

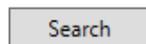
GETTING STARTED: QUICK REFERENCE GUIDE

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

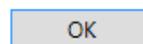
Define your target chemical by Chemical Name, CAS number, SMILES, drawing the molecule or selecting it from a list. To define a chemical by CAS number:



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 software interface. The 'Define' button is highlighted in the top toolbar. The main window displays the chemical structure of 4-Nitrobenzoyl chloride, along with its properties:

Structure info	Value
Additional Ids	EC Number:1484851
CAS Number	122-04-3
CAS Smiles relation	High
Chemical name(s)	4-Nitrobenzoyl chloride
Composition	
Molecular Formula	C7H4ClNO3
Predefined substance type	Mono constituent
SMILES	[O-][N+](=O)c1ccc(cc1)C(=O)Cl

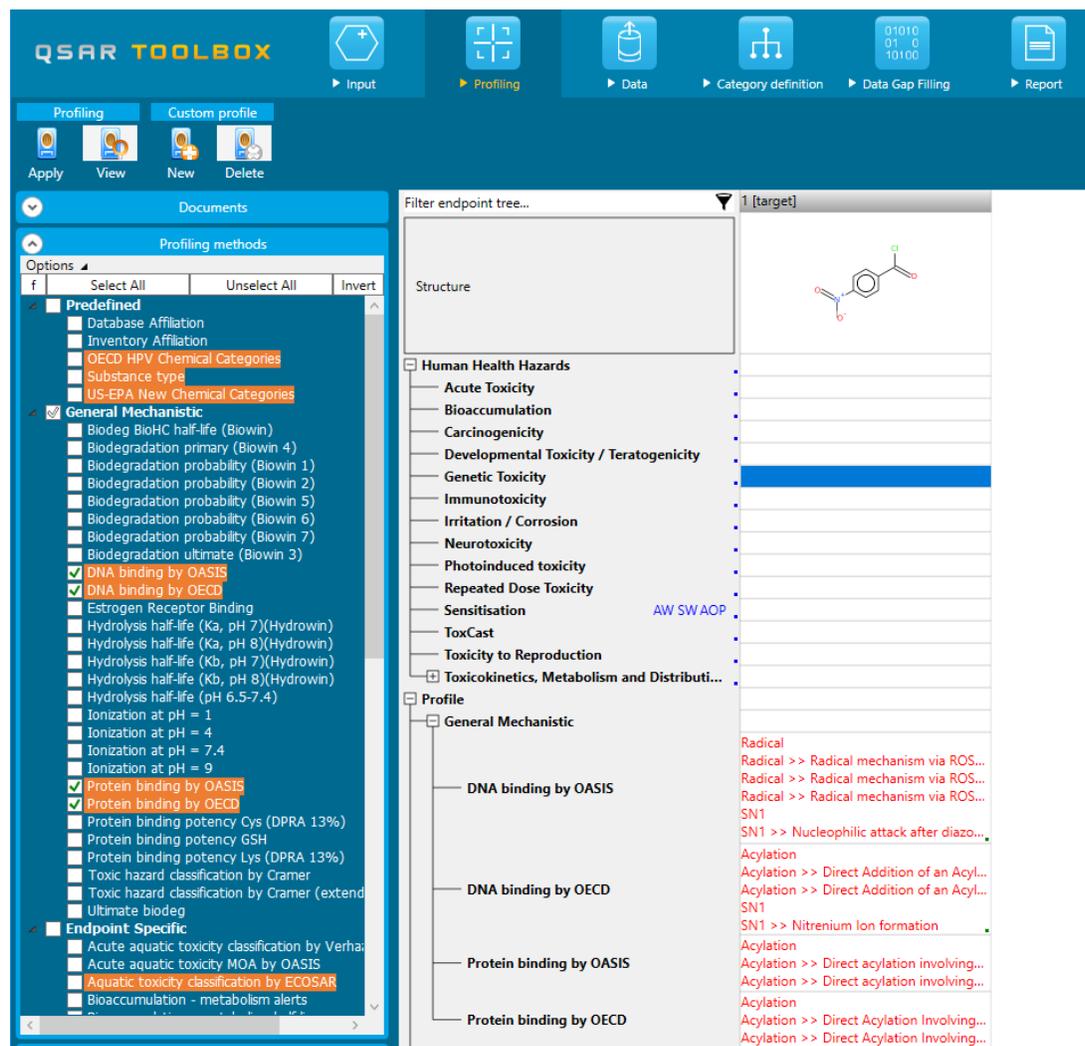


To define the target endpoint, which will be used for the predictions click



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 buttons for Input, Profiling, Data, Category definition, Data Gap Filling, and Report. Below this, there are sub-sections for Profiling and Custom profile, each with Apply, View, New, and Delete buttons. The main window is divided into several panels:

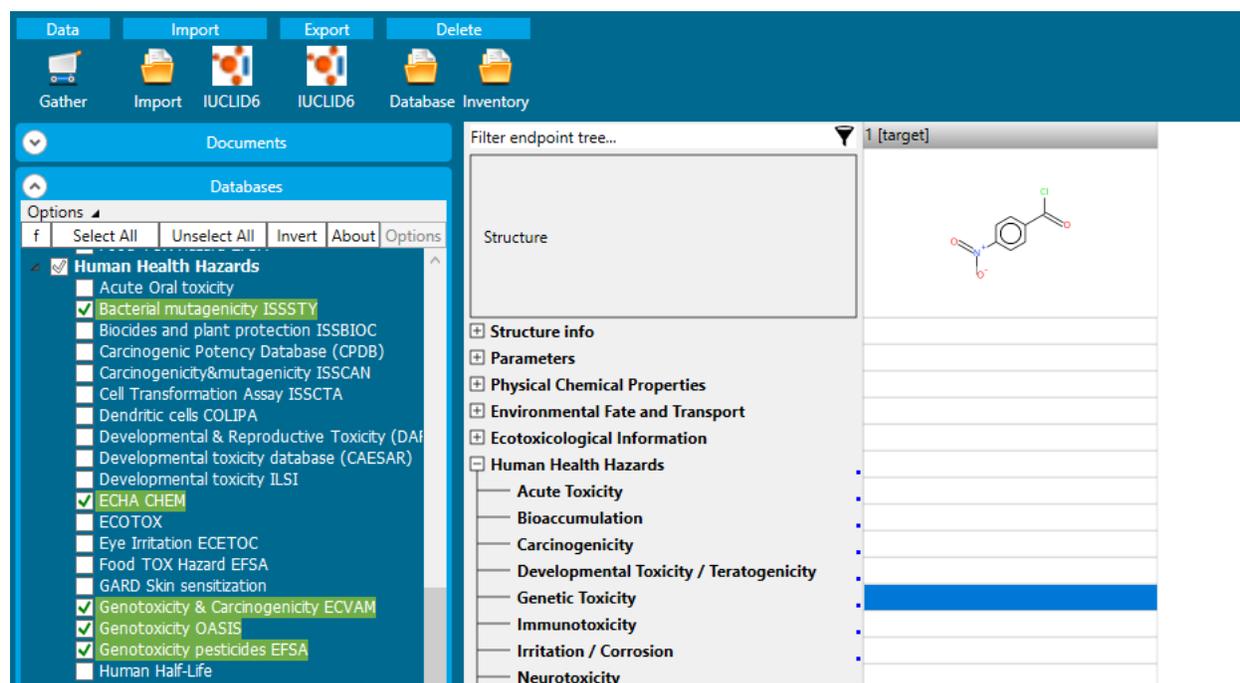
- Documents:** A list of documents with a search bar and options to Select All, Unselect All, or Invert.
- Profiling methods:** A tree view of various profilers. Under "General Mechanistic", several items are checked, including "DNA binding by OASIS" and "DNA binding by OECD".
- Filter endpoint tree...:** A tree view showing the structure of the selected endpoint. The "Profile" section is expanded, showing a list of profilers and their associated mechanisms. For example, "DNA binding by OASIS" is linked to "Radical" and "Acylation" mechanisms.

! 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:



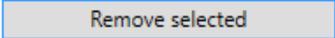
 To open the data tree: left-click on the nodes. To access detailed information on the experimental results: double-click on the result in the matrix.

 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

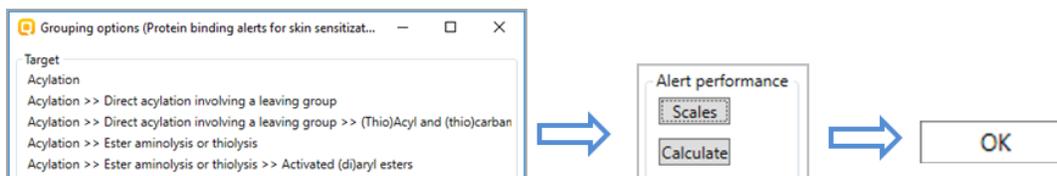
Select one grouping method according to the profile of your target chemical in the window **Grouping methods** → .

To refine the category, repeat the procedure by clicking on  and selecting other grouping methods. In the subcategorization procedure, the

function  deletes chemicals having different categories compared to the target.

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 the **Define (with metabolism) button** is selected then calculate the Alert performance



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. Three layers of information are considered important: Physicochemical similarity; Structural similarity and Mechanistic similarity.

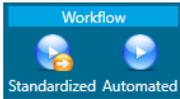
! The highlighted profiles correspond to the selected endpoint in the data matrix or to the previously defined endpoint if any.

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:

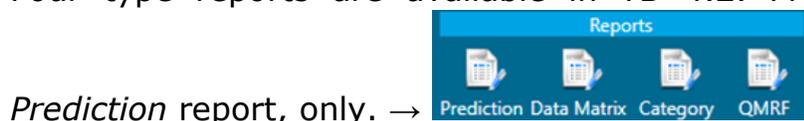
- Read-across: for “qualitative” endpoints (skin sensitization or mutagenicity e.g. positive, negative, equivocal) or for “quantitative endpoints” (e.g., 96h-LC50 for fish) if only very few analogues with

experimental results are identified. → 

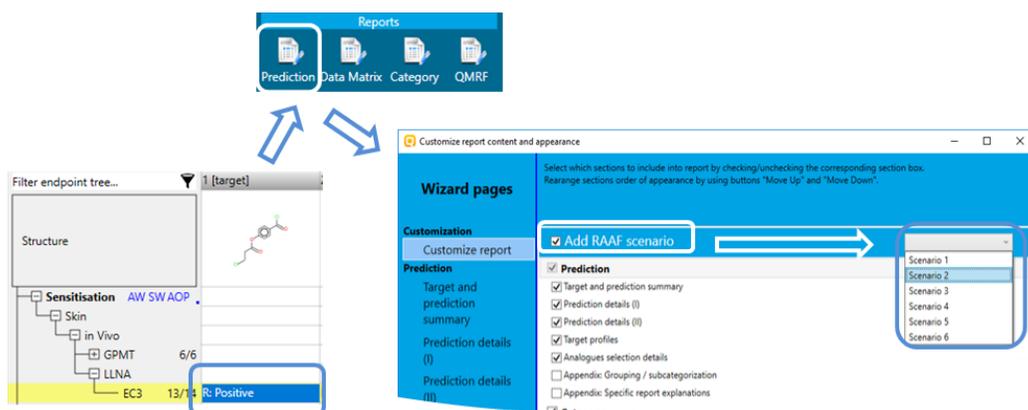
- Trend analysis: for “quantitative” endpoints if many analogues with experimental results are identified. → 
- (Q)SAR models: if no analogue with experimental results is identified or to build a weight of evidence case. → 
- Standardized and Automated workflows: once started, they follow the implemented logic and finish with prediction. They include read-across or trend analysis method depending on the endpoint → 

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

Four type reports are available in TB 4.2. Prediction is needed for the



Read across Assessment Elements could be included to the report automatically by selection of **RAAF scenario**



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