface every time when you open the software then check **Remember the choice** checkbox before selecting one of the two interfaces.

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

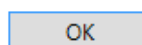
Define your target chemical by Chemical Name, CAS number, SMILES, drawing the molecule or selecting it from a list. To define a chemical by CAS number:



Click **CAS#** → enter the number, and then click



→ the program displays the structure →



The structure is displayed on the data matrix.

The screenshot shows the QSAR TOOLBOX interface. The 'CAS#' button is selected, and the number '122043' is entered. The 'Search' button is clicked, and the chemical structure of 4-Nitrobenzoyl chloride is displayed. The data matrix shows the following information:


| Structure | EC Number | CAS Number | CAS-SMILES relation | Chemical name(s)        | Comment | Identity   | Molecular formula | Predefined substance type | SMILES                        |
|-----------|-----------|------------|---------------------|-------------------------|---------|------------|-------------------|---------------------------|-------------------------------|
|           | 2045174   | 122-04-3   | High                | 4-Nitrobenzoyl chloride |         | Sources:15 | C7H4ClNO3         | Mono constituent          | [O-][N+](=O)c1ccc(cc1)C(=O)Cl |

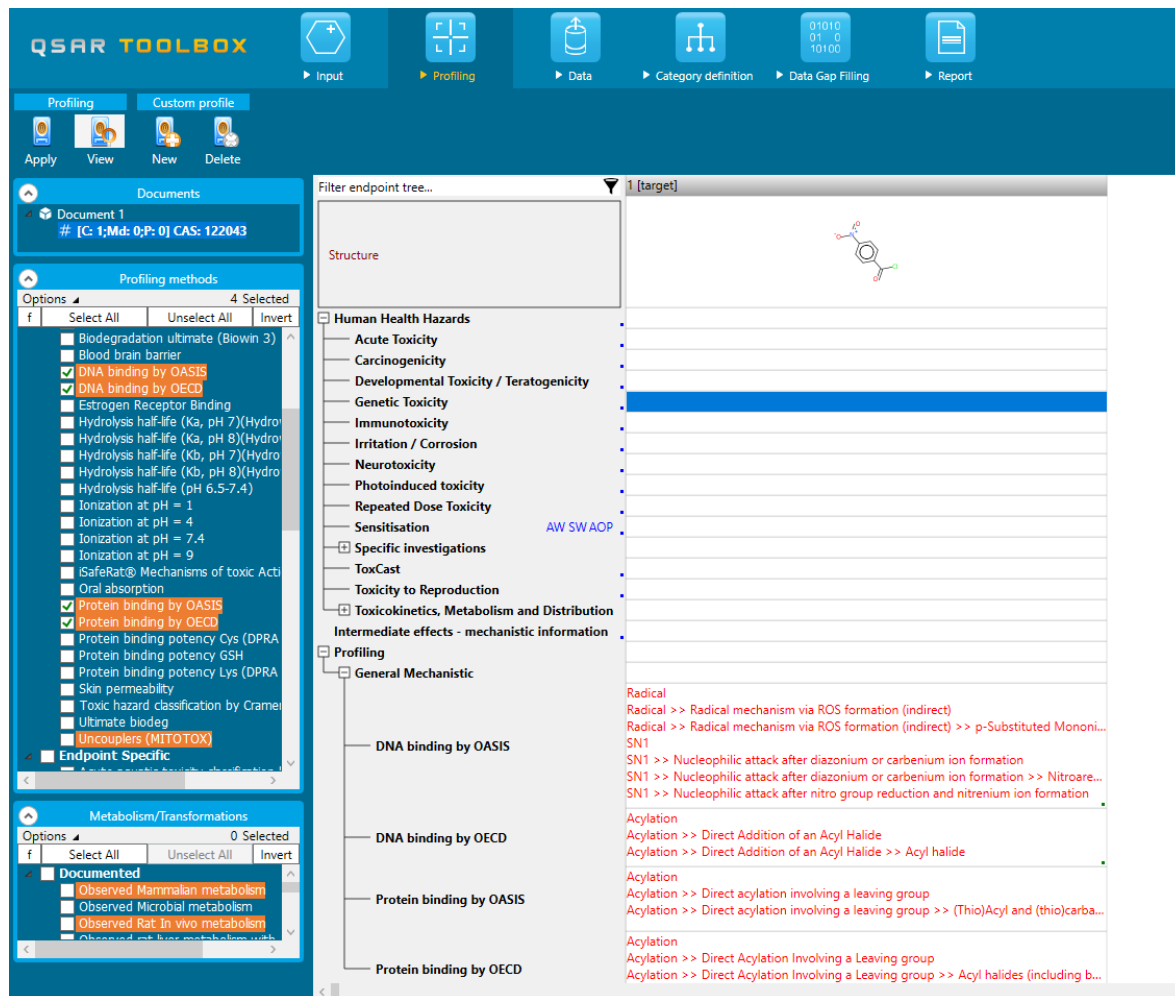


To define the target endpoint, which will be used for the predictions click



## 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.




The screenshot displays the QSAR TOOLBOX software interface. The top navigation bar includes icons for Input, Profiling (active), Data, Category definition, Data Gap Filling, and Report. Below this, the Profiling section is active, showing a list of profiling methods on the left and a list of endpoints on the right. The left panel, titled "Profiling methods", shows a list of methods with checkboxes. Selected methods include: DNA binding by OASIS, DNA binding by OECD, Protein binding by OASIS, Protein binding by OECD, and Uncouplers (MITOTOX). The right panel, titled "Endpoints", shows a list of endpoints with checkboxes. The "DNA binding by OASIS" endpoint is highlighted in blue. The "Structure" tab is active, showing the chemical structure of the target compound. The "Filter endpoint tree..." window is open, showing a tree structure of endpoints. The "DNA binding by OASIS" endpoint is selected, and its details are displayed on the right. The details include: Radical, Radical >> Radical mechanism via ROS formation (indirect), Radical >> Radical mechanism via ROS formation (indirect) >> p-Substituted Mononitro..., SN1, SN1 >> Nucleophilic attack after diazonium or carbenium ion formation, SN1 >> Nucleophilic attack after diazonium or carbenium ion formation >> Nitroare..., SN1 >> Nucleophilic attack after nitro group reduction and nitrenium ion formation, Acylation, Acylation >> Direct Addition of an Acyl Halide, Acylation >> Direct Addition of an Acyl Halide >> Acyl halide, Acylation, Acylation >> Direct acylation involving a leaving group, Acylation >> Direct acylation involving a leaving group >> (Thio)Acyl and (thio)carba..., Acylation, Acylation >> Direct Acylation Involving a Leaving group, Acylation >> Direct Acylation Involving a Leaving group >> Acyl halides (including b...

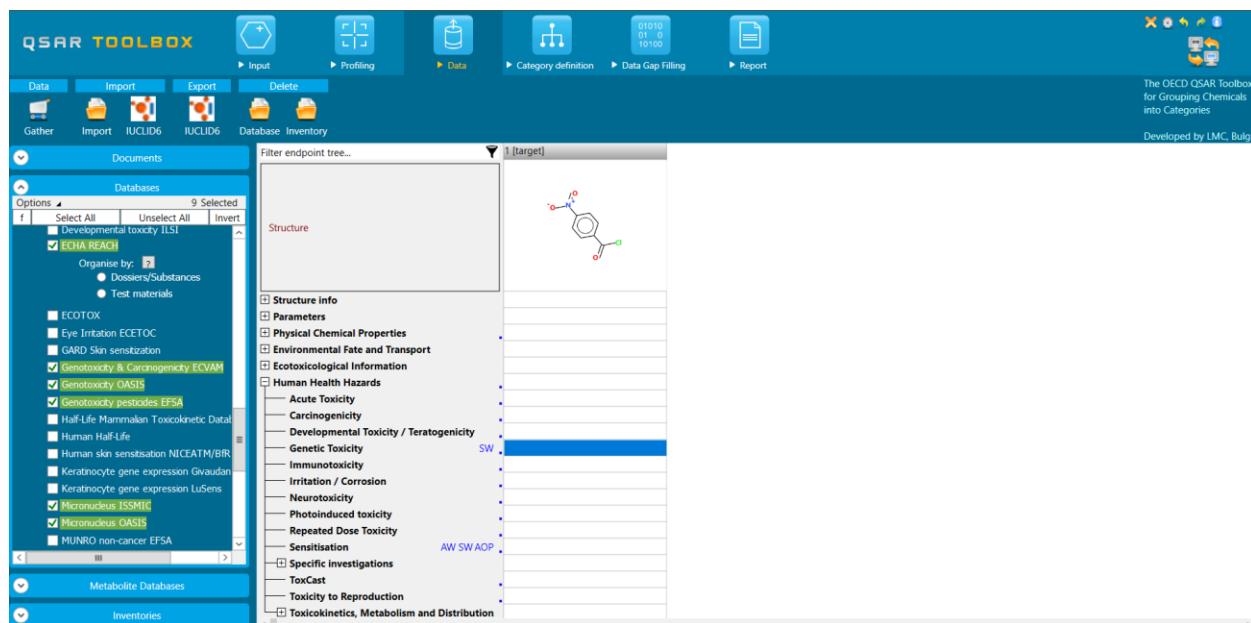
! To obtain the general background information on any profiler, right click on it and select **About**. To obtain the scientific information used to build the profiler, select

it and click .

! 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 → . The retrieved information is displayed according to four subsections in the endpoint tree:



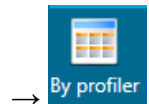
! To open the data tree: left-click on the nodes. To access detailed information on the experimental results: double-click on the result in the matrix.

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

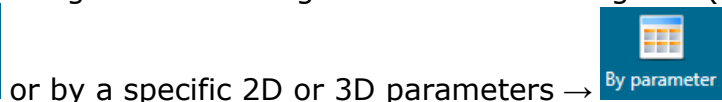
## Step 4: Category definition - Identify chemicals which could form a category with the "target" chemical

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

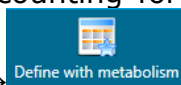
To identify the analogues of the target based on the profile of your target chemical



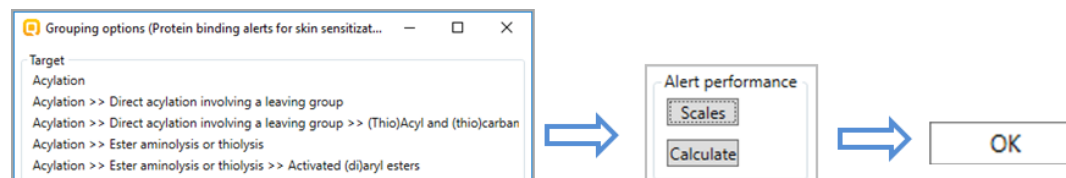
To identify the analogues of the target based on the fragment(s) identified in the



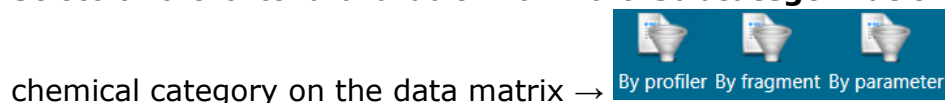
To identify the analogues of the target accounting for metabolic activation of the chemicals based on specific criteria select →



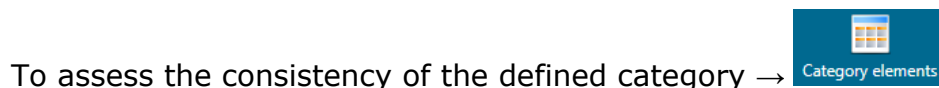
To check how much relevant to a target endpoint an alert is, once search **by profiler/with metabolism** is selected then calculate the Alert performance:



Select of the criteria available within the **Subcategorization section** to refine a



To identify the subgroups within an existing category that are determined by the



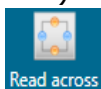
! The category consistency is endpoint specific. Four layers of information are considered important: Physicochemical similarity; Structural similarity and Mechanistic similarity and ADME similarity.

! 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. →



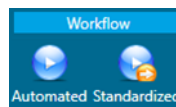
- Trend analysis: for “quantitative” endpoints if many analogues with experimental results are identified. →



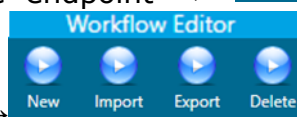
- (Q)SAR models: if no analogue with experimental results is identified or to build a weight of evidence case. →



- 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 →



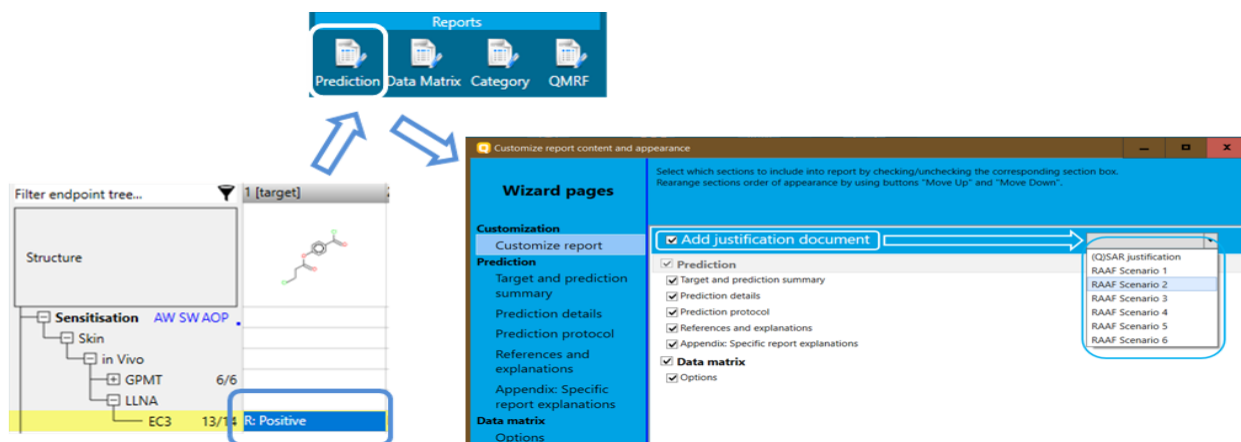
import/export your own workflows →



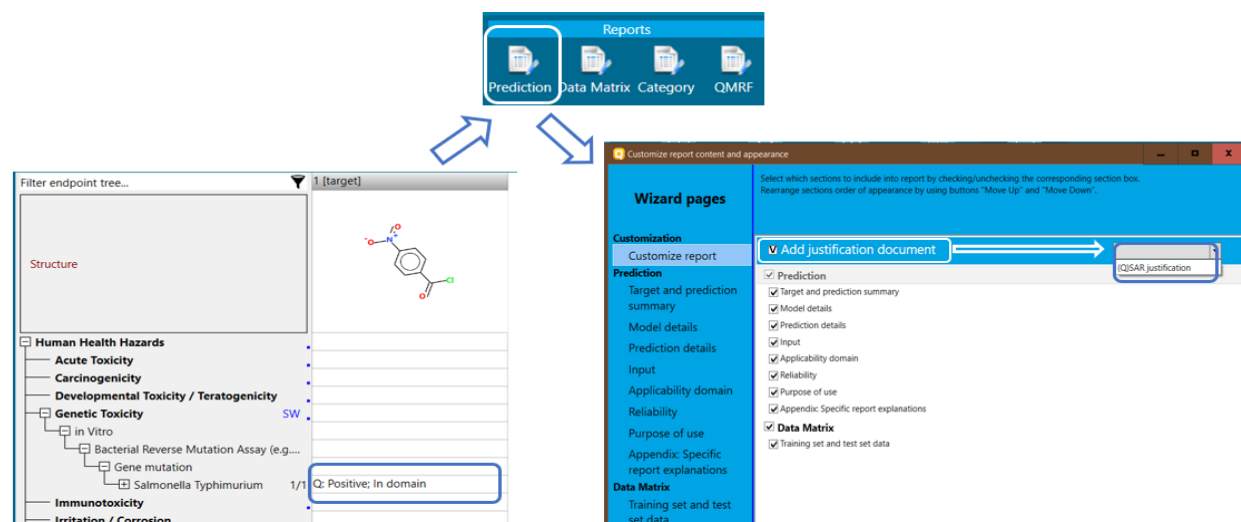
## Step 6: Report – Obtain a detailed report for your prediction or category

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**.

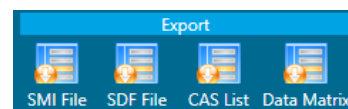


For predictions from a (Q)SAR model, the **(Q)SAR justification** document including (Q)SAR assessment elements, can be selected.



Four export types are also available in Toolbox v.4.8 →

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).