

## GETTING STARTED: QUICK REFERENCE GUIDE

### Step 1: Input - Define chemical of interest (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:



CAS# → enter the number without hyphens,

Search → the program displays the structure → OK

The structure is displayed on the data matrix.

The screenshot shows the QSAR Toolbox software interface. The top menu bar includes options like Document, Single Chemical, Chemical List, Search, and Target Endpoint. The 'Define' button is highlighted. The main window displays the chemical structure of 4-Nitrobenzoyl chloride and its properties:


Filter endpoint tree...	1 [target]
Structure	
Structure info	
CAS Number	122-04-3
CAS Smiles relation	High
Chemical name(s)	4-Nitrobenzoyl chloride
Composition	
Molecular Formula	C7H4ClNO3
Predefined substance type	Mono constituent
Structural Formula	[O-][N+](=O)c1ccc(cc1)C(C)=O
Parameters	
Physical Chemical Properties	
Environmental Fate and Transport	
Ecotoxicological Information	
Human Health Hazards	

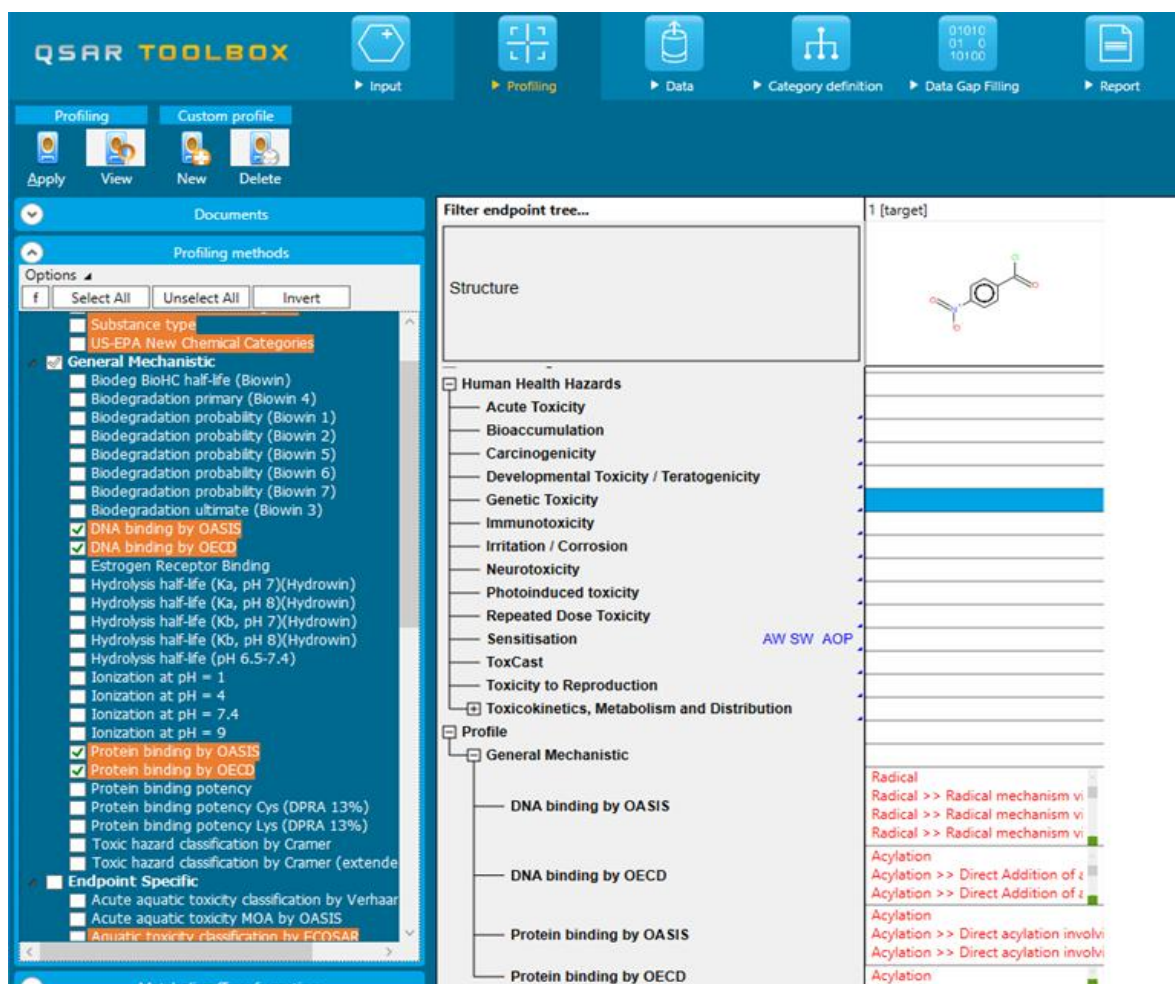


To define the target endpoint, which will be used for predictions click



## 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 tabs for Profiling and Custom profile, with sub-buttons for Apply, View, New, and Delete. The main workspace is divided into three panels:

- Documents Panel (Left):** Shows "Profiling methods" with a search bar and buttons for "Select All", "Unselect All", and "Invert". A list of methods is shown, with "DNA binding by OASIS" and "DNA binding by OECD" checked. Other methods include "Substance type", "US-EPA New Chemical Categories", "General Mechanistic" (with various Biowin and hydrolysis options), "Protein binding by OASIS/OECD", and "Endpoint Specific".
- Filter endpoint tree... Panel (Middle):** A tree view showing "Structure" at the top, followed by "Human Health Hazards" (with sub-items like Acute Toxicity, Bioaccumulation, etc.), "Toxicokinetics, Metabolism and Distribution", and "Profile". Under "Profile", "General Mechanistic" is expanded to show "DNA binding by OASIS", "DNA binding by OECD", "Protein binding by OASIS", and "Protein binding by OECD".
- 1 [target] Panel (Right):** Displays a chemical structure of a benzene ring with a nitro group and a chlorine atom. Below the structure is a table with columns for "Radical" and "Acylation", showing various mechanisms like "Radical >> Radical mechanism vi" and "Acylation >> Direct Addition of z".


! To obtain the general background information on any profiling scheme, right-click on it and select **About**. To obtain the scientific information used

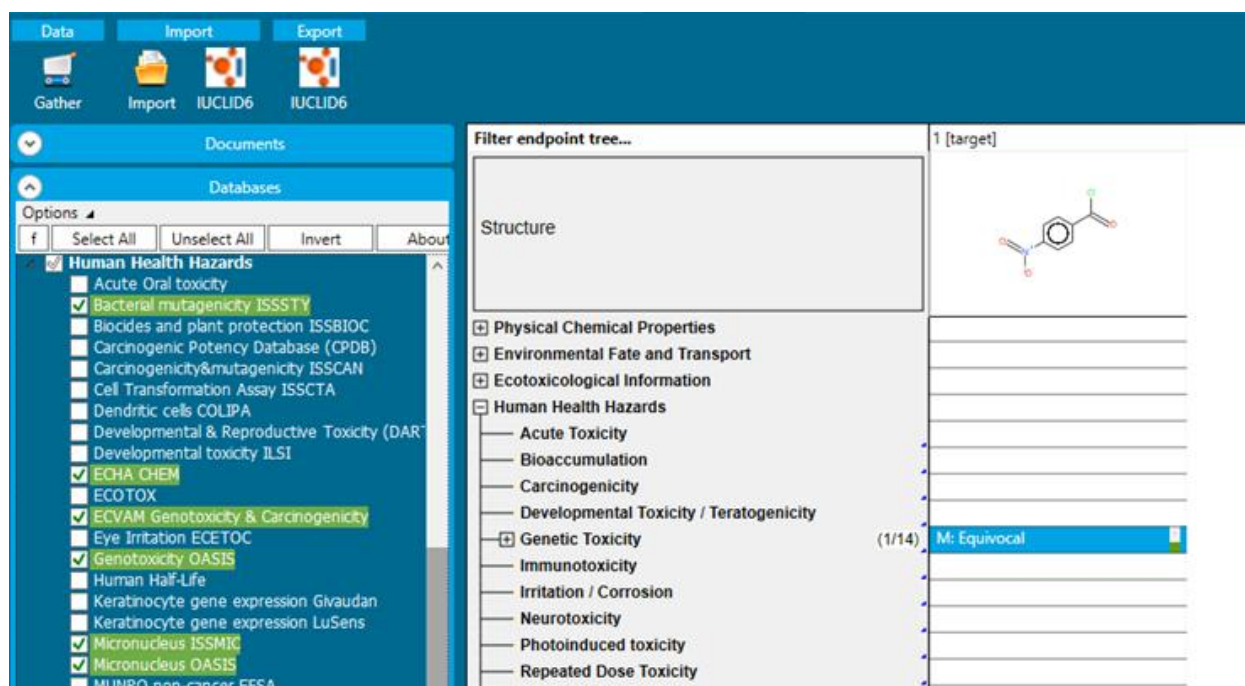
to build the profiling scheme, select it and click



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

### Step 3: Data - Retrieve experimental results from the resident databases

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



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

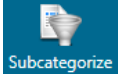
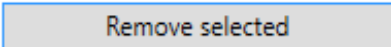
! The highlighted databases correspond to the selected endpoint in the data matrix or to the previously defined endpoint if any.


### 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** →  Define.

You are prompted to confirm the query details and the retrieval of experimental data. Click  each time.

To refine the category, repeat the procedure by clicking  and selecting other grouping methods. In the subcategorization procedure, the function  deletes chemicals having different categories compared to the target.

 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**

Click the cell in the data matrix with missing experimental data, 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. → 

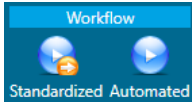
- Trend analysis: for “quantitative” endpoints if many analogues with

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 4.1. Prediction is needed only for the

*Prediction* report. ->

