

## OECD QSAR Toolbox v.4.4.1

Step by step example on how to predict acute aquatic toxicity to Daphnia for 3-ethyl-5-methyl-3-methoxyphenol by the trend analysis approach

# Outlook

- **Background**
- Keywords
- Objectives
- Specific Aims
- Trend analysis
- The exercise
- Workflow of the exercise

# Background

- This is a step-by-step presentation designed to take the user of the Toolbox through the workflow of a data gap filling exercise by trend analysis approach.

# Outlook

- Background
- **Keywords**
- Objectives
- Specific Aims
- Trend analysis
- The exercise
- Workflow of the exercise

# Keywords

**TARGET CHEMICAL** – a chemical of interest

**MODULE** – a Toolbox module is a section dedicated to specific actions and options (e.g. Profiling)

**WORKFLOW** – the use, in combination, of the different modules (e.g. prediction workflow: from input to report)

**PROFILER** - algorithm (rule set) for the identification of specific features of the chemicals. Several types of profilers are available, such as structural (e.g. organic functional groups), mechanistic (e.g. Protein binding by OECD) and endpoint-specific (e.g. in vitro in vitro mutagenicity (Ames test) alerts by ISS) profilers.

**ALERT** - the profilers consist of sets of rules or alerts. Each of the rules consists of a set of queries. The queries could be related to the chemical structure, physicochemical properties, experimental data, comparison with the target or list with substances and external queries from other predefined profilers (reference queries).

**CATEGORY** – “group” of substances sharing same characteristics (e.g. the same functional groups or mode of action). In a typical Toolbox workflow, it consists of the target chemical and its analogues gathered according to the selected profilers

**ENDPOINT TREE** – Endpoints are structured in a branched scheme, from a broader level (Phys-Chem properties, Environmental Fate and transport, Ecotoxicology, Human health hazard) to a more detailed one (e.g. EC3 in LLNA test under Human health hazard-Skin sensitization)

**DATA MATRIX** – Table reporting the chemical(s) and data (experimental results, profilers outcomes, predictions). Each chemical is in a different column and each data in a different row

**PREDICTION** – An outcome obtained for the target chemical by different gap filling approach methods (e.g. read-across, trend analysis, QSAR model predictions)

**TREND ANALYSIS** - The appropriate data-gap filling method for “quantitative endpoints” (e.g., 96h-LC50 for fish) if a high number of analogues with experimental results are identified.

**IUCLID 6 (IU6)** – IUCLID is a software to record, store, maintain and exchange data on intrinsic and hazard properties of chemical substances. Toolbox has a functionality to export a prediction or import of data to/from IU6

# Outlook

- Background
- Keywords
- **Objectives**
- Specific Aims
- Trend analysis
- The exercise
- Workflow of the exercise

# Objectives

- **This presentation reviews a number of functionalities of the Toolbox:**
  - Identify analogues for a target chemical
  - Retrieve experimental results available for those analogues
  - Fill data gaps by trend-analysis

# Outlook

- Background
- Keywords
- Objectives
- **Specific Aims**
- Trend analysis
- The exercise
- Workflow of the exercise



## Specific Aims

- To review the workflow of the Toolbox.
- To review the six modules of the Toolbox.
- To reacquaint the user with the basic functionalities within each module.
- To explain the rationale behind each step of the exercise.

# Outlook

- Background
- Keywords
- Objectives
- Specific Aims
- **Trend analysis**
- The exercise
- Workflow of the exercise

# Trend Analysis Overview

- For a given (eco)toxicological endpoint, the members of a category are often related by a trend (e.g. increasing, decreasing or constant). The trend could be related to molecular mass, carbon chain length, or to some other physicochemical property.
- A demonstration of consistent trends in the behaviour of a group of chemicals is one of the desirable attributes of a chemical category and one of the indicators that a common mechanism for all chemicals is involved. When some chemicals in a category have measured values and a consistent trend is observed, missing values can be estimated by simple scaling from the measured values to unmeasured values as a means of filling data gaps.

# Outlook

- Background
- Keywords
- Objectives
- Specific Aims
- Trend analysis
- **The exercise**
- Workflow of the exercise

## Exercise

- In this exercise we will predict the acute toxicity to daphnids for an untested compound, (3-ethyl-5-methyl-4-methoxyphenol), which is the “target” chemical.
- The target endpoint is LC50, 48h, Mortality, *D.magna*.
- This prediction will be accomplished by collecting a set of test data for chemicals considered to be in the same category as the target molecule.
- The category will be defined using the following categorization schemes:
  - *Acute aquatic toxicity classification by ECOSAR* – for primary grouping.
  - *Acute aquatic toxicity MOA by OASIS* – for mechanistic refining the category.

# Outlook

- Background
- Keywords
- Objectives
- Specific Aims
- Trend analysis
- The exercise
- **Workflow of the exercise**

## Workflow

- **Toolbox has six modules which are used in a sequential workflow:**
  - Chemical Input
  - Profiling
  - Data
  - Category Definition
  - Filling Data Gaps
  - Report

# Outlook

- Background
- Keywords
- Objectives
- Specific Aims
- Trend analysis
- The exercise
- **Workflow of the exercise**
  - **Chemical Input**



# Chemical Input Overview

- This module provides several means of entering the chemical of interest or the target chemical.
- Since all subsequent functions are based on chemical structure, the goal here is to make sure the molecular structure assigned to the target chemical is the correct one.

# Chemical Input

## Ways of Entering a Chemical

### User Alternatives for Chemical ID:

#### A. Single target chemical

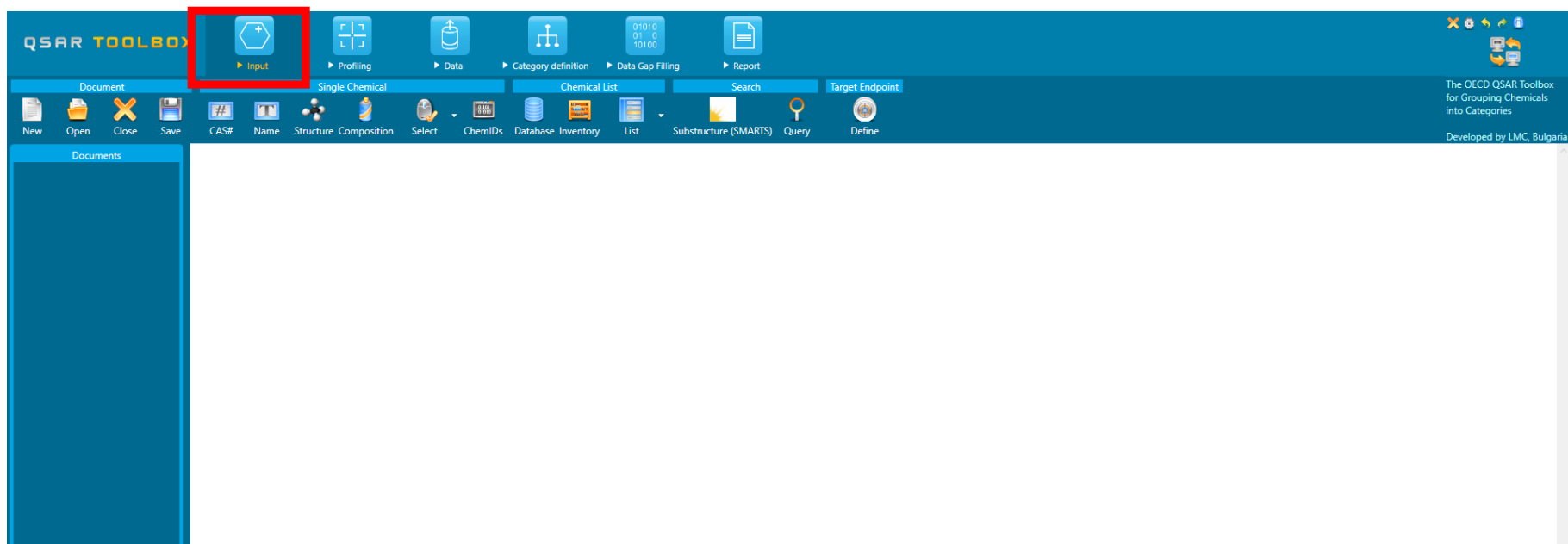
- Chemical Name
- Chemical Abstract Services (CAS) number (#)
- SMILES (simplified molecular information line entry system) notation/InChi
- Drawing chemical structure
- Select from User List/Inventory/Databases
- Substructure by using SMART

#### B. Group of chemicals

- User List/Inventory
- Specialized Databases

# Getting Started

- Open Toolbox.
- Click “Input”.

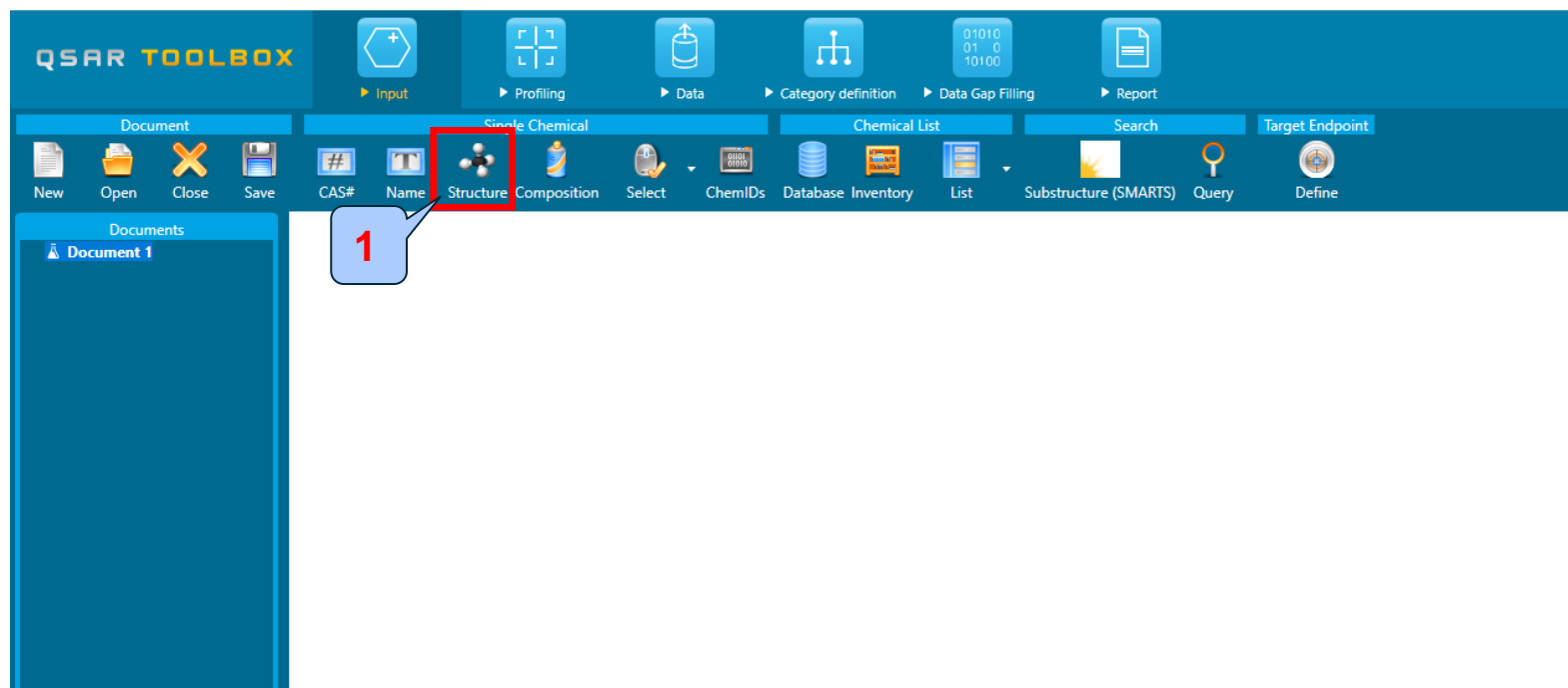


## Chemical Input by Drawing

- Input of the target chemical by drawing varies in difficulty with the structural complexity of the molecule.
- It is accomplished by a series of point-click-move-click operations within the 2D-editor which drops down when you click on "structure" (see next screen shot).
- The subsequent series of slides will take you through the process for inputting the target chemical.

# Chemical Input Screen

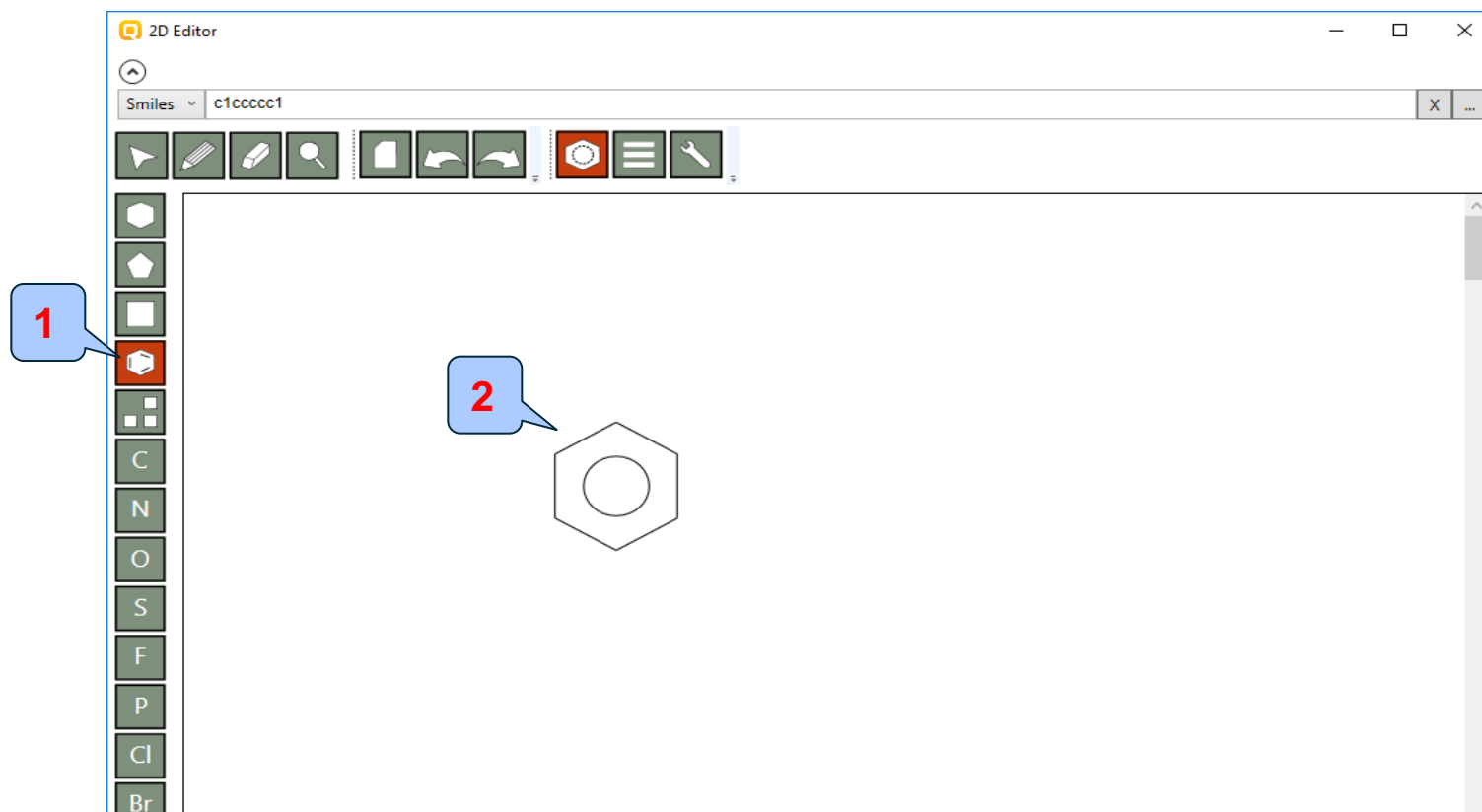
## Input target chemical by drawing



1. Click **Structure** button.

# Chemical Input

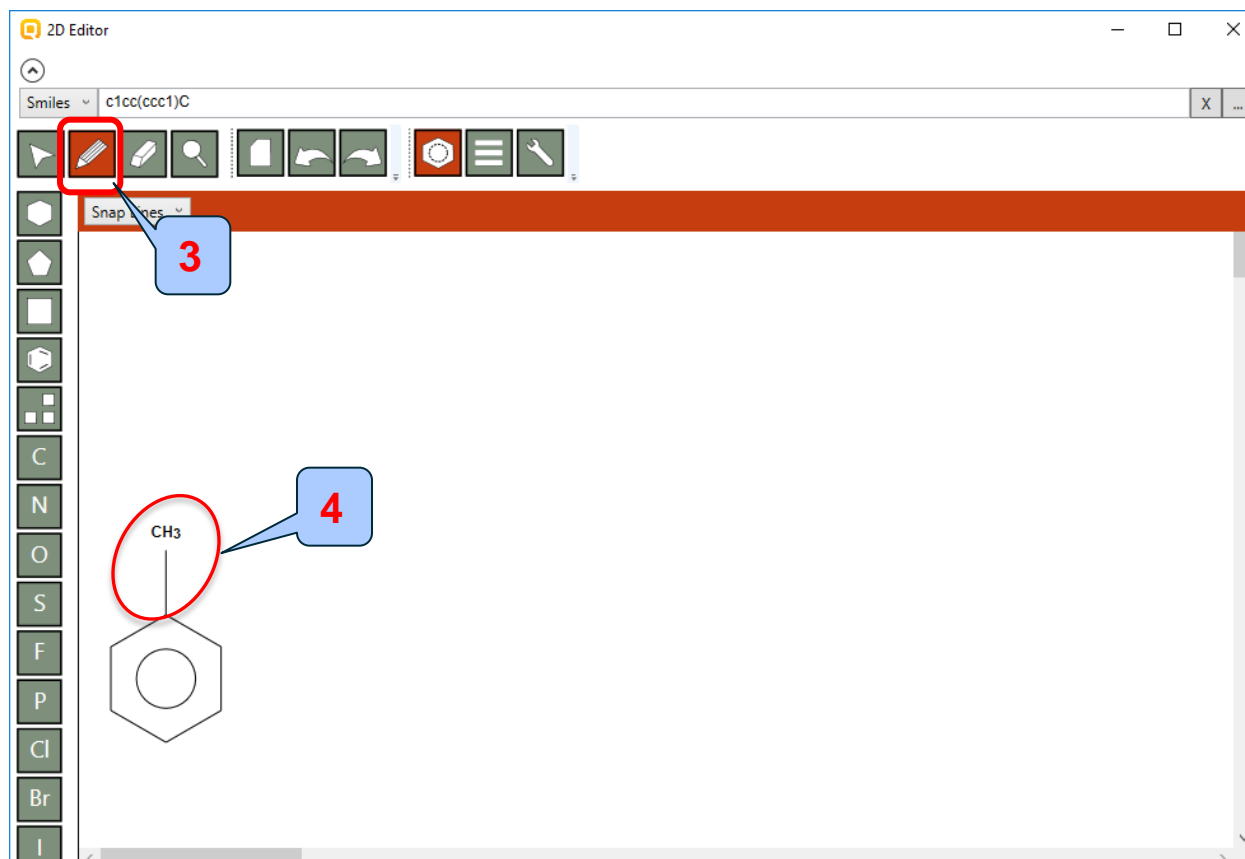
Drawing the target "3-ethyl-5-methyl-4-methoxyphenol" by 2-D editor




1. Left-click on the appropriate template form (in this case the benzene ring).
2. Move the cursor to the large clear area and left-click again, this puts the selected template in the plot.


# Chemical Input

Drawing the target "3-ethyl-5-methyl-4-methoxyphenol" by 2-D editor



3. Click on the  pencil button to draw a single bond.
4. Drag the mouse (pointing finger) to the appropriate atom and left-click to create a single bond.

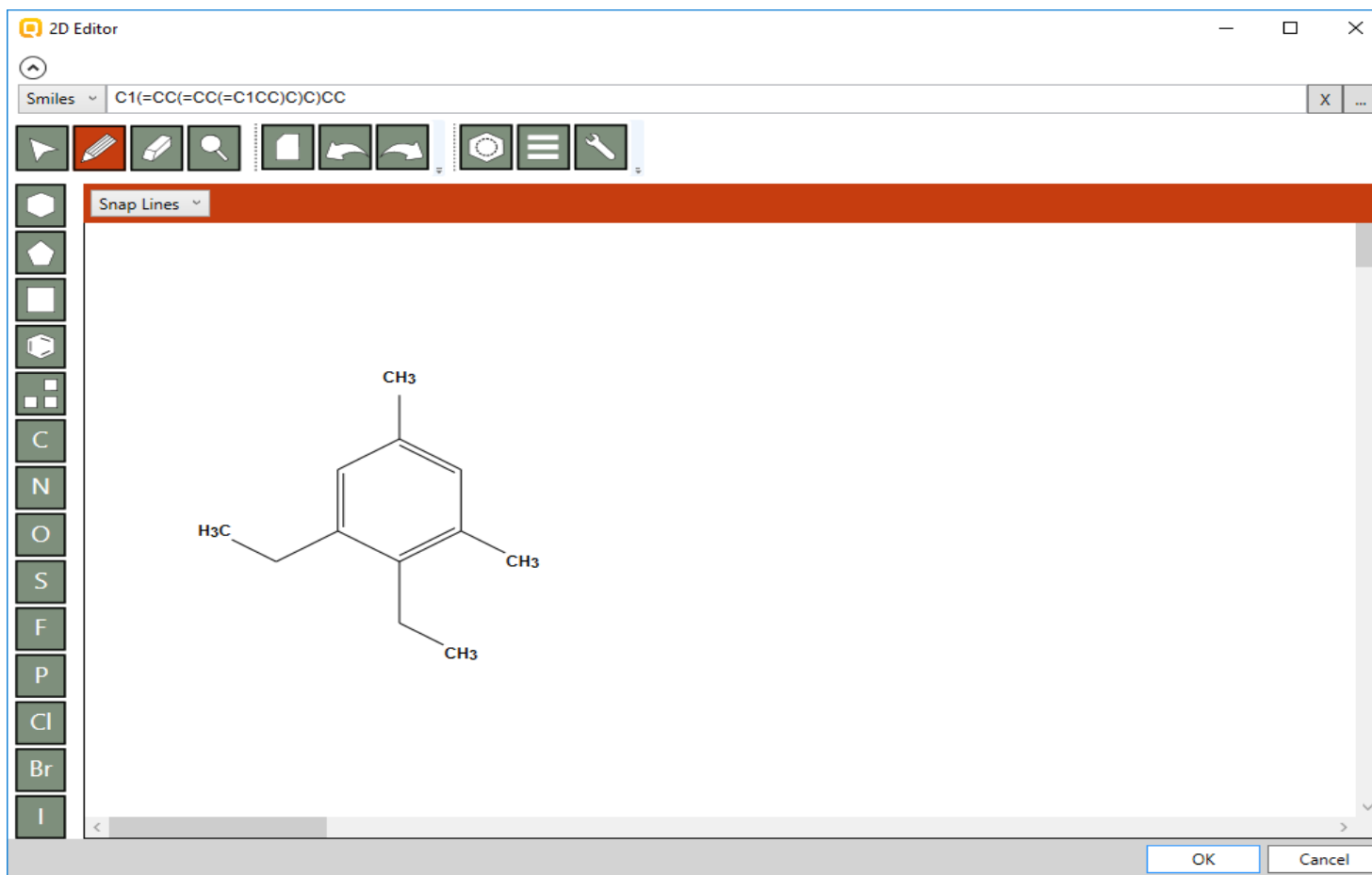
## Chemical Input by Drawing

- Note the default is addition of a CH<sub>3</sub>-group.
- By moving the 'finger' to other C-atoms and left clicking the mouse adds other hydrocarbon fragments.
- If you make an incorrect entry you can click the 'undo' icon (  ) in the upper corner of the screen to remove the addition.
- This process allows you to build the hydrocarbon skeleton of the target molecule (see next screen shot).



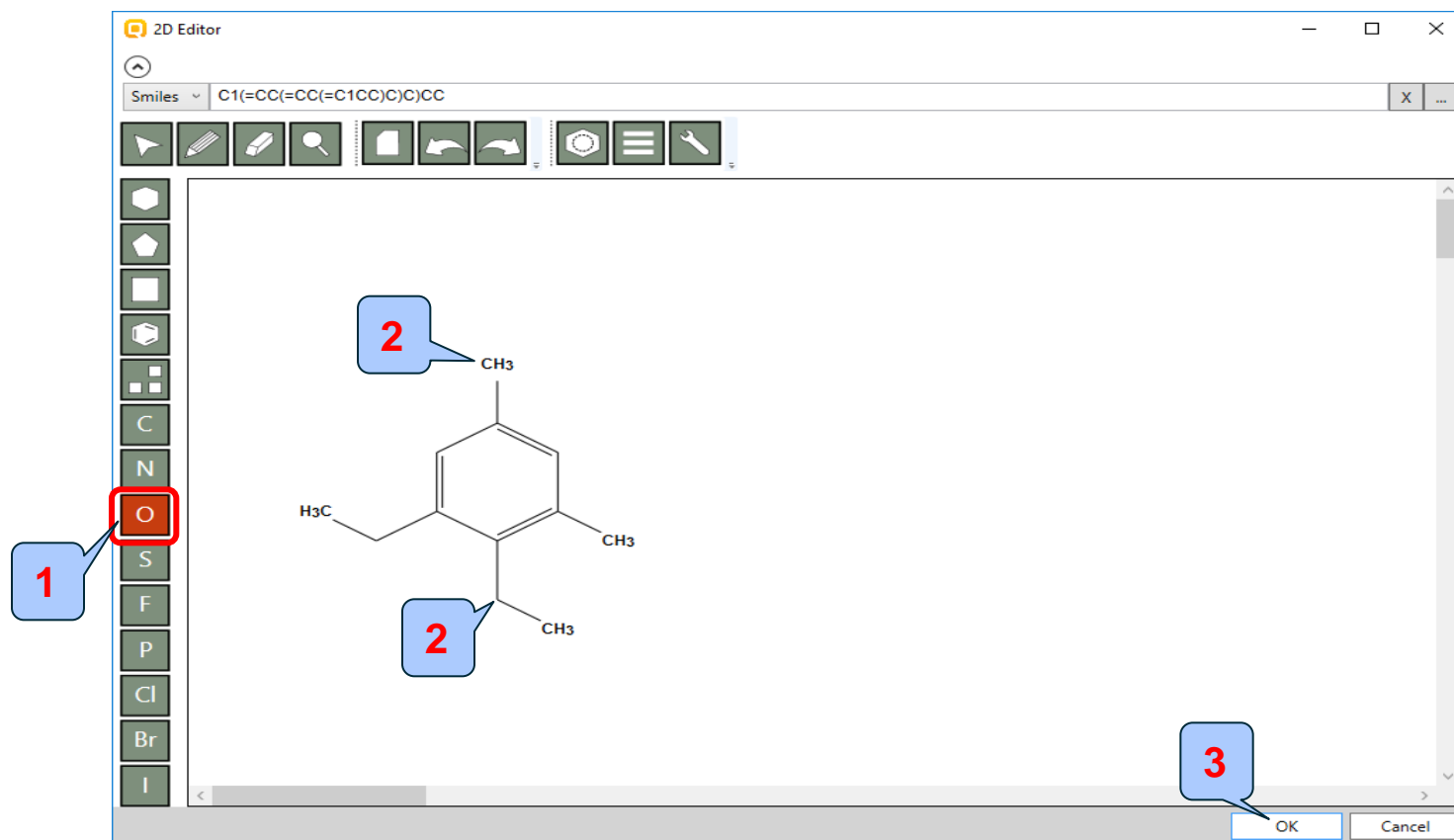
# Chemical Input

Drawing the target "3-ethyl-5-methyl-4-methoxyphenol" by 2-D editor



# Chemical Input

Drawing the target "3-ethyl-5-methyl-4-methoxyphenol" by 2-D editor



1. Click **O** to add an oxygen atom; 2. Left-click with mouse over the methyl group to insert an oxygen atom; 3. Click **OK**.

# Chemical Input

## Target chemical identity

- The already drawn target structure automatically appears on the data matrix
- Note that no CAS number or name is displayed for this chemical. This means the target chemical is not listed in the chemical inventories/databases implemented in the Toolbox (see next slide).

# Chemical Input

## Target chemical identity

The screenshot shows the QSAR Toolbox interface with the 'Chemical Input' module selected. The 'Target Endpoint' tab is active, showing a chemical structure and its associated information. A red dashed box highlights the 'Structure info' section, which includes the following data:

Structure info	Value
Additional Ids	
CAS Number	No CAS number
CAS-SMILES relation	Not applicable
Chemical name(s)	
Composition	
Molecular formula	C10H14O2
Predefined substance type	Mono constituent
SMILES	CCc1cc(O)cc(C)c1OC

The workflow on the first module is now complete, and the user can proceed to the next module.

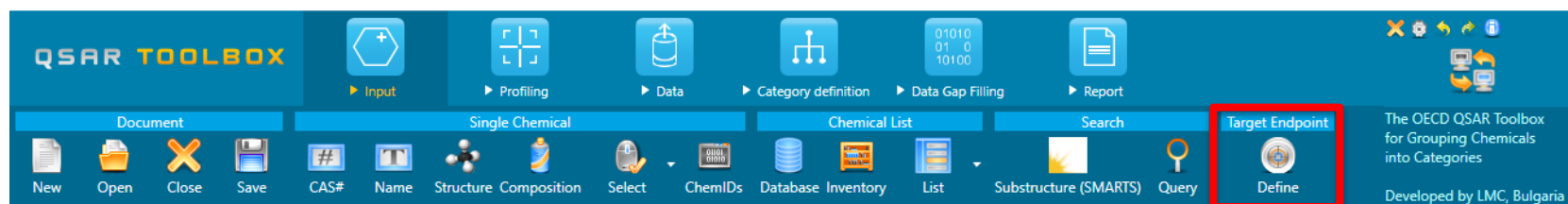
# Outlook

- Background
- Keywords
- Objectives
- Specific Aims
- Trend analysis
- The exercise
- **Workflow of the exercise**
  - Chemical Input
    - **Define target endpoint**

# Input

## Define target endpoint

- Defining of the endpoint allows entering the endpoint of interest e.g. EC3, LC50, gene mutation etc., along with specific metadata information. Based on the metadata, relevancy of the profiles and databases is provided expressed in different color highlighting:
  - In green are highlighted the most suitable profilers related to the endpoint and databases including data for the defined target endpoint,
  - In orange are colored profilers which are plausible with respect to the defined target endpoint.



# Input

## Define target endpoint

The screenshot shows the QSAR Toolbox software interface. The top toolbar contains several icons, with the 'Define' button (a target icon) highlighted by a red box and labeled with a blue callout '1'. Below the toolbar, the 'Documents' panel on the left shows 'Document 1' with a chemical structure. The 'Filter endpoint tree...' panel in the center shows a tree view with 'Ecotoxicological Information' expanded, and 'Aquatic Toxicity' highlighted by a red box and labeled with a blue callout '2'. The 'Select endpoint' dialog box is open, showing a list of endpoints. 'Aquatic Toxicity' is selected, and the 'LC50' endpoint is chosen from the 'Endpoint' dropdown menu, labeled with a blue callout '4'. The 'Effect' dropdown is set to 'Mortality', 'Duration' is set to '48h', and 'Test organisms (species)' is set to 'Daphnia magna', all labeled with a blue callout '5'. The 'Next' button is labeled with a blue callout '3'. The 'Finish' button is labeled with a blue callout '6'. A blue callout '3' also points to the 'Next' button.

By clicking **Define** (1) you could select the target endpoint.  
 In this tutorial the target endpoint is LC50 which is related to aquatic toxicity. In this respect select **Aquatic toxicity** in the *Ecotoxicological information* (2).  
 Click **Next** (3).  
 You need first to select the **LC50** endpoint (4) from the drop-down menu and then consecutively add the following metadata:  
*Effect: Mortality, Duration: 48h, Test organism (species): D.magna* (5).  
 Finally click **Finish** (6).

# Input

## Define target endpoint

The screenshot displays the QSAR Toolbox software interface. The 'Define' tab is active, showing the 'Filter endpoint tree...' panel. The tree is expanded to the 'LC50' endpoint, which is highlighted in yellow. A red rectangle is drawn around the path from 'Ecotoxicological Information' to 'LC50'. The 'Structure' panel shows the chemical structure of 2,4-dimethylphenol (2,4-DMP). The 'Parameters' panel shows a table with one row containing the chemical structure and the text '1 [target]'.

The endpoint tree is automatically expanded to the level of the defined endpoint and the row is highlighted in yellow



# Input

## Input results

- 1) In module *Input*, you have entered the target chemical by drawing it.
- 2) The target endpoint (aquatic toxicity, LC50) is defined using “Define target endpoint” functionality.
- 3) Based on the defined target endpoint the relevant profiles and databases become highlighted in color (see next slides).

# Outlook

- Background
- Keywords
- Objectives
- Specific Aims
- Trend analysis
- The exercise
- **Workflow of the exercise**
  - Chemical Input
  - **Profiling**

# Profiling Overview

- "*Profiling*" module refers to the electronic process of retrieving relevant information on the target compound, other than environmental fate, ecotoxicity and toxicity data, which are stored in the Toolbox database;
- Available "profilers" includes likely mechanism(s) of action, which could be useful in forming categories that include the target chemical;
- "Profilers" are a collection of empirical and mechanism knowledge which could be used to analyse the structural properties of chemicals;
- The "profilers" identify the affiliation of the target chemical(s) to preliminary defined categories (functional groups/alerts);
- The "Profiling" module contains also observed and simulated metabolisms/transformations, which could be used in combination with the profilers;
- The outcome of the profiling determines the most appropriate way to search for analogues, but they are also useful for preliminary screening or prioritization of substances;
- The "profilers" are not (Q)SARs, i.e. they are not prediction models themselves;
- Based on the "profilers' relevancy" (determined by the defined target endpoint), the most suitable and plausible ones are getting colour highlighted.

# Profilers Background

Summary information of the different profilers are provided in the "About".

The screenshot shows the QSAR Toolbox interface. The top toolbar has icons for Profiling (1), Data, and Category definition. The Profiling icon is highlighted with a red box. Below the toolbar, the 'Documents' panel shows a search for '[C: 1;Md: 0;P: 0] Search chemical'. The 'Filter endpoint tree...' panel on the right shows a tree structure with 'Structure info' expanded, showing 'Parameters', 'Physical Chemical Properties', 'Environmental Fate and Transport', and 'Ecotoxicological Information'. The 'Ecotoxicological Information' section is expanded, showing 'Aquatic Toxicity' and 'Sediment Toxicity'. The 'Aquatic Toxicity' section is expanded, showing 'Mortality' and 'LC50'. The 'Mortality' section is expanded, showing '48 h', 'Animalia (animals)', 'Arthropoda (arthropods)', 'Branchiopoda (branchiopods)', and 'Daphnia magna'. The 'Daphnia magna' section is expanded, showing 'LC50'. The 'About' window is open, showing the 'US-EPA New Chemical Categories' profiler. The 'About' window has a 'Name' field with 'US-EPA New Chemical Categories' and a 'Short Description' field. The 'Disclaimer' section states: 'The rules coded in the US-EPA New Chemical Program profiler reproduces the original categories cited in the document "TSCA New Chemicals Program (NCP)/ Chemical Categories" - an official document of U.S. EPA Office of Pollution Prevention and Toxics. However, not all of the categories have been coded because they are very broad and limits are mostly based on physical considerations and do not include structure based rules. These categories are listed below: - Category: Acid Dyes and Amphoteric Dyes - Category: Cationic Dyes - Category: Polyanionic Polymers (& Monomers) - Category: Polycationic Polymers - Category: Respirable, Poorly soluble Particulates'. The 'Donor(s)' field is 'United States Environmental Protection Agency (EPA), USA'. The 'Author(s)' field is empty. The 'Profiling methods' panel at the bottom shows a list of methods, including 'Suitable' and 'Plausible'. The 'US-EPA New Chemical Categories' method is highlighted with a red box (2). The 'About' button is highlighted with a red box (3). The 'Close' button (X) is highlighted with a red box (4).

1. Go to **Profiling** module
2. Click on the profiler (US-EPA New Chemical category);
3. Click **About**;
4. After acquiring the information you desire, **close** the window by clicking "x";

# Profilers

## Background

- For most of the profilers, background information can be retrieved by highlighting one of the profilers (for example, *US-EPA New Chemical Categories*) and clicking **View** (see next slide).

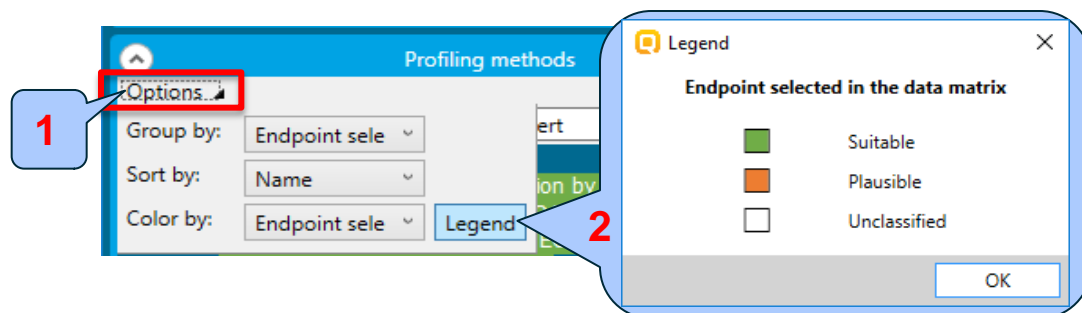
# Profiler Background

The screenshot shows the QSAR Toolbox Profiler interface. The main window is titled 'US-EPA New Chemical Categories (Predefined) - Profiling Scheme Browser'. It has several tabs: Definition, Properties, Training Set, Literature, MetaInfo Table, Custom Captions, and Scheme. The 'Literature' tab is selected, showing detailed information for the 'Anilines Environmental Toxicity' category. A list of chemical categories is visible on the left, with 'Anilines (Acute toxicity)' highlighted. The 'Profiling methods' section on the bottom left shows various methods, with 'US-EPA New Chemical Categories' selected. The 'Structure info' section on the right shows a tree view of chemical properties, with 'Anilines (Acute toxicity)' highlighted. The 'Literature' tab displays a detailed description of the category, including its definition, hazard concerns, and SARs.

1. Click the profiler;
2. Click **View**;
3. Click one of the structural alerts (for example *Anilines*);
4. Go to the **Literature** tab to see the mechanistic justification for the category.

# Profiler Background

- Once the endpoint is selected, the relevant profiles and metabolic transformations are highlighted. The meaning of the colors can be seen within the **Options** (1) by click **Legend** (2).



- Suitable** - developed using data/knowledge for the target endpoint;
  - Plausible** - not endpoint specific; structure-based; form broader group of analogues;
  - Unclassified** - all profilers, which are not classified in any of the categories above.
- Select the Profiling methods related to the target endpoint by ticking the checkbox next to the profilers name.
- This selects (a green check mark appears) or deselects (the green check disappears) profilers.

# Profiling

## Profiling the target chemical

1. Select the row corresponding to the *Aquatic Toxicity*;

2. Tick the checkboxes of the suitable profilers;

3. Click **Apply**.



# Profiling

## Profiling the target chemical

- The actual profiling will take several seconds depending on the number and type of selected profilers.
- The results of profiling automatically appear as a dropdown box under the target chemical.
- Please note the specific profiling results obtained by the most suitable profilers.
- These results will be used to search for suitable analogues in the next steps of the exercise.

# Profiling

## Profiles of the target "3-ethyl-5-methyl-4-methoxyphenol"

The screenshot shows the QSAR Toolbox software interface. The top menu bar includes 'Input', 'Profiling', 'Data', 'Category definition', 'Data Gap Filling', and 'Report'. The 'Profiling' tab is active, showing a 'Filter endpoint tree...' window. The tree lists various endpoints, with 'Acute aquatic toxicity classification by Verhaar (Modified)' selected. The left sidebar shows 'Profiling methods' and 'Metabolism/Transformations' sections. The right sidebar shows the chemical structure of 3-ethyl-5-methyl-4-methoxyphenol and a list of categories including 'Phenols (Acute toxicity)'.

# Profiling

## Profiling results

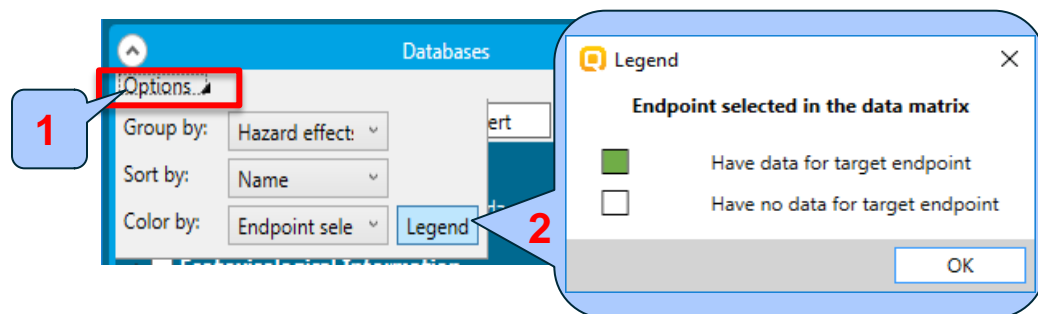
- 1) In module *Profile*, you have profiled the target chemical according to the suitable profilers (green) related to the target endpoint.
- 2) The target chemical is categorized as “phenol” based on predefined Acute aquatic toxicity US-EPA profiler (hereafter called US-EPA) and the two endpoint-specific profilers (Acute aquatic toxicity classification by ECOSAR (hereafter called ECOSAR) and Acute aquatic toxicity MOA by OASIS (hereafter called MOA))
- 3) By the endpoint-specific “Acute aquatic toxicity classification by Verhaar” the target is categorized as “Class 3 (unspecific reactivity)”
- 4) In general the target is classified as “phenol”
- 5) All of the above mentioned profilers could be used for categorization purposes (collecting analogues)
- 6) In this case ECOSAR profiler will be used for categorization purpose (primary grouping).

# Outlook

- Background
- Keywords
- Objectives
- Specific Aims
- Trend analysis
- The exercise
- **Workflow of the exercise**
  - Chemical Input
  - Profiling
  - **Data**

# Data

- *Data* module refers to the electronic process of retrieving the environmental fate, ecotoxicity and toxicity data that are stored in the Toolbox databases.
- Data gathering can be executed in a global fashion (i.e. collecting all data of all endpoints) or on a more narrowly defined basis (i.e. collecting data for a single or limited number of endpoints).
- Once the endpoint is selected, the relevant databases are highlighted. Meaning of the colors could be seen within the **Options** (1) by click **Legend** (2).



- In this example, we limit our data gathering to the common aquatic toxicity endpoints from databases containing aquatic toxicity data (Aquatic OASIS, ECHA REACH, ECOTOX, Food TOX Hazard EFSA).

# Data

## Gather data using database relevancy

The screenshot shows the QSAR Toolbox software interface. The top toolbar has a 'Data' icon (a blue square with a white database cylinder) highlighted with a red box and a callout bubble containing the number '1'. Below the toolbar, the 'Databases' panel on the left shows a list of databases with checkboxes. Four databases are selected and highlighted in green: 'Aquatic OASIS', 'ECHA REACH', 'ECOTOX', and 'Food TOX Hazard EFSA'. A red circle and a callout bubble with the number '2' are around this selection. The 'Gather' button (a blue square with a white folder icon) is also highlighted with a red circle and a callout bubble with the number '3'. The main window displays a 'Filter endpoint tree...' on the left and a 'Structure' panel on the right showing a chemical structure of a phenol derivative.

1. Go to **Data** module;
2. Select the green highlighted databases corresponding to the *Aquatic toxicity* (*Aquatic OASIS*, *ECHA REACH*, *ECOTOX*, *Food TOX Hazard EFSA*);
3. Click **Gather**.

# Data

## Process of collecting data

Toxicity information on the target chemical is electronically collected from the selected datasets.

A window with "Read data?" appears. Now the user could choose to collect "all" or "endpoint specific" data.

The screenshot displays the QSAR Toolbox software interface. The main window shows a 'Filter endpoint tree...' on the left with a hierarchical list of endpoints. The 'Aquatic Toxicity' branch is expanded, showing 'Mortality' and '48 h' under it. The 'Daphnia magna' endpoint is highlighted in yellow. A chemical structure is shown in the top right corner. A 'Read data?' dialog box is open on the right, with the 'All endpoints' radio button selected. The 'OK' button is highlighted with a red circle and the number '1'. A blue callout box with the number '1' points to the 'OK' button.

1. Click **OK** to read all available data.

# Data

## Process of collecting data

In this example, an insert window appears stating that no experimental data is available for the chemical of interest.

The screenshot displays the QSAR Toolbox software interface. The top menu bar includes 'Data', 'Import', 'Export', and 'Delete'. The 'Data' tab is active, showing a 'Filter endpoint tree...' window. This window lists various endpoints under 'Ecotoxicological Information', with 'Daphnia magna LC50' selected. A message window is open, stating 'No experimental data are available on the chemicals of interest.' with an 'OK' button. A blue callout box with the number '1' points to the 'OK' button.

25

1. Click **OK** to close the window.



## Recap

- You have entered the target chemical being sure of the correct structure.
- You have profiled the target chemical and found no experimental data is currently available for this structure.
- In other words, you have identified a data gap, which you would like to fill.
- Now you are ready to continue with next step of the workflow - *Category Definition*.

# Outlook

- Background
- Keywords
- Objectives
- Specific Aims
- Trend analysis
- The exercise
- **Workflow of the exercise**
  - Chemical Input
  - Profiling
  - Data
  - **Category definition**

# Category Definition

## Overview

- This module provides the user with several means of grouping chemicals into a toxicologically meaningful category that includes the target molecule.
- This is the critical step in the workflow.
- Several options are available in the Toolbox to assist the user in defining the category definition.

# Category Definition

## Grouping methods

- The different grouping methods allow the user to group chemicals into chemical categories according to different measures of “similarity” so that within a category data gaps can be filled by trend-analysis.
- For this example, starting from the target chemical a specific ECOSAR classification is identified (“phenols”), subsequently analogues are found within the same specific classification (“phenols”) for which experimental results are available.

# Category Definition

## ECOSAR categories - overview

- ECOSAR has been used by the U.S. Environmental Protection Agency since 1981 to predict the aquatic toxicity of new industrial chemicals in the absence of test data.
- The *Aquatic toxicity classification by ECOSAR* profiling scheme in the Toolbox is used for grouping of chemicals by structural similarity which may or may not have mechanistic meaning. Experience has shown ECOSAR to be a robust profiler which makes it a logical choice in an initial profiling scheme.

# Category Definition

## Defining ECOSAR category

The screenshot illustrates the process of defining an ECOSAR category in the QSAR Toolbox. The steps are numbered 1 through 4:

- Go to the **Category definition** module (indicated by a red box and callout 1).
- Select the highlighted **Aquatic toxicity classification by ECOSAR** document in the Documents panel (indicated by a red box and callout 2).
- Click **Define** in the menu bar (indicated by a red box and callout 3).
- Confirm the category "Phenols" by clicking **OK** in the Grouping options dialog box (indicated by a red box and callout 4).

1. Go to **Category Definition** module
2. Select the highlighted **Aquatic toxicity classification by ECOSAR**;
3. Click **Define**;
4. Confirm the category "Phenols" by clicking **OK**.

# Category Definition

## Defining ECOSAR category

The screenshot displays the QSAR Toolbox software interface. The top toolbar includes icons for Input, Profiling, Data, Category definition, Data Gap Filling, and Report. The 'Category definition' panel is active, showing a 'Filter endpoint tree...' on the left and a grid of chemical structures on the right. The tree structure includes categories like 'Structure', 'Parameters', 'Physical Chemical Properties', 'Environmental Fate and Transport', 'Ecotoxicological Information', 'Aquatic Toxicity', 'Sediment Toxicity', 'Terrestrial Toxicity', 'Human Health Hazards', and 'Profiling'. The 'Aquatic Toxicity' category is expanded, showing sub-categories like 'Mortality', '48 h', 'Animalia (anima...', 'Arthropoda', 'Branchio...', and 'Dapt...'. A 'Grouping results' dialog box is open in the center, displaying '1167 chemical(s) found.' and an 'OK' button. A red speech bubble with the number '1' points to the 'OK' button. The background shows the main software interface with various toolbars and panels.

1. Click **OK** to confirm the result and to gather experimental data.

**Note:** The number of chemicals depends on the database version you are working with.

## Category Definition

### Analogues

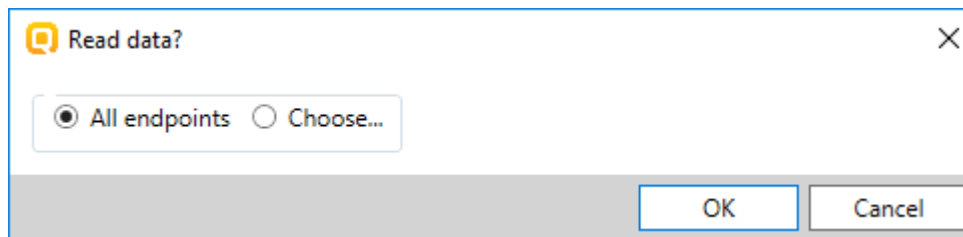
- The Toolbox now identifies all chemicals corresponding to the ECOSAR classification of *Phenols* which are listed in the selected databases within the *Data* module.
- 1167 analogues are identified. Along with the target they form a category (Phenols) which can be used for data gap filling.



## Category Definition

### Read data for Analogues

- The Toolbox automatically requests the user to select the endpoint that should be retrieved.
- The user can either select the specific endpoint or by default choose to retrieve data on all endpoints (see below).



- In this example, since only databases that contain information for Eco-toxicological endpoints are selected, both options give the same results.
- As the Toolbox must search the database, this may take some time.

# Category Definition

## Summary information of Analogues

The screenshot shows the QSAR Toolbox software interface. The main window is titled 'Category definition' and includes a toolbar with icons for Input, Profiling, Data, Category definition, Data Gap Filling, and Report. The 'Category definition' tab is active, showing a 'Filter endpoint tree...' window. The 'Ecotoxicological Information' section is expanded, listing various endpoints such as Aquatic Toxicity, Accumulation, Adult Behaviour, Adult Mortality, Avoidance, Behavior, Biochemistry, Biomass, Cell Number, Cell(s), Coagulation of The Embryo, Development, Ecosystem Process, Enzyme(s), Feeding Behavior, Fertility, Frond Number, Genetics, Gonadal Histology, Growth, Growth Inhibition, Growth Rate, Histology, Hormone(s), and Immobilisation. A 'Gather data' dialog box is open, displaying '78914 points added across 1166 chemicals.' A red callout bubble with the number '1' points to the 'OK' button in the dialog box.

1. Click **OK** on window that provides information for common number collected data across the initial group of chemicals.

**Note:** The number of data points depends on the database version you are working with.



59

# Category Definition

## Summary information of Analogues

The screenshot shows the QSAR Toolbox software interface. The 'Data points' window is open, displaying a table of experimental data points. A red box highlights a cell containing 'M: 10 mg/L', and a blue callout bubble with the number '1' points to it. The background shows the main software interface with various toolbars and a document list on the left.

Datapoints	#	Value	Original value	Additional	Applicable
Ecotoxicological Information;Aquatic Toxicity;Mortality;24 h;Animalia (animals);Chordata (chordates);Actinopterygii (ray-finned fishes,spiny rayed fishes);Oncorhynchus kisutch;Undefined Endpoint	1	M: 10 mg/L (Mass concentration)	1E+04 µg/L (Mass concentration)	BAGS// CONC/ ONLY CONC TESTED//	1 Dosed x time(s) per study period
Ecotoxicological Information;Aquatic Toxicity;Mortality;24 h;Animalia (animals);Chordata (chordates);Actinopterygii (ray-finned fishes,spiny rayed fishes);Oncorhynchus kisutch;Undefined Endpoint	2	M: 10 mg/L (Mass concentration)	1E+04 µg/L (Mass concentration)	BAGS// CONC/ ONLY CONC TESTED//	1 Dosed x time(s) per study period
Ecotoxicological Information;Aquatic Toxicity;Behavior;24 h;Animalia (animals);Chordata (chordates);Actinopterygii (ray-finned fishes,spiny rayed fishes);Ptychocheilus oregonensis;Undefined Endpoint	3	M: 10 mg/L (Mass concentration)	1E+04 µg/L (Mass concentration)	BAGS// CONC/ ONLY CONC TESTED//	1 Dosed x time(s) per study period

Below the 'Data points' window, a detailed table of experimental data is visible. A red box highlights a cell containing 'M: 10 mg/L'. A blue callout bubble with the number '1' points to it.

Ecotoxicological Information	Value	Original value	Additional	Applicable
M: 10 mg/L	M: ≥1.5 mg/L	M: 0.00382 mg/L	M: =2.5 mg/L	M: >1E+03 mg/L
M: 10 mg/L	M: >1.5 mg/L	M: 0.00382 mg/L	M: =2.5 mg/L	M: >1E+03 mg/L
M: 10 mg/L	M: >9.2 mg/L	M: 0.00382 mg/L	M: =2.5 mg/L	M: >1E+03 mg/L
M: 5 ppm	M: 9.2 mg/L	M: 0.1 mg/L	M: =2.5 mg/L	M: >1E+03 mg/L
M: 5 ppm	M: >9.2 mg/L	M: 0.11 mg/L	M: =2.5 mg/L	M: >1E+03 mg/L
M: 5 ppm	M: ≥9.2 mg/L	M: 0.15 mg/L	M: =2.5 mg/L	M: >1E+03 mg/L
M: 5 ppm	M: >9.2 mg/L	M: 0.319 mg/L	M: =2.5 mg/L	M: >1E+03 mg/L
M: 5 ppm	M: >9.2 mg/L	M: 0.4 mg/L	M: =2.5 mg/L	M: >1E+03 mg/L
M: 5 ppm	M: >9.2 mg/L	M: 1 mg/L	M: =2.5 mg/L	M: >1E+03 mg/L
M: 5 ppm	M: ≥11.2 mg/L	M: 1 mg/L	M: =2.5 mg/L	M: >1E+03 mg/L

1. Double-click on the cell with measured data opens a table which provides detailed information for all experimental data of the focused chemical.

## Recap

- You have identified a category of 1166 chemicals (*Phenols*) with the *Aquatic toxicity classification by ECOSAR* profiler for the target chemical 3-ethyl-5-methyl-4-methoxyphenol.
- The available experimental results for these 1166 analogues have been collected from the selected databases (*Aquatic OASIS, ECHA REACH, ECOTOX and Food TOX Hazard EFSA*).
- But before the user can proceed with the *Filling Data Gap* module, he/she should navigate through the endpoint tree and find the specific gap that will be filled.

# Category Definition

## Navigation through the endpoint tree

- The user can navigate through the data tree by opening (or closing) the nodes of the tree.
- The data tree is extensive but logically constructed. It can be mastered with a practice.
- In this example, the “48 h LC50 Mortality for *Daphnia magna*” is the target endpoint.
- As already mentioned the row with the defined target endpoint is highlighted in yellow. (see next slide)

# Category Definition

## Navigation through the endpoint tree

The image shows three overlapping screenshots of the 'Filter endpoint tree' dialog in the QSAR Toolbox, illustrating the navigation path to a specific endpoint. The path is marked with numbered callouts 1 through 8.

- 1**: Expanding the **Ecotoxicological Information** category.
- 2**: Expanding the **Aquatic Toxicity** sub-category.
- 3**: Expanding the **Mortality** sub-category.
- 4**: Expanding the **48 h** duration.
- 5**: Expanding the **Animalia (animals)** taxonomic group.
- 6**: Expanding the **Arthropoda (arthropods)** taxonomic group.
- 7**: Expanding the **Daphnia magna** species.
- 8**: Selecting the **LC50** endpoint.

**Endpoint Tree Structure (from rightmost screenshot):**

- Structure
  - Inhibition of Nitrification Rate
  - Inhibition of Total Respiration
  - Injury
  - Intoxication
  - Length
  - Mobility
  - Morphology
  - Mortality
    - Undefined Duration
      - 24
      - 96
      - 0 d
      - 2.5 min
      - 3 min
      - 4.02 min
      - 4.5 min
    - 46 h (4/5)
    - 47 h (1/1)
    - ca.48 h (1/5)
    - 48 h
      - Animalia (animals)
        - Annelida (annelids) (9/36)
        - Arthropoda (arthropods)
          - Arachnida (arac) (1/33)
          - Branchiopoda (branchiopods)
            - Artemia franc... (1/1)
            - Artemia part... (1/3)
            - Artemia salina (5/7)
            - Artemia sinica (3/3)
            - Ceriodaphnia... (1/3)
            - Ceriodaphnia... (13/57)
            - Ceriodaphnia... (1/1)
            - Ceriodaphnia... (2/5)
            - Chydorus sph... (1/1)
            - Daphnia cari... (2/3)
            - Daphnia cucu... (3/4)
            - Daphnia gale... (1/2)
            - Daphnia long... (1/1)
            - Daphnia magna
              - ECO (1/1)
              - EC0 (1/1)
              - EC100 (1/1)
              - EC50 (21/29)
              - EL50 (2/2)
              - LC10 (1/2)
              - LC50 (63/277)
              - LC90 (1/2)
              - LOEC (2/2)
              - NOEC (10/22)

**Navigation Summary:**

Expand: the **Ecotoxicological Information** >>  
**Aquatic Toxicity** (1) >>  
**Mortality** (2) >>  
**48h** (3) >>  
**Animalia (animals)** (4) >>  
**Arthropoda (arthropods)** (5) >>  
**Branchiopoda (branchiopods)** (6) >>  
**Daphnia magna** (7) - this is the species related to target endpoint **LC50** (8).

## Recap

- You have now retrieved the available experimental data on aquatic toxicity for 1166 chemicals classified as “phenols” by the “ECOSAR” profiler found in the databases Aquatic OASIS, ECHA REACH, ECOTOX and Food TOX Hazard EFSA.
- You have identified the target endpoint of “48 h LC50 Mortality for *Daphnia magna*”.
- You are ready to fill in the data gap so click *Data Gap Filling* (see next few slides).



# Outlook

- Background
- Keywords
- Objectives
- Specific Aims
- Trend analysis
- The exercise
- **Workflow of the exercise**
  - Chemical Input
  - Profiling
  - Data
  - Category definition
  - **Data Gap Filling**

# Data Gap Filling

## Overview

- *Data Gap Filling* module gives access to five different data gap filling tools:
  - Read-across
  - Trend analysis
  - (Q)SAR models
  - Standardized workflow (SW)
  - Automated workflow (AW)
- The most relevant data gap mechanism is used , taking into account the following considerations:
  - *Read-across* is the appropriate data-gap filling method for “qualitative” endpoints like skin sensitisation or mutagenicity for which a limited number of results are possible (e.g. positive, negative, equivocal). Furthermore read-across is recommended for “quantitative endpoints” (e.g., 96h-LC50 for fish) if only a low number of analogues with experimental results are identified.
  - *Trend analysis* is the appropriate data-gap filling method for “quantitative endpoints” (e.g., 96h-LC50 for fish) if a high number of analogues with experimental results are identified.
  - *(Q)SAR models* can be used to fill a data gap if no adequate analogues are found for a target chemical.
  - *Automated and standardized workflows* follow preliminary implemented logic. The AW is not affected by the user activities (proceeding or subsequent), while the SW stops at the each step of the workflows allowing the user to make different selection.
- In this example we will use trend analysis.

# Data Gap Filling

## Apply Trend analysis

**1** Click **Data Gap Filling** in the top menu.

**2** Click **Trend analysis** in the left sidebar.

**3** Click **OK** in the **Possible data inconsistency** dialog box.

**4** Click **OK** in the **Information** dialog box.

**Target endpoint**

Endpoint	Chemicals	Data
EC0	1/1	
EC10	1/1	
EC100	2/2	
EC50	4/4	
EL50	2/2	
LC10	1/2	
<b>LC50</b>	<b>63/278</b>	
LC90	1/2	
LOEC	3/3	
NOEC	20/23	
NOEL	1/1	
NR-LETH	1/1	
NR-ZERO	3/4	
Other En...	1/3	

**Possible data inconsistency**

Metadata

- Class
- Duration
- Effect
- Endpoint
- Kingdom
- Native scale/unit
  - ☒ M (14 chemicals; 14 data)
  - ☒ mg/L (25 chemicals; 74 data)
  - ☒ mmol/L (1 chemicals; 1 data)
  - ☒ mol/L (45 chemicals; 45 data)
  - ☒ ppm (11 chemicals; 11 data)
  - ☒ µM (1 chemicals; 1 data)
  - ☒ µg/L (36 chemicals; 132 data)
- Phylum

Select scale/unit to use

- ☐ M [14 native data and 253 converted]
- ☐ g/m³ [0 native data and 267 converted]
- ☒ log(1/mol/L) [0 native data and 267 converted]
- ☐ mg/L [74 native data and 193 converted]
- ☐ mmol/L [1 native data and 266 converted]
- ☐ mol/L [45 native data and 222 converted]
- ☐ µmol/L [10 native data and 267 converted]

Converted data

14 from scale/unit M  
74 from scale/unit mg/L  
1 from scale/unit mmol/L  
45 from scale/unit mol/L  
1 from scale/unit µmol/L

Chemicals 63/63; Data 267/278

**OK** **Cancel**

1. Go to **Data Gap filling** module; 2. Click **Trend analysis**; 3. A pop-up window alerting you to possible data inconsistencies appears. Click **OK**; 4. A pop-up message informs about the number of chemicals (e.g. mixtures or UVCB substances) that will not be included in the Trend analysis prediction due to missing X descriptor value(s), which by default is LogKow. Click **OK**.

# Data Gap Filling

## Interpreting Trend analysis

- The resulting plot outlines the log of the experimental LC50 results of all analogues (Y axis) according to a descriptor (X axis) with Log *Kow* being the default descriptor (see next slide).
- The **RED** points represent the predicted value for the target chemical.
- The **BLUE** points represent the experimental results available for the analogues used in the trend analysis.
- The square-shaped signs in the right side of the data gap filling window are the so-called “helpers”. The helpers are notifying messages that provide different type of information related to the used data points in the prediction.
- Before accepting the estimated result for the target chemical, the trend analysis should be further refined by subcategorization (see the next slides).

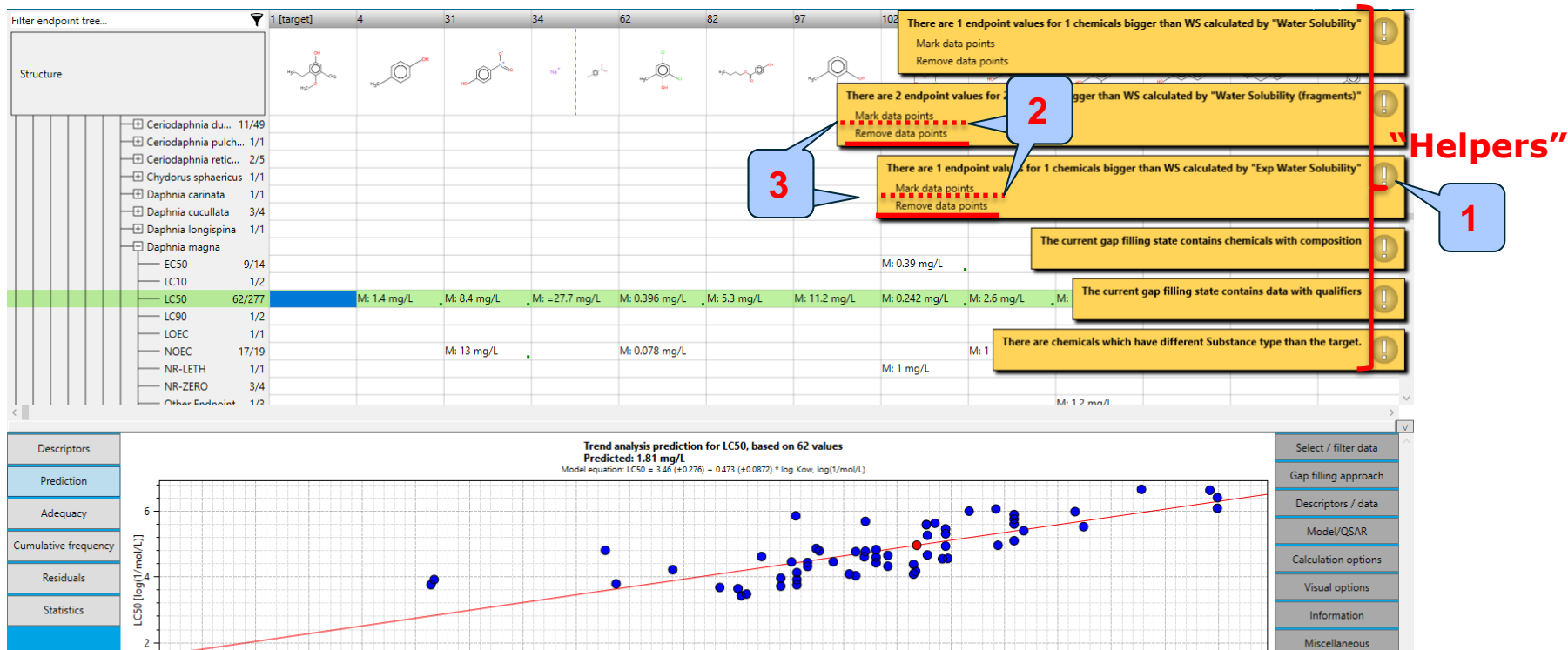
# Data Gap Filling

## Results of Trend analysis



# Data Gap Filling

## Results of Trend analysis



1. Click the helpers to see the information that they provide;
2. Click on "**Mark data points**" to mark the chemicals meeting the criteria explained in the helper (e.g. mark the chemicals which have 2 endpoint values (LC50) bigger than the water solubility (WS) of the chemical);
3. Click **Remove data points** in order to eliminate the data points that have values bigger than WS of the chemical (click on all helpers). Once the data points are removed the helpers disappear.

# Data Gap Filling

## Subcategorization

- Remember in the Toolbox, a category refers to a group of chemicals which have the same profiling result according to one of the profilers listed in the module *Profiling*.
- Subcategorization refers to the process of applying additional profilers to the previously defined category. The subcategorization identifies chemicals which have differing profiling results and eventually eliminating these chemicals from the final category.

# Data Gap Filling

## Subcategorization

In this example, subcategorization allows for the elimination of analogues which are dissimilar to the target chemical with respect to:

- OASIS Mode of action (all except phenols and anilines)

The categorization based on mode of action identifies analogues having the same mode of action as the target which is in the group of phenols and anilines.

- Chemical elements

The profiler aimed to identify analogues consisting of same elements as those presented in the target chemical

Subcategorization is demonstrated in the next 2 slides.

**Note:** Expert judgement should always be used when removing chemicals.



# Data Gap Filling

## Subcategorization by Acute-aquatic toxicity MOA

1 [target] 4 31 34 62 82 97 102 118 130 185 199 202

Structure

Subcategorization

Options

Select All Unselect All Invert About Options

Toxic hazard Ultimate bio Uncouplers

2

Acute aquatic toxicity classification by Verhaar (1) Acute aquatic toxicity MOA by OASIS Acute Oral Toxicity Aquatic toxicity classification by ECOSAR Bioaccumulation - metabolism alerts Bioaccumulation - metabolism half-lives Biodegradation fragments (BioWIN MITI) Carcinogenicity (genotox and nongenotox) alerts

Metabolisms

Select All Unselect All Invert

Do not account metabolism Documented Observed Mammalian metabolism Observed Microbial metabolism Observed Rat In vivo metabolism Observed rat liver metabolism with quantitative c Observed Rat Liver S9 metabolism Simulated Autoxidation simulator Autoxidation simulator (alkaline medium) Dissociation simulator Hydrolysis simulator (acidic)

3

Adjust options

Target

Phenols and Anilines

Differ from target by

At least one category All categories

STOP

Analogues

(1) (N/A) (1) Aldehydes (3) Basesurface narcotics (54) Phenols and Anilines (4) Reactive unspecified

8 (53/61)

Select different Remove selected

Trend analysis prediction for LC50, based on 61 values Predicted: 1.81 mg/L Model equation:  $LC50 = 3.56 (\pm 0.313) + 0.440 (\pm 0.0990) * \log Kow, \log(1/mol/L)$

1

Select / filter data

Subcategorize

Mark chemicals by WS

Mark chemicals by descriptor value

Mark outliers

Filter points by test conditions

Mark focused chemical

Mark focused points

Cumulative frequency

Residuals

Statistics

LC50 [log(1/mol/L)]

1. Click **Subcategorize**;
2. Select **Acute aquatic toxicity MOA by OASIS**;
3. Click **Remove selected** to eliminate the dissimilar chemicals.

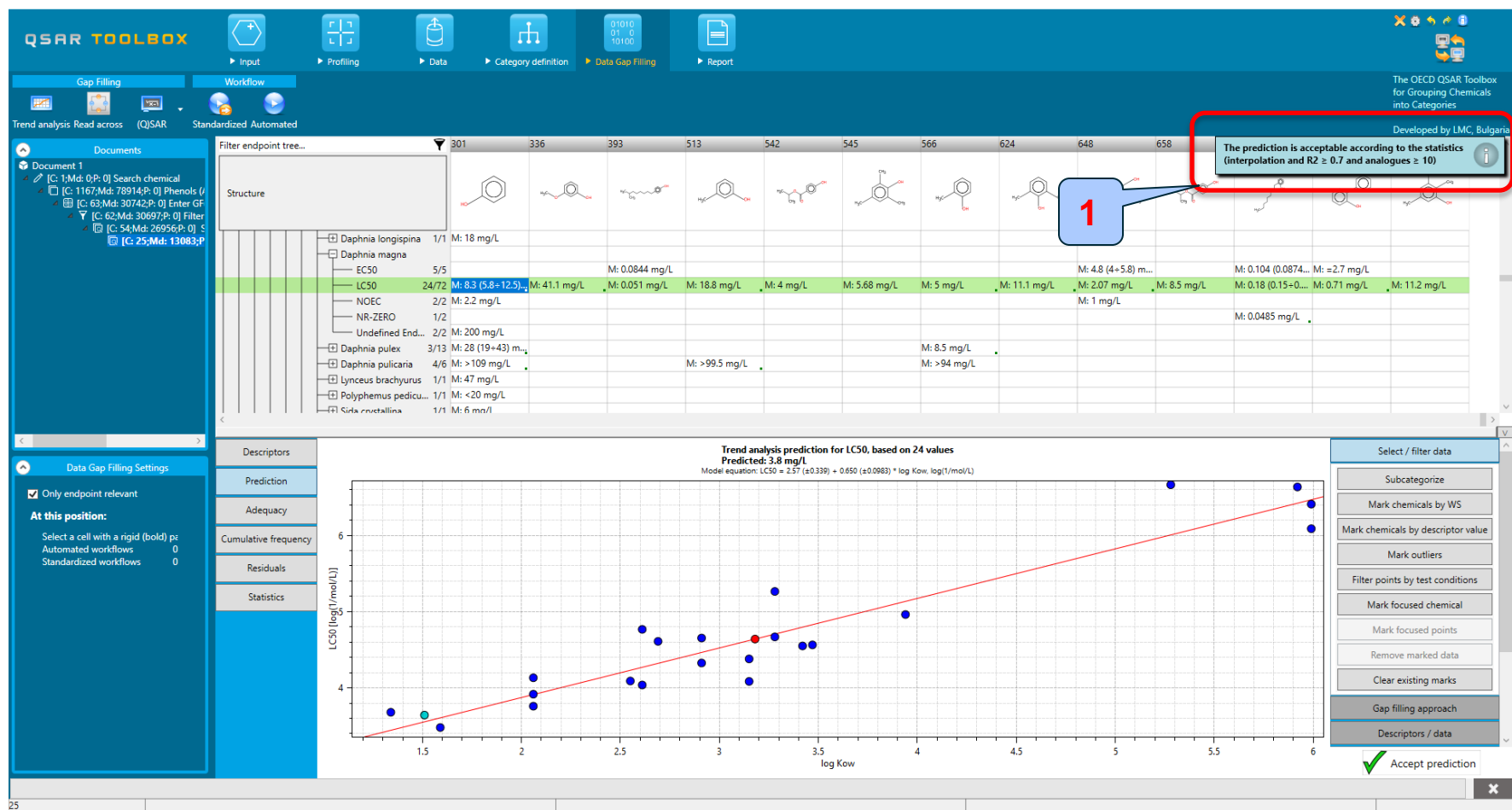
# Data Gap Filling

## Subcategorization by Chemical elements

The screenshot displays the OECD QSAR Toolbox interface for Subcategorization. The left sidebar shows various tool categories, with 'Chemical elements' highlighted under the 'Empiric' section. The central plot area shows a trend analysis prediction for LC50, based on 53 values, with a predicted value of 2 mg/L. The plot includes a red regression line and data points. The right sidebar contains a 'Select / filter data' section with options like 'Subcategorize', 'Mark chemicals by WS', and 'Mark chemicals by descriptor value'. A context menu is visible over the plot, showing options like 'Show all data points', 'Hide all of type', and 'Differences to target'. A table of chemical structures and their corresponding LC50 values is also displayed.

1. Right-click over one of the outliers; 2. Select **Differences to target**; 3. A new subcategorization window appears where some of the profilers are red highlighted. They indicate that categories of the analogues differs from the categories of target. In our case select **Chemical elements**; 4. Click **Remove selected** to eliminate the dissimilar

# Data Gap Filling Results



1. Helper indicating that the prediction is acceptable according to the statistic appears.

## Data Gap Filling Results

- All the chemicals remaining in the graph have a consistent profile relevant for aquatic toxicity (i.e. Substance type, Classification by ECOSAR, MOA by OASIS and Chemical elements) – they all are phenols
- By **accepting the prediction** the data gap is filled (see next screen shot).

# Data Gap Filling

## Accepting prediction result

The screenshot displays the QSAR Toolbox software interface during the Data Gap Filling process. A 'Confirm' dialog box is open, asking 'Are you sure you want to accept this prediction?' with 'Yes' and 'No' buttons. A red circle highlights the 'Accept prediction' button in the bottom right corner. A red arrow points to the 'Yes' button in the dialog box. A scatter plot shows the trend analysis prediction for LC50 based on 24 values, with a predicted value of 3.8 mg/L. The plot includes a regression line and data points. The interface also shows a list of chemicals and their predicted values.

**Confirm Dialog:**

Are you sure you want to accept this prediction?

**Accept Prediction:**

**1. Click **Accept prediction**;**

**2. Click **Yes** to confirm the prediction.**

The prediction is accepted successfully and the system automatically returns you to the data matrix.

# Outlook

- Background
- Keywords
- Objectives
- Specific Aims
- Trend analysis
- The exercise
- **Workflow of the exercise**
  - Chemical Input
  - Profiling
  - Data
  - Category definition
  - Data Gap Filling
  - **Export a prediction to IUCLID6**

# Export prediction to the IUCLID 6

## Overview

- The OECD QSAR Toolbox allows the users to export predicted results (by means of the Filling Data Gap tools) to IUCLID 6.
- The way of exporting is connecting to an IUCLID 6 server (via WebServices) and assigning the predicted endpoint data to a selected substance.
- A wizard will guide the user through the different steps of exporting (see next screenshot).

# Exporting the prediction to IUCLID 6

## Case study

The screenshot shows the QSAR Toolbox software interface. The top menu bar includes 'Data', 'Import', 'Export', and 'Delete'. The 'Data' module is selected, indicated by a red box and a callout '1'. The 'Export' button is highlighted with a red box and a callout '3'. The 'IUCLID6' button is also highlighted with a red box and a callout '3'. The main window displays a list of endpoints and their predictions. The 'LC50' endpoint is highlighted in yellow, and its prediction '3.8 (0.841-17.2) mg/L' is highlighted in blue, with a callout '2' pointing to it. The 'LC50' endpoint is also highlighted in yellow. The 'LC50' endpoint is highlighted in yellow. The 'LC50' endpoint is highlighted in yellow.

1. Go to **Data** module;

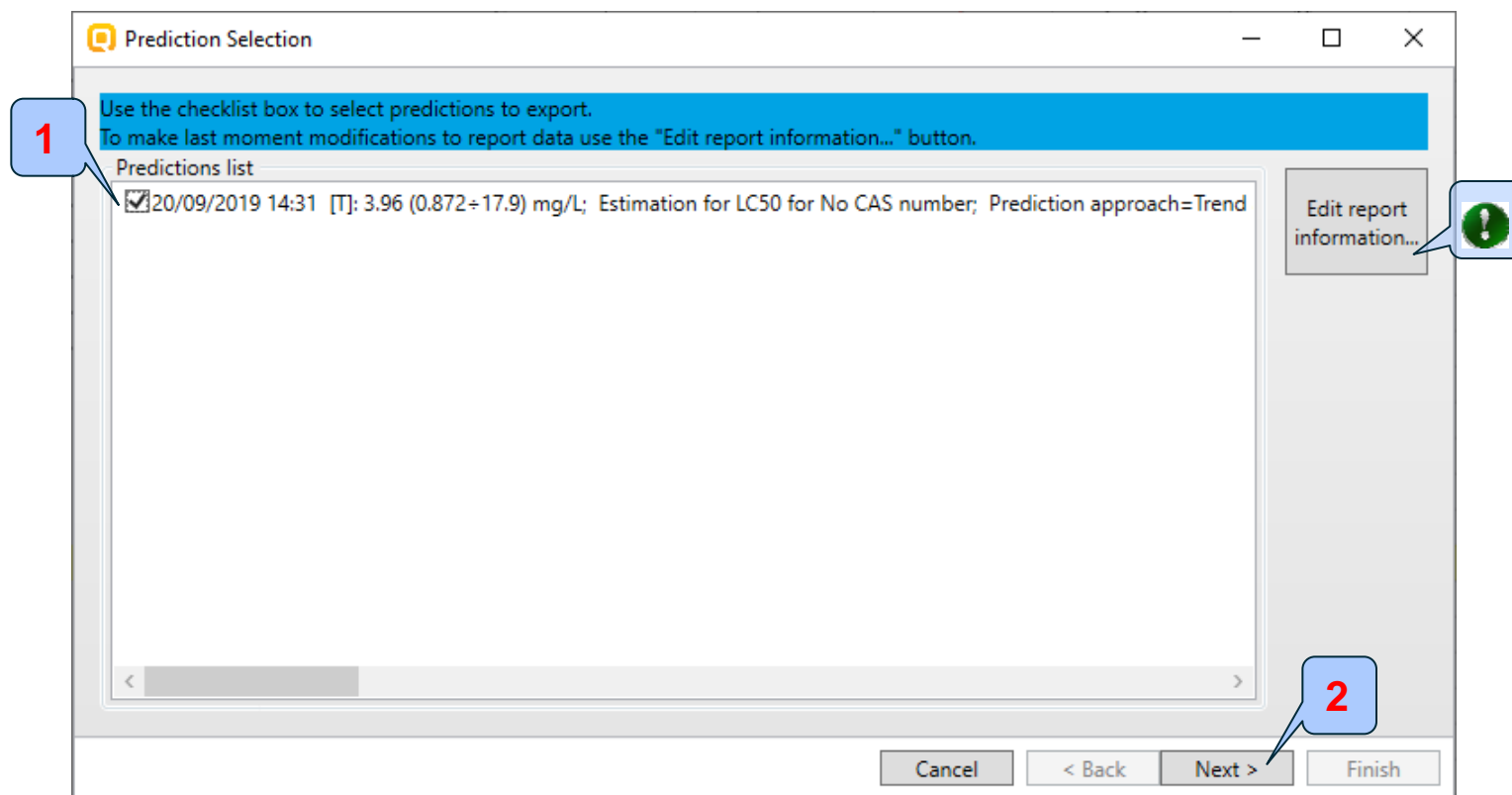
2. Click the cell containing the prediction;

3. Click **IUCLID6**.



# Exporting the prediction to IUCLID 6

## Case study



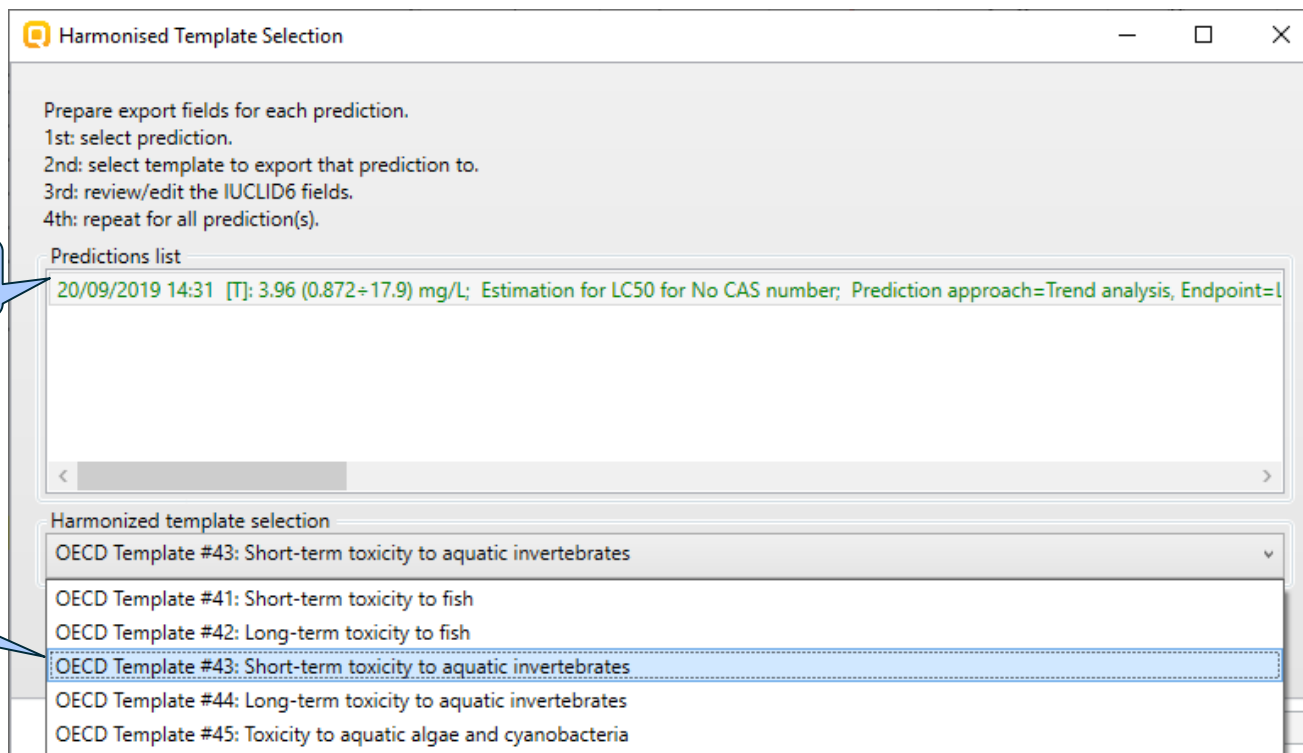
1. Tick the prediction to export;
2. Click **Next** to move through the next step of the export.



The user could also edit the report information.

# Exporting the prediction to IUCLID 6

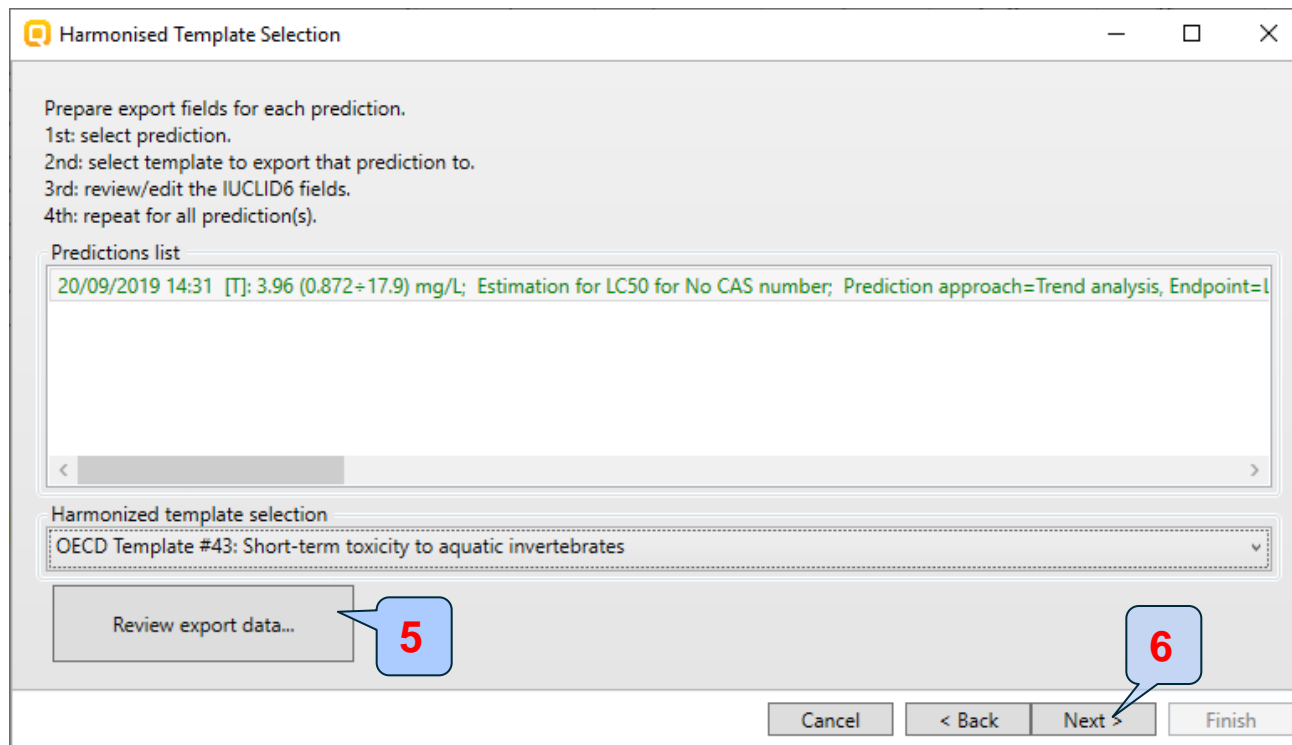
## Case study



3. Select the prediction;
4. Select a template to export the prediction;

# Exporting the prediction to IUCLID 6

## Case study



5. Review/edit the IUCLID6 fields;
6. Click **Next**;

# Exporting the prediction to IUCLID 6

## Case study

**Connection Settings**

**Connect to an IUCLID6 server**

In order to use a IUCLID server you should establish a network connection with it. Please provide the needed connection parameters below and then click Next

IUCLID Server:  Port:

Username:  Password:

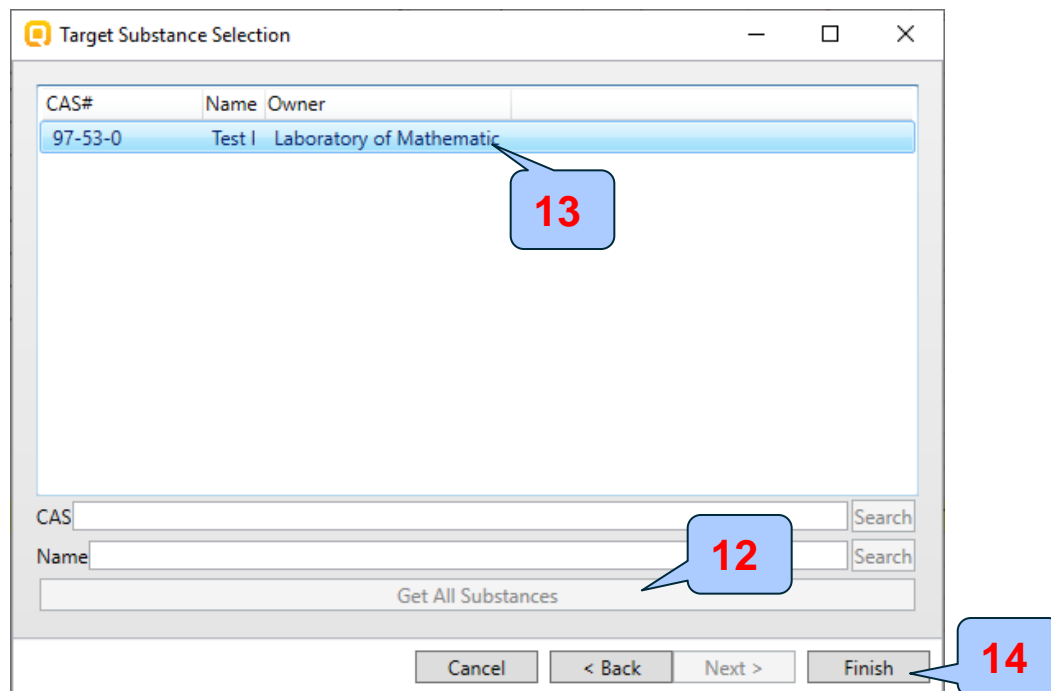
7. Write **IUCLID Server** name;
8. Fill in the **Port** number;
9. Fill in the **Username**;
10. Fill in the **password**: root;
11. Click **Next**.

### Note:

In case you don't know your IUCLID account, please contact your administrator.

# Exporting the prediction to IUCLID 6

## Case study



12. Click **Get All Substances**;
13. Select the chemical to which the prediction to be exported;
14. Click **Finish**.

# Outlook

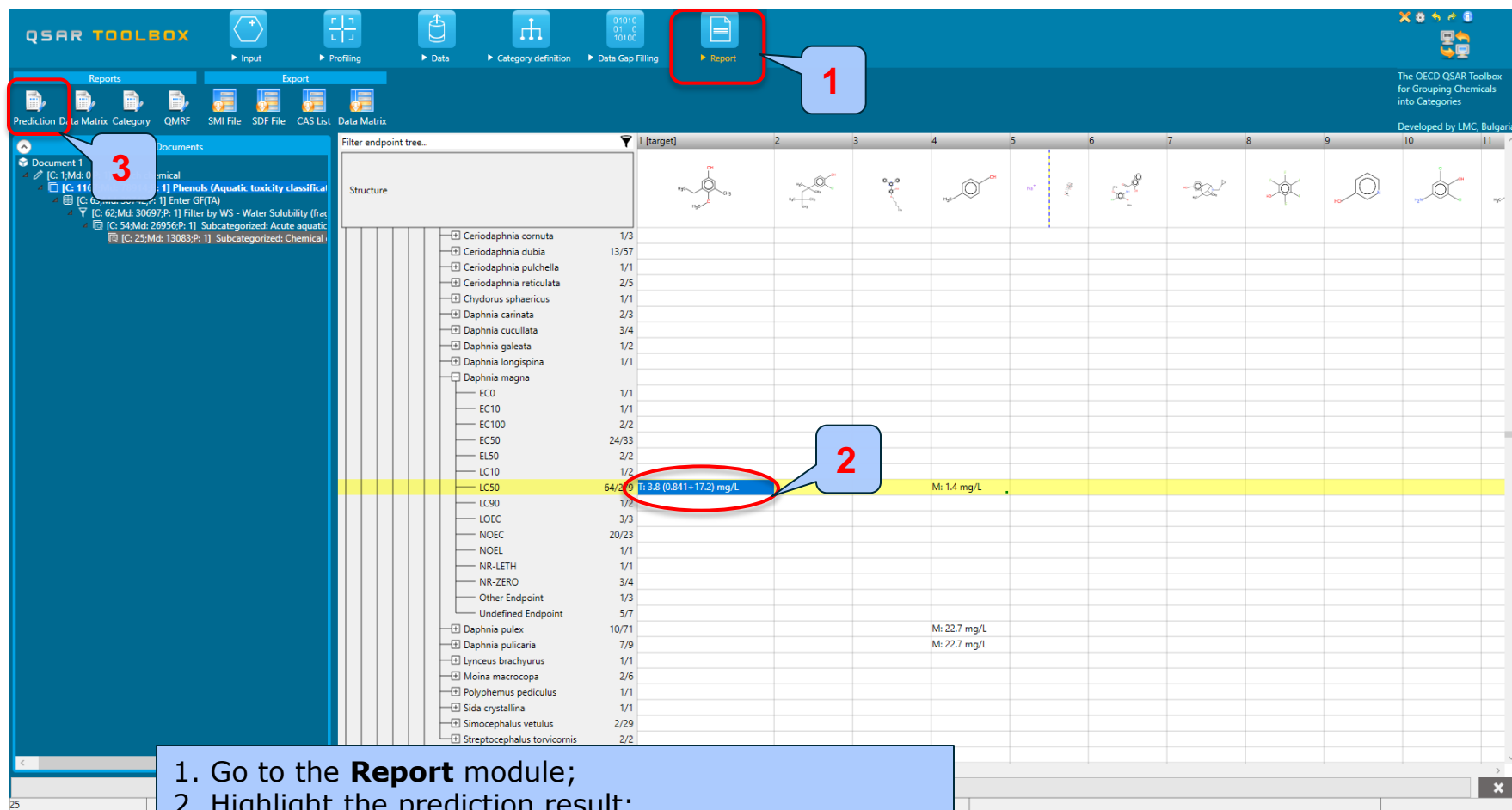
- Background
- Keywords
- Objectives
- Specific Aims
- Trend analysis
- The exercise
- **Workflow of the exercise**
  - Chemical Input
  - Profiling
  - Data
  - Category definition
  - Data Gap Filling
  - Export a prediction to IUCLID6
  - **Report**

# Report Overview

- The report module can generate a report on any of predictions performed with the Toolbox.
- The report module contains predefined report templates, which can be customized.
- The report can then be printed or saved in different formats.

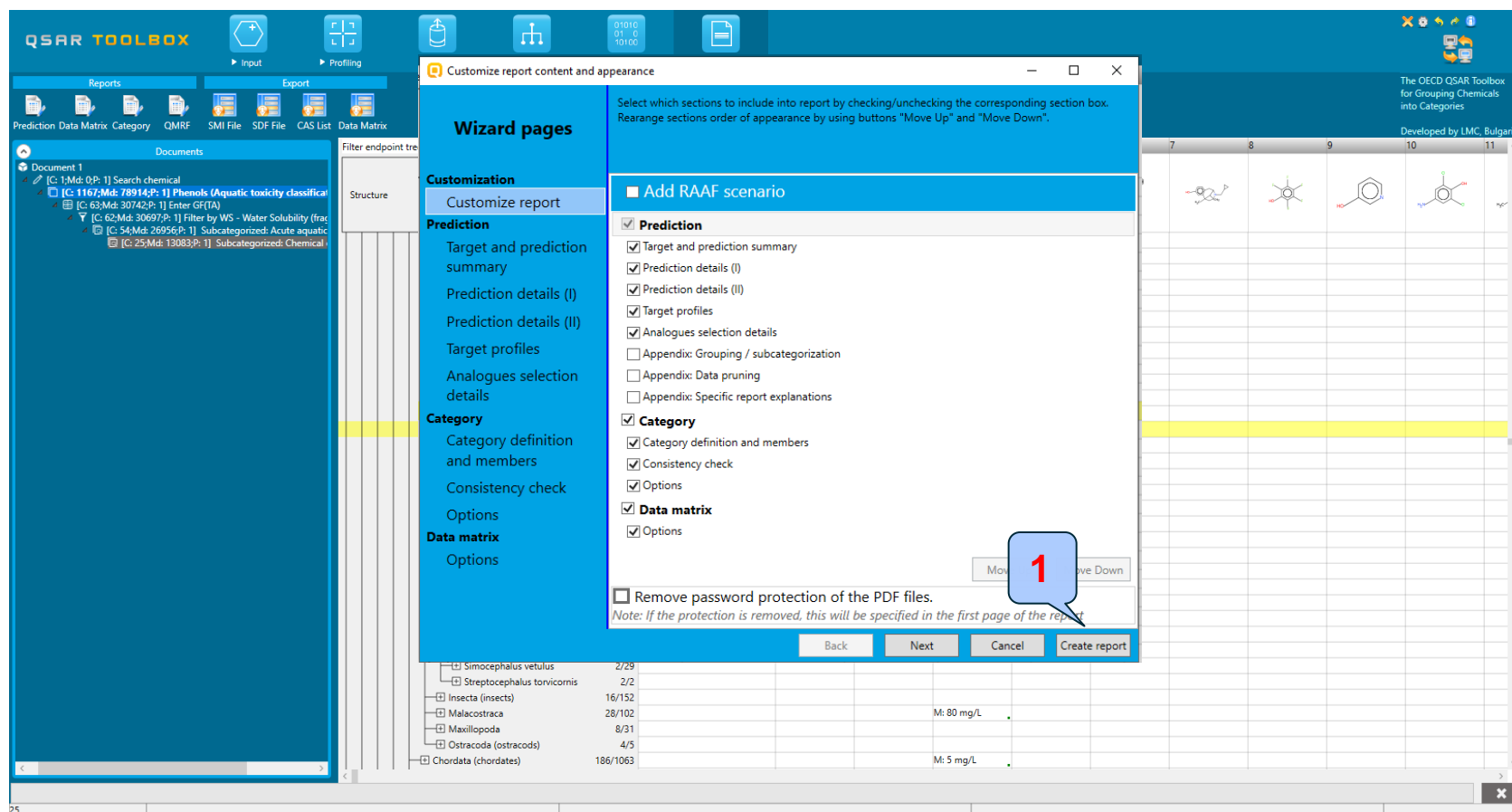
# Report

## Generation report





# Report Generation report



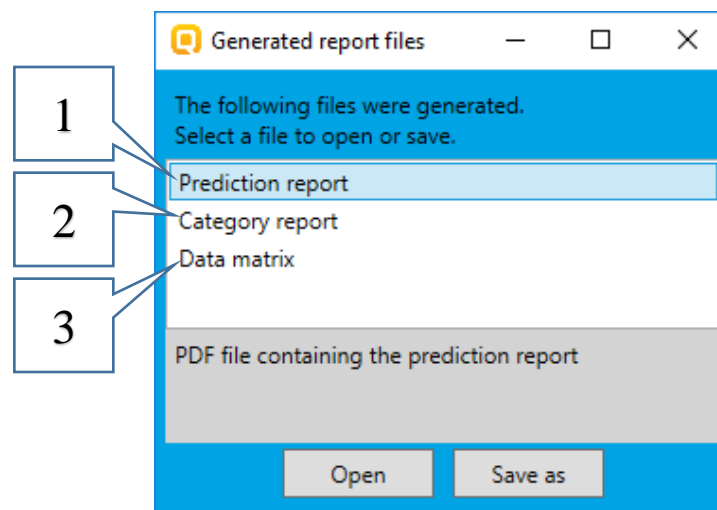
Report wizard pages appears, where the user could customize the report content and appearance. Some of the fields in the report are automatically populated by the system.  
1. Click **Create report** to generate the report.

# Report Generation

After clicking *Create report* button, *Generated report files* window appears. It contains three type of files:

- 1) Prediction report** - a PDF file containing the prediction information related to the target.
- 2) Category report** - a PDF file containing information for the consistency of the final category (target plus used analogues)
- 3) Data matrix** - a MS Excel file containing chemicals used for prediction along with their data for selected parameters, profiles and endpoint tree positions.

**Note:** All generated files should be provided when submit a prediction.



# Report

## Generated report files

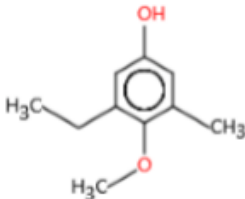
### Prediction report

Prediction of LC50 for CCc1cc(O)cc(C)c1OC

1 / 6

#### QSAR Toolbox prediction for single chemical

Date: 3 Apr 2020  
Author(s):  
Contact details:

Target information		
Structural information	Numerical identifiers	Chemical names
SMILES: CCc1cc(O)cc(C)c1OC	CAS#: No CAS number Other: N/A	
Structure		
		

#### Prediction summary

Predicted endpoint: LC50; Mortality; Daphnia magna; 48 h; No guideline specified  
Predicted value: 3.8 (from 0.841 to 17.2)  
Unit/scale: mg/L  
Data gap filling method: Trend analysis  
Summary: manually editable field  
Not provided by the user

Prediction of LC50 for CCc1cc(O)cc(C)c1OC

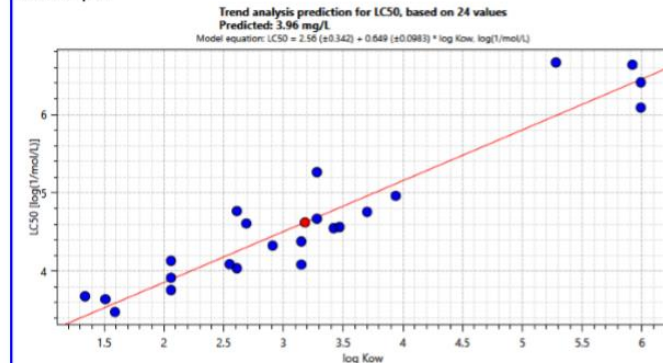
2 / 6

#### Prediction details (I)

Predicted value: 4.62 log(1/mol/L), conf.range: (3.97 ; 5.28) at 95.0%

Predicted endpoint (OECD Principle 1 - Defined endpoint): Ecotoxicological Information -> Aquatic Toxicity -> Mortality -> LC50 -> 48 h -> Animalia (animals) -> Arthropoda (arthropods) -> Branchiopoda (branchiopods) -> Daphnia magna

Prediction plot:



Calculation approach (OECD principle 2 - Unambiguous algorithm): Linear approximation

Model equation:  $LC50 = 2.56 (\pm 0.342) + 0.649 (\pm 0.0983) * \log Kow, \log(1/mol/L)$

Active descriptor: log Kow (calculated)

Data usage: Arithmetic mean (average) value\*

Statistics of the prediction model:

N = 24; count of data points

R2 = 0.895; coefficient of determination

R2adj = 0.890; adjusted coefficient of determination

SSR = 2.12; sum of squared residuals

s = 0.297; sample standard deviation of residuals

F = 187; Fisher function

\*When multiple values are available for the same chemical, their arithmetic mean (average) value is taken in prediction calculations

# Report Generated report files

## Category report

### QSAR Toolbox report for category

#### 1. Category definition

##### 1.1. Category definition

###### Category name

Not provided by the user

manually editable field

###### Covered (target) endpoint(s)

- Ecotoxicological Information/Aquatic Toxicity: LC50, Daphnia magna, Branchiopoda (branchiopods), Arthropoda (arthropods), Animalia (animals), Mortality, Duration=48 h

###### Category hypothesis

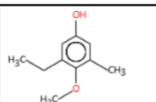
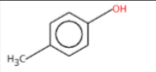
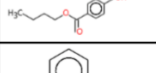
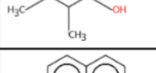

Not provided by the user

manually editable field

##### 1.2. Category members

###### Information of category members

Table of category members

#	CAS	Name	SMILES	Structure
1	No CAS number		<chem>CC1ccc(O)cc(C)C1OC</chem>	
2	106-44-5	Cresol	<chem>Cc1ccc(O)cc1</chem>	
3	94-26-8	Butylparaben	<chem>CCCC(=O)Oc1ccc(O)cc1</chem>	
4	526-75-0	2,3-xynolol	<chem>Cc1ccc(O)cc1C</chem>	
5	135-19-3	135-19-3	<chem>Oc1ccc2ccccc2c1</chem>	

## Data matrix report

Data matrix\_3,3\_U\_17\_16\_16\_16\_16 - Microsoft Excel

	A1	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W
1																							
2																							
3																							
4																							
5																							
6																							
7																							
8																							
9																							
10																							
11																							
12																							
13																							
14																							
15																							
16																							
17																							
18																							
19																							
20																							
21																							

# Outlook

- Background
- Keywords
- Objectives
- Specific Aims
- Trend analysis
- The exercise
- Workflow of the exercise
- **Save the prediction result**

## Saving the prediction result

- This functionality allow storing/restoring the current state of Toolbox documents including loaded chemicals, experimental data, profiles, predictions etc., on the same computer. The functionality is implemented based on saving the sequence of actions that led to the current state of the Toolbox document and later executing these actions in the same sequence in order to get the same result(s).
- Saving/Loading the file with TB prediction is shown on next screenshots

# Saving the prediction result

1. Go to the **Input** module;

2. Click **Save** button;

3. Click **Yes** to confirm;

4. Define name of the file;

5. Click **Save**.

# Open file

The screenshot shows the QSAR Toolbox software interface. The top menu bar includes options like Input, Profiling, Data, Category definition, Data Gap Filling, and Report. Below the menu is a toolbar with icons for Document, Single Chemical, Chemical List, Search, and Target Endpoint. The 'Open' dialog box is open, showing a file list with 'Tutorial\_LC50.tb4' selected. The file name 'Tutorial\_LC50.tb4' is entered in the 'File name' field, and the file type is set to 'Toolbox documents (\*.tb4)'. The 'Open' button is highlighted.

To open a file:

1. Click **Open**;
2. Find and select the file;
3. Click **Open**.



# Congratulations!

- You have now been introduced to the work flow of the Toolbox and completed the tutorial on data gap filling by trend analysis and exported the prediction to IUCLID 6.
- You have been introduced to the six modules of the Toolbox, the basic functionalities within each module and the rationale behind each module.
- Remember, proficiency comes with practice!