

OECD QSAR Toolbox v.4.4.1

Step-by-step example for building QSAR model

Outlook

- **Background**
- Keywords
- Objectives
- The exercise
- Workflow of the exercise

Background

- This is a step-by-step presentation designed to take you through the workflow of the Toolbox for building a QSAR model for predicting aquatic toxicity.
- By now you have some experience in using the Toolbox so there will be multiple key strokes between screen shots.

Note: Please note that building of custom items (such as profilers, (Q)SAR models as well as importing of custom databases) is only enabled in single user mode. So, if your Toolbox is installed in multiuser mode, you will be not able to follow this tutorial.

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Keywords

TARGET CHEMICAL - 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

(Q)SAR - (Q)SAR models can be used to fill a data gap if no adequate analogues are found for a target chemical

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Objectives

- **This presentation demonstrates building a QSAR model for predicting acute toxicity of aldehydes to *Tetrahymena pyriformis*. The presentation addresses specifically:**
 - predicting acute toxicity for a target chemical;
 - building a QSAR model based on the prediction;
 - applying the model to other aldehydes;
 - exporting the predictions to a file.

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The Exercise

- **This exercise includes the following steps:**
 - select a target chemical – Furfural, CAS 98-01-1;
 - extract available experimental results;
 - search for analogues;
 - estimate the target endpoint: 48h-IGC50 for *Tetrahymena pyriformis* by using trend analysis;
 - improve the data set by either:
 - subcategorizing by “Protein binding” mechanisms, or
 - assessing the difference between outliers and the target chemical
 - evaluate and save the model;
 - use the model to display its training set, visualize its applicability domain and perform predictions.

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Workflow of the exercise

- **Remember the Toolbox has 6 modules which are used in a sequential workflow:**
 - Input
 - Profiling
 - Data
 - Category Definition
 - Data Gap Filling
 - Report

Outlook

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- **Workflow of the exercise**
 - **Input**

Input

The screenshot shows the QSAR Toolbox software interface. The main window has a menu bar with options: Document, Single Chemical, Chemical List, Search, and Target Endpoint. Below the menu bar is a toolbar with icons for New, Open, Close, Save, CAS#, Name, Structure, Composition, Select, ChemIDs, Database, Inventory, List, Substructure (SMARTS), Query, and Define. A search dialog box is open, showing the search results for CAS# 98-01-1. The dialog box has a search input field with the text "98011" and a "Search" button. Below the search input field are buttons for "Select All", "Unselect All", and "Invert Selection". The search results are displayed in a table with the following columns: CAS, SMILES, CS Relation, Substance, Composition, Name, and Sources. The first result is selected, and its chemical structure is shown on the right side of the dialog box.

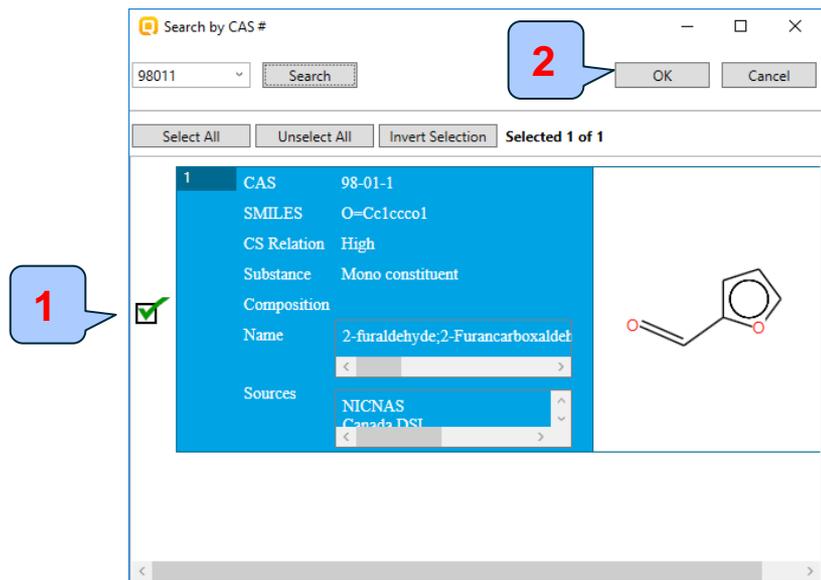
CAS	SMILES	CS Relation	Substance	Composition	Name	Sources
98-01-1	O=Cc1ccco1	High	Mono constituent		2-furaldehyde;2-Furancarboxaldehyd	NICNAS Canada DSI

1. Click on **CAS#** 2. Enter CAS# 98-01-1; 3. Click **Search**;

Input

Target chemical identity

The Toolbox now searches the Toolbox databases and inventories for the presence of the chemical with structure related to the current CAS number. It is displayed as a 2D image. Note it is unselected by default.



1. Mark desired chemical (in case there is only one chemical it is marked by default);
2. Click **OK** to add chemical in data matrix;

Input

Target chemical identity

- Target chemical is displayed on the data matrix.
- To see chemical identification click on the box next to "Structure info" (see next screen shot).

Chemical Input

Target chemical identity

The screenshot displays the QSAR Toolbox software interface. The top menu bar includes options like 'Input', 'Profiling', 'Data', 'Category definition', 'Data Gap Filling', and 'Report'. Below this, a secondary menu bar shows 'Document', 'Single Chemical', 'Chemical List', 'Search', and 'Target Endpoint'. The 'Target Endpoint' menu is currently active, showing a dropdown list of target endpoints. The first item, '1 [target]', is selected and highlighted with a red circle. To the left of this list is a 'Structure' field containing a chemical structure diagram of 2-furaldehyde. Below the structure is a table of properties for the selected target endpoint:

EC Number:	2026277
CAS Number	98-01-1
CAS-SMILES relation	High
Chemical name(s)	2-furaldehyde
Composition	
Molecular formula	C5H4O2
Predefined substance type	Mono constituent
SMILES	O=Cc1ccco1

The left sidebar shows a 'Documents' panel with 'Document 1' selected, displaying its CAS number: '# [C: 1; Md: 0; P: 0] CAS: 98011'. The bottom of the interface shows a status bar with a close button.

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 - **Input**
 - **Define Target Endpoint**

Input

Define Target Endpoint

- In this exercise we will build a QSAR model to estimate the following endpoint:

*Ecotoxicological Information#Aquatic
Toxicity#Growth#IGC50#48h#Protozoa#Ciliophora#Ciliatea
#Tetrahymena pyriformis*

- For defining the target endpoint the “Define target endpoint” functionality is used (see next few slides)

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 highlighting:
 - In green are highlighted the most suitable profilers related to the endpoint and databases including data for the defined target endpoint, while
 - in the orange are colored profilers which are plausible with respect to the defined target endpoint.



Input

Define target endpoint

1. Click **Define**; 2. Select **Aquatic Toxicity**; 3. Click **Next** and consecutively add the following endpoint and metadata (4): **Endpoint** – IGC50; **Effect** – **Growth**; **Duration** – **48h**; **Test organism (species)**: ***Tetrahymena pyriformis***; 5. Click **Finish**

Input

Define target endpoint

The screenshot shows the QSAR Toolbox software interface. The 'Define' tab is active, and the 'Filter endpoint tree...' dialog is open. The tree structure is as follows:

- Structure
- Structure Info
- Parameters
- Physical Chemical Properties
- Environmental Fate and Transport
 - Ecotoxicological Information
 - Aquatic Toxicity (AW SW)
 - Growth
 - 48 h
 - Protozoa
 - Ciliophora
 - Ciliatea
 - Tetrahymena pyriformis (highlighted in yellow)
- Sediment Toxicity
- Terrestrial Toxicity

- Human Health Hazards

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

! As mentioned above (slide 19) defining the target endpoint lead to highlighting of relevant profilers and databases (see next slides)

Outlook

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 - 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.

Profiling

Profiling the target chemical

- Select the “Profiling methods” related to the target endpoint
- This selects (a **green** check mark appears) or deselects (**green** check disappears) profilers.
- In this case select all green (the most suitable to the target endpoint) profilers – see next slide

Profiling

Profiling the target chemical

The screenshot shows the QSAR Toolbox Profiling module. The top navigation bar includes 'Input', 'Profiling', 'Data', 'Category definition', 'Data Gap Filling', and 'Report'. The 'Profiling' button is circled in red and labeled '1'. Below the navigation bar, the 'Profiling' section has 'Apply', 'View', and 'Delete' buttons. The 'Apply' button is circled in red and labeled '3'. The 'Filter endpoint tree' window shows a tree structure with 'Tetrahymina pyriformis' and 'IGCS0' highlighted in yellow. The 'Suitable' list of profilers is shown, with several items checked and highlighted in green, circled in red and labeled '2'. The list includes:

- Acute aquatic toxicity classification by Verhaar (Modified)
- Acute aquatic toxicity MOA by OASIS
- Aquatic toxicity classification by ECOSAR
- Protein binding by OASIS
- Protein binding potency GSH
- US-EPA New Chemical Categories

1. Go to **Profiling** module
2. Select all suitable (marked in green) profilers
3. Click **Apply** to apply knowledge of the selected profilers to the target chemical

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 appeared as a dropdown box under the target chemical (see next screen shot).
- Green rectangles in some result boxes indicate there is more than one profiling result and the field needs to be expanded.

Profiling

Profiling the target chemical – profiling results

The screenshot shows the QSAR Toolbox interface. On the left, the 'Filter endpoint tree...' is visible, with 'Acute aquatic toxicity classification by Verhaar (Modified)' selected. The main window displays a list of categories under 'US-EPA New Chemical Categories', with 'Aldehydes (Acute toxicity)' highlighted. A red dashed box surrounds this category. To the right, the 'Explanation for US-EPA New Chemical Categories -> Aldehydes (Acute toxicity)' window is open, showing a 'Literature' tab with a date 'September, 1988; Revised July, 1999 and January, 1997'. A blue callout box with the number '2' points to this literature information. Below the literature, there is a chemical structure diagram of an aldehyde and a 'Map 1' section. A red dashed box also highlights the 'Aldehydes (Acute toxicity)' category in the list, with a blue callout box containing the number '1' pointing to it.

1. Double click on the cell with "Aldehydes (Acute toxicity)" results based on US-EPA Chemical New Chemical Categories to see why the chemical is categorized as aldehyde
2. Literature information is displayed. The knowledge explained here is used for coding the structural boundaries of the category

Continued on next slide

Profiling

Profiling the target chemical – Boundaries of the profilers

The screenshot displays the 'Explanation for: US-EPA New Chemical Categories -> Aldehydes (Acute toxicity)' window. The 'Definition' tab is active, showing a 'Category tree' with three nodes (1, 2, 3) connected to an 'AND' node. A red circle highlights this tree structure, with callout 1 pointing to it. Below, the 'Query details' section shows a SMARTS query: [#6h][=][#8][#6,#1], with callout 2 pointing to it. The 'View mode' is set to 'Facade' and 'Navigation mode' is 'Cascade'. A chemical structure visualization shows a carbonyl group with callout 3 pointing to it. On the left, the 'Categories' list includes 'Aldehydes (Acute toxicity)' highlighted in red. The 'Explanation' section shows a chemical structure of an aldehyde with a red highlight on the carbonyl group, also with callout 3 pointing to it.

1. Structural boundaries of the category- Aldehydes (Acute toxicity); The boundaries which are met are ticked with green
2. Definition of the SMARTS used for coding the knowledge; Visualization of the common fragment used for coding the knowledge;
3. The target molecule and highlighted (red) part of the molecule meeting the structure boundary.

Profiling

Profiling results

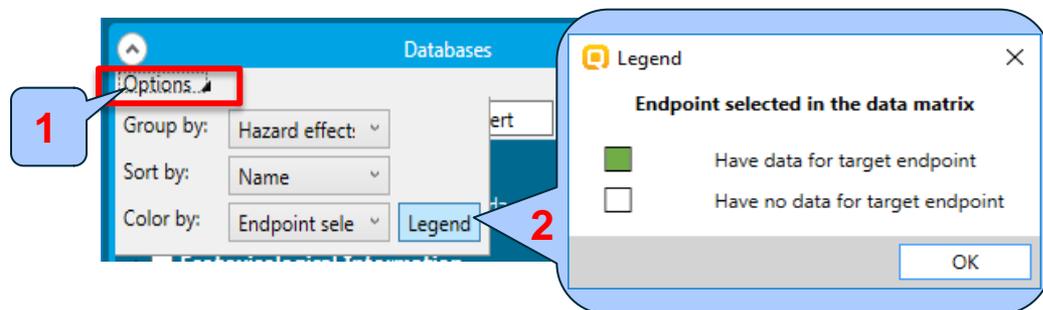
- 1) In module *Profile*, you have profiled the target chemical according to the suitable profilers (green) related to the target endpoint.
- 2) The target chemical is categorized as “aldehyde” based on predefined Acute aquatic toxicity US-EPA profiler (hereafter called US-EPA) and the two endpoint-specific 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) Moreover the target is categorized as “aldehyde” based on Protein binding by OASIS reacting by Schiff-base formation mechanism
- 5) In general the target is classified as “aldehyde”
- 6) All of the above mentioned profilers could be used for categorization purposes (collecting analogues)
- 7) In this case US-EPA profiler will be used for categorization purpose (primary grouping).

Outlook

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 - 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 databases containing aquatic toxicity data for the defined target endpoint (Aquatic OASIS).

Data

Extracting endpoint values

The screenshot shows the QSAR Toolbox interface. The 'Data' module is selected in the top toolbar (callout 1). In the 'Databases' panel on the left, 'Aquatic OASIS' is selected (callout 2). The 'Gather' button is highlighted in the 'Data' section (callout 3). A dialog box displays '3 points added across 1 chemicals.' with an 'OK' button (callout 4). The 'Filter endpoint tree' on the right shows a tree structure with 'Aquatic Toxicity' expanded, and 'Tetrahymena pyriformis' highlighted in yellow (callout 2).

1. Go to **Data** module
2. Select the green highlighted database
3. Click **Gather**. 3 data points are collected for the target. A single data point is found for the target endpoint; We will try to reproduce it.
4. Click **OK**

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 - Data
 - **Category definition**

Category definition

Defining US-EPA category

- As mentioned before, the initial search for analogues is based on structural similarity, of US EPA categorization
- **Select** US-EPA New Chemical Category
- **Click** Define (see next screen shot)

Category definition

Defining US-EPA category

1. Go to **Category definition** module; 2. Highlight **“US-EPA New Chemical Categories”**; 3. Click **Define**; 4. Put a tick in the Strict box (see next screen shot); 5. Click OK to confirm the category **Aldehydes (Acute toxicity)**;

Category definition

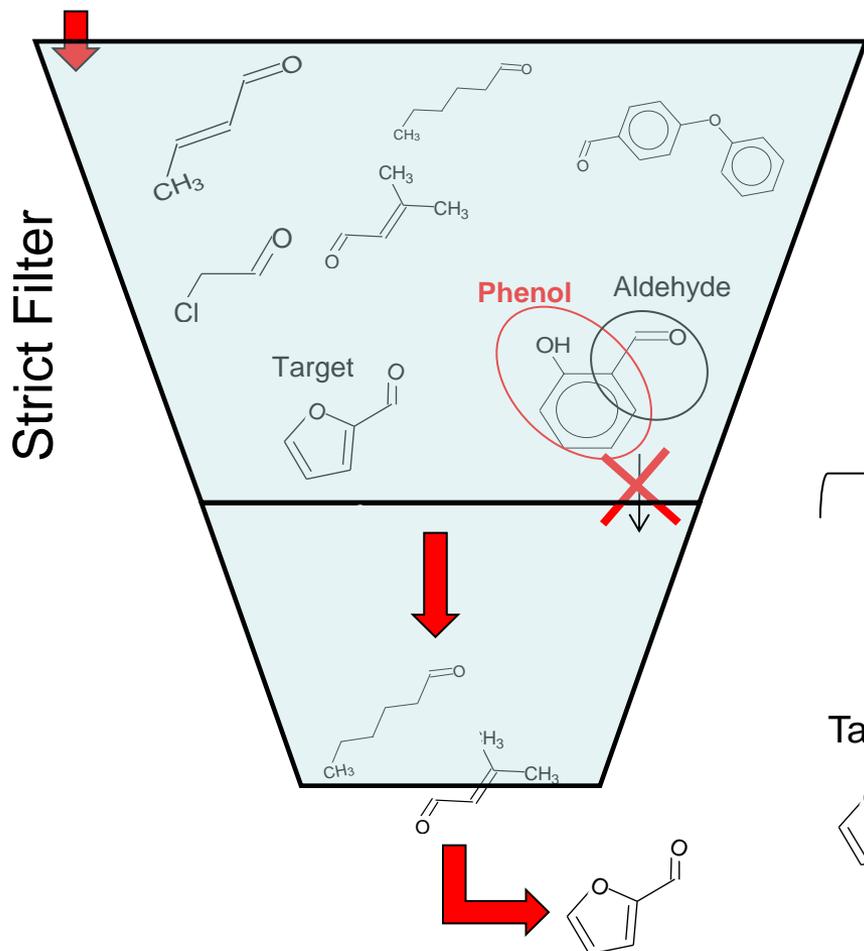
Defining US-EPA category strict functionality

- The **Strict** functionality means that the software will group analogues having **ONLY** the categories of the target and will exclude the analogues having any other categories according to the profiler used in the grouping method.
- For example, if the profiling for the target results in *Aldehydes (Acute toxicity)* **ONLY** according to US-EPA category, the group of analogues will include *Aldehydes (Acute toxicity)* **ONLY**. (See next screen shot)

Category definition

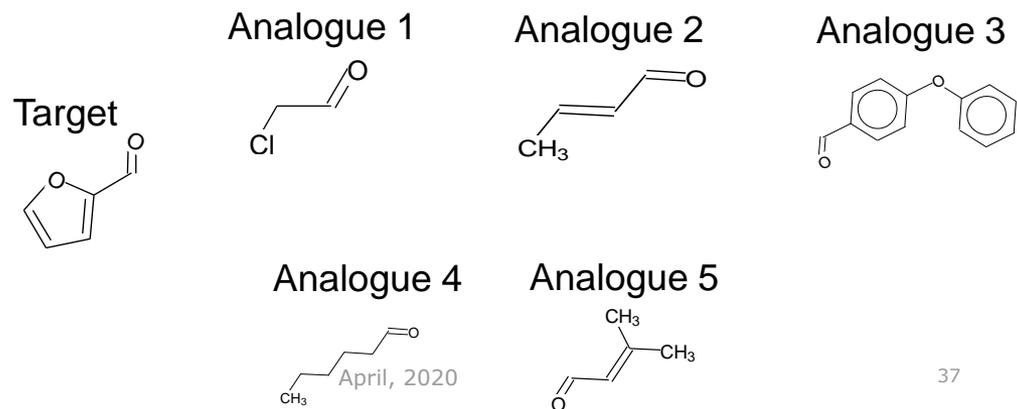
Defining US-EPA category strict functionality

Input



The target and analogues have *Aldehydes* **ONLY** according to US-EPA category

Defined Category



Category definition

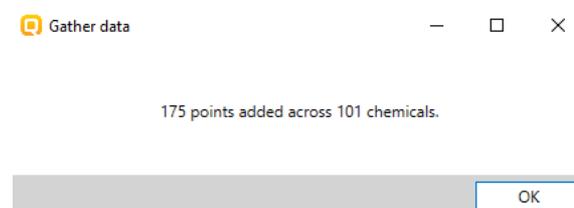
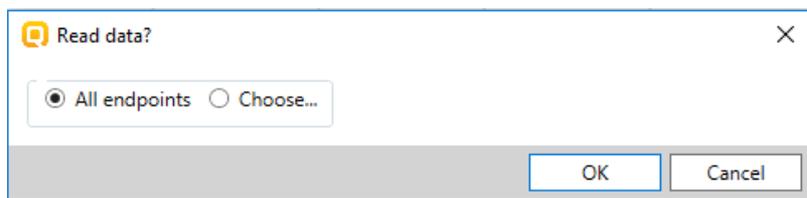
Analogues

- The Toolbox now identifies all chemicals corresponding to *Aldehydes (Acute toxicity)* by US-EPA listed in the databases selected under “Data”.
- 101 analogues including the target chemical are identified; they form a mechanistic category “**Aldehydes (Acute toxicity)**”, which will be used for gap filling.

Category definition

Reading data for Analogues

- The Toolbox automatically request 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). Click OK to read all available data. 175 data points are collected for the list of 101 analogues



Category definition

Summary information for Analogues

After a message for number of data collected, the experimental results for the target and analogues are inserted into the matrix.

The screenshot displays the QSAR Toolbox software interface during the 'Category definition' phase. The main window shows a data matrix with 12 columns representing different chemical entities and rows representing various endpoints. The 'Acute aquatic toxicity MOA by OASIS' endpoint is highlighted in yellow for the first entity.

Endpoint	1 [target]	2	3	4	5	6	7	8	9	10	11	12
Acute aquatic toxicity MOA by OASIS	M: 145 mg/L	M: 31.7 mg/L	M: 112 mg/L	M: 3.9 mg/L	M: 14 mg/L	M: 7.96 mg/L	M: 8.2 mg/L	M: 937 mg/L	M: 191 mg/L	M: 167 mg/L	M: 632 mg/L	
Mortality	M: 10.5 mg/L	M: 6.62 mg/L	M: 7.77 mg/L				M: 3.19 mg/L		M: 20 mg/L	M: 5.01 mg/L		
Intoxication	1/1											
Physiology	19/22			M: 1.66 mg/L	M: 14.6 mg/L	M: 5.64 mg/L						

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 - 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 (IGC 50 48h of *T. pyriformis*) Apply Trend analysis

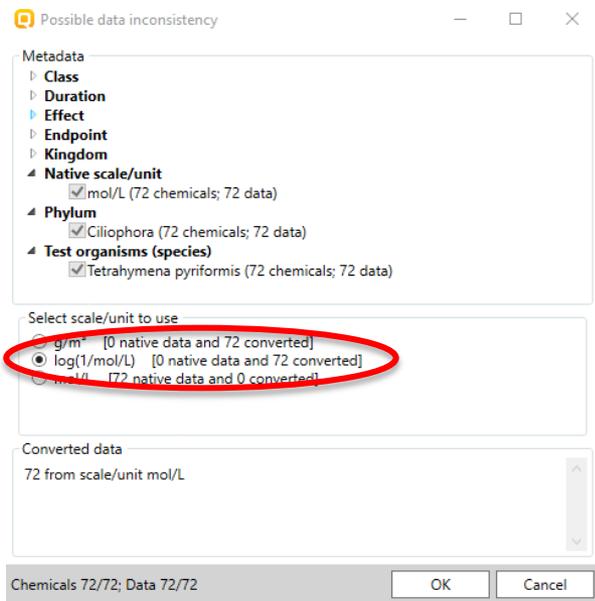
The screenshot displays the QSAR Toolbox interface. The top menu bar has 'Data Gap Filling' highlighted with a red box and a callout '1'. The left sidebar has 'Trend analysis' highlighted with a red box and a callout '3'. The central data table shows a grid of chemical structures and their corresponding IGC50 values. The cell containing 'M: 145 mg/L' is highlighted with a red box and a callout '2'. The table data is as follows:

Structure	1	2	3	4	5	6	7	8	9	10	11	12	13
Tetrahymena pyriformis	M: 145 mg/L	M: 31.7 mg/L	M: 112 mg/L	M: 3.9 mg/L	M: 14 mg/L	M: 7.96 mg/L	M: 8.2 mg/L	M: 937 mg/L	M: 191 mg/L		M: 167 mg/L	M: 6.32 mg/L	M: 10.3 mg/L
IGC50	72/80												
Intoxication	1/1												
Mortality	60/80	M: 10.5 mg/L	M: 6.62 mg/L	M: 7.77 mg/L			M: 3.19 mg/L		M: 20 mg/L	M: 5.01 mg/L			
Physiology	19/22			M: 1.66 mg/L	M: 14.6 mg/L	M: 5.64 mg/L							
Sediment Toxicity													
Terrestrial Toxicity													
Human Health Hazards													
Profile													

1. Go to **Data Gap Filling**; 2. Highlight the **data gap** corresponding to target endpoint: IGC50, *Tetrahymena pyriformis* under the target chemical; 3. Select **Trend analysis**;

Data Gap Filling (IGC 50 48h of *T. pyriformis*) Apply Trend analysis

- A message for possible data inconsistency appears
- It is recommended the $\log(1/\text{mol/L})$ scale to be chosen



- The resulting plot can be seen on next screen shot

Data Gap Filling (IGC 50 48h of *T. pyriformis*)

QSAR TOOLBOX

Input Profiling Data Category definition Data Gap Filling Report

Gap Filling Workflow

Trend analysis Read across (QSAR) Standardized Automated

The OECD QSAR Toolbox for Grouping Chemicals into Categories
Developed by LMC, Bulgaria

Documents

- Document 1
 - # [C: 1;Md: 3;P: 0] CAS: 98011
 - [C: 101;Md: 175;P: 0] Aldehydes (Acute toxicity) Strict (US-EPA)
 - [C: 72;Md: 135;P: 0] Enter GF (TA)

Filter endpoint tree... [target]

Structure

Structure info
Parameters
Physical Chemical Properties
Environmental Fate and Transport
Ecotoxicological Information
Aquatic Toxicity
Growth
48 h
Protozoa
Ciliophora
Ciliata
Tetrahymena pyriformis
IGC50
Mortality
Physiology

72/72	M: 145 mg/L	M: 31.7 mg/L	M: 112 mg/L	M: 3.9 mg/L	M: 14 mg/L	M: 7.96 mg/L	M: 8.2 mg/L	M: 937 mg/L	M: 191 mg/L	M: 167 mg/L	M: 6.32 mg/L	M: 10.3 mg/L
33/47	M: 10.5 mg/L	M: 6.62 mg/L	M: 7.77 mg/L	M: 1.66 mg/L	M: 14.6 mg/L	M: 5.64 mg/L	M: 3.19 mg/L	M: 20 mg/L				
15/16												

Sediment Toxicity
Terrestrial Toxicity

Data Gap Filling Settings

Only endpoint relevant

At this position:

- QSARs 0
- Automated workflows 0
- Standardized workflows 0

In nodes below:

- QSARs 0
- Automated workflows 0
- Standardized workflows 0

Descriptors
Prediction
Adequacy
Cumulative frequency
Residuals
Statistics

Trend analysis prediction for IGC50, based on 71 values
Observed: 145 mg/L; Predicted: 101 mg/L
Model equation: $IGC50 = 2.65 (\pm 0.301) + 0.395 (\pm 0.135) * \log Kow, \log(1/mg/L)$

Select / filter data
Gap filling approach
Descriptors / data
Model/QSAR
Calculation options
Visual options
Information
Miscellaneous

Accept prediction

Data Gap Filling (IGC 50 48h of *T. pyriformis*) Interpreting dots on the graph

- The resulting plot outlines the experimental results of all analogues (Y axis) according to a descriptor (X axis) with LogKow being the default descriptor (see previous screen shot).
- The **RED** dot represents the predicted value for target chemical.
- The **ORANGE** dot represents the observed data value for the target chemical.
- The **BLUE** dots represent the experimental results available for the analogues.
- The **LIGHT BLUE** dots (see the following screen shots) represent analogues belonging to different subcategories.

Data Gap Filling (IGC 50 48h of *T. pyriformis*) An accurate analysis of data set

- In this example, the mechanistic properties of the analogues are consistent.
- Subcategorization can be performed based on protein binding mechanisms. This is the second stage of analogue search - requiring the same interaction mechanism.
- Acute effects are associated with covalent interaction of chemicals within cell proteins, i.e. with protein binding.
- Chemicals with a different protein binding mechanism / reactions compared to the target chemical will be removed.

Data Gap Filling (IGC 50 48h of *T. pyriformis*) Subcategorization

- After the available data has been retrieved, the user can then further subcategorize the results according to the following endpoint-specific subcategorizations:
 - Acute aquatic toxicity MOA by OASIS
 - Protein binding by OASIS
 - Aquatic toxicity classification by ECOSAR
- These steps are summarized in the next screen shots.

Data Gap Filling (IGC 50 48h of *T. pyriformis*)

Subcategorization 1: Acute aquatic toxicity MOA by OASIS

The screenshot displays the QSAR Toolbox interface for subcategorization. The 'Subcategorization' window is active, showing 'Options' and 'Profilers' tabs. The 'Profilers' tab is selected, and 'MOA by OASIS' is highlighted in green. A red dashed box labeled '2' points to this selection. The 'Data Gap Filling' table shows a list of chemicals with their respective IGC50 values and predicted values. A red dashed box labeled '1' points to the 'Select / filter data' panel on the right, which includes a 'Subcategorize' button. A red dashed box labeled '3' points to the 'Remove selected' button in the 'Selected 4 (67/71)' section. The 'Trend analysis prediction' plot shows a scatter plot of log(I) vs log(I) with a red regression line. The 'Analogues' list shows 'Reactive unspecified' as a category.

1. Click **Select / filter data**, then **Subcategorize**; 2. Select **"MOA by OASIS"** (Note: the most suitable profilers for subcategorization are again green highlighted); 3. **Click "Remove selected"** to eliminate dissimilar to the target analogues (in this case analogues categorized as "reactive unspecified" based on MOA profiler will be eliminated)

Data Gap Filling (IGC 50 48h of *T. pyriformis*) Subcategorization 2: Protein binding by OASIS

The screenshot shows the QSAR Toolbox interface. On the left, the 'Subcategorization' window is open. Under 'Endpoint Specific', 'Protein binding by OASIS' is selected (indicated by a red '1'). In the 'Analogues' section, several items are selected and highlighted with a red dashed box (indicated by a red '2'), including '(18) Michael addition', '(3) Michael addition >> Michael ac', '(16) No alert found', and '(1) Schiff base formation >> Direct'. The main window displays a table of chemical structures and their IGC50 values. Below the table is a scatter plot titled 'Trend analysis prediction for IGC50, based on 67 values' showing a positive correlation between log Kow and IGC50. The plot includes a model equation: $IGC50 = 2.37 (\pm 0.242) + 0.488 (\pm 0.107) * \log Kow$. The observed value is 145 mg/L and the predicted value is 161 mg/L. A red dashed box highlights a cluster of points in the plot.

Chemical Structure	IGC50	M: 145 mg/L	M: 31.7 mg/L	M: 112 mg/L	M: 3.9 mg/L	M: 7.96 mg/L	M: 8.2 mg/L	M: 937 mg/L	M: 191 mg/L	M: 167 mg/L	M: 6.6
<chem>C1=CC=C(C=C1)C=O</chem>	68/68	M: 145 mg/L	M: 31.7 mg/L	M: 112 mg/L	M: 3.9 mg/L	M: 7.96 mg/L	M: 8.2 mg/L	M: 937 mg/L	M: 191 mg/L	M: 167 mg/L	M: 6.6
<chem>CC(=O)C1=CC=C(C=C1)</chem>	32/43	M: 10.5 mg/L	M: 6.62 mg/L	M: 7.77 mg/L			M: 3.19 mg/L		M: 20 mg/L		
<chem>CC(C)C=O</chem>	13/14				M: 1.66 mg/L	M: 5.64 mg/L					

1. Select "Protein binding by OASIS";
2. Click "Remove selected" to eliminate dissimilar to the target analogues.

Data Gap Filling (IGC 50 48h of *T. pyriformis*)

Subcategorization 3: Aquatic toxicity classification by ECOSAR

The screenshot displays the 'Subcategorization' window in the QSAR Toolbox. On the left, the 'Endpoint Specific' section is active, with 'Aquatic toxicity classification by ECOSAR' selected. A red dashed arrow points from this selection to the 'Analogues' list, where '(1) Imidazoles' is highlighted. A second red dashed arrow points from a 'Remove selected' button to the same analogue. Below the analogue list, a 'Trend analysis prediction' plot shows a scatter of data points with a red regression line. The plot is titled 'Trend analysis prediction for IGC50, based on 28 values' and includes the equation: $IGC50 = 2.09 (\pm 0.238) + 0.130 (\pm 0.106) * \log \text{Kow, } \log(1/\text{mol/L})$. The observed value is 145 mg/L and the predicted value is 281 mg/L. A table of analogues is shown above the plot, listing chemical structures and their IGC50 values for various target categories.

Target	3	4	7	8	9	17	22	27	31	37	42		
hymena pyriformis													
GC50	29/29	M: 145 mg/L	M: 112 mg/L	M: 3.9 mg/L	M: 8.2 mg/L	M: 937 mg/L	M: 191 mg/L	M: 216 mg/L	M: 296 mg/L	M: 148 mg/L	M: 103 mg/L	M: 152 mg/L	M: 104 mg/L
	19/28	M: 10.5 mg/L	M: 7.77 mg/L	M: 1.66 mg/L	M: 3.19 mg/L	M: 20 mg/L	M: 14.9 mg/L	M: 18.6 mg/L	M: 1.36 mg/L	M: 9.79 mg/L	M: 13 mg/L	M: 61 mg/L	
6/7													

1. Select "Aquatic toxicity classification by ECOSAR";
2. Click "Remove selected" to eliminate the single analogue;

Data Gap Filling (IGC 50 48h of *T. pyriformis*) Results after subcategorisation

The screenshot displays the QSAR Toolbox interface during a 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 blue callout box with the number '2' points to the 'Yes' button. Below the dialog, a 'Data Gap Filling Settings' panel is visible, with 'Only endpoint relevant' checked. To the right, a 'Trend analysis prediction for IGC50, based on 27 values' scatter plot shows a positive correlation between log Kow and IGC50 (log(l/mo/l)). The observed value is 145 mg/L and the predicted value is 268 mg/L. The model equation is $IGC50 = 2.12 (\pm 0.256) + 0.520 (\pm 0.106) \cdot \log Kow$. On the far right, a 'Select / filter data' panel is shown, with the 'Accept prediction' button circled in red and a blue callout box with the number '1' pointing to it. The background shows a table of chemical structures and their predicted values.

9	17	22	27	31	37	42	48
<chem>CC(=O)O</chem>	<chem>CC=O</chem>	<chem>CC(=O)O</chem>	<chem>C1=CC=CC=C1</chem>	<chem>CC(=O)O</chem>	<chem>CCCC</chem>	<chem>CCCC</chem>	<chem>CCCC</chem>
M: 191 mg/L M: 20 mg/L	M: 216 mg/L M: 14.9 mg/L	M: 296 mg/L M: 18.6 mg/L	M: 148 mg/L	M: 103 mg/L M: 1.36 mg/L	M: 152 mg/L M: 9.79 mg/L	M: 104 mg/L M: 13 mg/L	M: 235 mg/L M: 61 mg/L

1. Click "Accept prediction"; 2. Click "Yes" ("No" allows to continue with the subcategorization).

Data Gap Filling (IGC 50 48h of *T. pyriformis*) Evaluation of the model

- To assess the model accuracy use:
 - Adequacy (predictions after leave-one-out)
 - Statistics
 - Cumulative frequency
 - Residuals
- See next four screen shots

Data Gap Filling (IGC 50 48h of *T. pyriformis*) Evaluation of the model - Adequacy

The screenshot displays the QSAR Toolbox software interface during the 'Data Gap Filling' workflow. The top navigation bar includes 'Input', 'Profiling', 'Data', 'Category definition', 'Data Gap Filling', and 'Report'. The left sidebar shows a document tree with a selected endpoint: '[G: 28;Md: 63;P: 1] Subcategorized: Aquatic toxicity'. The center panel shows a filter endpoint tree with 'IGC50' selected. The right panel displays a data table with columns for various endpoints and their corresponding values. The bottom panel shows the 'Adequacy of prediction' scatter plot, which compares observed vs. predicted IGC50 values. The plot includes a regression line and a legend for 'Adequacy of prediction' with model statistics: $R^2 = 0.802$, $R^2_{adj} = 0.795$, $s = 0.303$. A 'Select / filter data' panel on the right contains buttons for 'Subcategorize', 'Mark chemicals by WS', 'Mark chemicals by descriptor value', 'Mark outliers', 'Filter points by test conditions', 'Mark focused chemical', 'Mark focused points', 'Remove marked data', and 'Clear existing marks'. A green checkmark and 'Accept prediction' button are visible at the bottom right.

1. Position on the last level of document tree; 2. Click "Adequacy";

Data Gap Filling (IGC 50 48h of *T. pyriformis*) Evaluation of the model - Cumulative frequency

The screenshot shows the QSAR Toolbox interface with the 'Data Gap Filling' workflow selected. The main window displays a filter endpoint tree on the left, a table of predicted values for various endpoints, and a cumulative frequency histogram at the bottom. A callout box with the number '1' points to the 'Cumulative frequency' option in the Descriptors list.

Filter endpoint tree...

- Structure
 - Ciliophora
 - Ciliata
 - Tetrahymena pyriformis
 - IGC50
 - M: 145 mg/L
 - M: 112 mg/L
 - M: 3.9 mg/L
 - M: 8.2 mg/L
 - M: 191 mg/L
 - M: 216 mg/L
 - M: 296 mg/L
 - M: 148 mg/L
 - M: 103 mg/L
 - M: 152 mg/L
 - M: 104 mg/L
 - M: 235 mg/L

Table of Predicted Values:

Endpoint	1	3	4	7	9	17	22	27	31	37	42	48
Mortality	19/28	M: 10.5 mg/L	M: 7.77 mg/L	M: 1.66 mg/L	M: 3.19 mg/L	M: 20 mg/L	M: 14.9 mg/L	M: 18.6 mg/L	M: 136 mg/L	M: 9.79 mg/L	M: 13 mg/L	M: 61 mg/L
Physiology	6/7											
Sediment Toxicity												
Terrestrial Toxicity												
Human Health Hazards												
Profiling												
Predefined												
US-EPA New Chemical Categories												
General Mechanistic												

Data Gap Filling Settings:

- Only endpoint relevant
- At this position:
 - Select a cell with a rigid (bold) path
 - Automated workflows: 0
 - Standardized workflows: 0

Descriptors:

- Prediction
- Adequacy
- Cumulative frequency** (1)
- Residuals
- Statistics

95% of Residuals ≤ 0.492, log(1/mol/L)

Cumulative frequency [%]

Residuals, Y - Y_{calc}

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
- Remove marked data
- Clear existing marks
- Gap filling approach

Accept prediction

1. Click "Cumulative frequency"; The residuals abs (obs-predicted) for 95% of analogues are comparable with the experimental error.

Data Gap Filling (IGC 50 48h of *T. pyriformis*) Evaluation of the model - Residuals

The screenshot displays the QSAR Toolbox interface during the 'Data Gap Filling' process. The 'Data Gap Filling Settings' panel on the left has 'Residuals' selected, indicated by a callout box with the number '1'. The central table shows the distribution of residuals for IGC50 across various descriptors. The scatter plot at the bottom, titled 'Distribution of residuals for IGC50 vs descriptors in use', plots IGC50 (residuals) [log¹⁰/mg/L] against log Kow.

Descriptor	IGC50	M: 145 mg/L	M: 112 mg/L	M: 3.9 mg/L	M: 8.2 mg/L	M: 191 mg/L	M: 216 mg/L	M: 296 mg/L	M: 148 mg/L	M: 103 mg/L	M: 152 mg/L	M: 104 mg/L	M: 235 mg/L
Mortality	19/28	M: 10.5 mg/L	M: 7.77 mg/L		M: 3.19 mg/L	M: 20 mg/L	M: 14.9 mg/L	M: 18.6 mg/L		M: 1.36 mg/L	M: 9.79 mg/L	M: 13 mg/L	
Physiology	6/7			M: 1.66 mg/L									M: 61 mg/L

1. Click "Residuals"

Data Gap Filling (IGC 50 48h of *T. pyriformis*) Evaluation of the model - Statistics

The screenshot shows the QSAR Toolbox interface. On the left, the 'Data Gap Filling Settings' panel is open, with the 'Statistics' option selected. A red circle with the number '1' highlights this option. The main window displays a filter endpoint tree for '48 h' and a table of predicted values for various chemical structures.

Structure	1 (target)	3	4	7	9	17	22	27	31	37	42	48
Structure												
48 h												
Protozoa												
Ciliophora												
Ciliata												
Tetrahymena pyriformis												
IGC50	28/29 M: 145 mg/L	M: 112 mg/L	M: 3.9 mg/L	M: 8.2 mg/L	M: 191 mg/L	M: 216 mg/L	M: 296 mg/L	M: 148 mg/L	M: 103 mg/L	M: 152 mg/L	M: 104 mg/L	M: 235 mg/L
Mortality	19/28 M: 10.5 mg/L	M: 7.77 mg/L		M: 3.19 mg/L	M: 20 mg/L	M: 14.9 mg/L	M: 18.6 mg/L		M: 1.36 mg/L	M: 9.79 mg/L	M: 13 mg/L	
Physiology	6/7		M: 1.66 mg/L								M: 61 mg/L	
Sediment Toxicity												
Terrestrial Toxicity												

The 'Data Gap Filling Settings' panel shows the following options:

- Only endpoint relevant
- At this position:**
 - QSARs: 0
 - Automated workflows: 0
 - Standardized workflows: 0
- In nodes below:**
 - QSARs: 0
 - Automated workflows: 0
 - Standardized workflows: 0

The 'Statistics' section in the 'Data Gap Filling Settings' panel is highlighted with a red circle and the number '1'. The statistics shown are:

Descriptors	Statistical characteristics	TA model
Prediction	Number of data points, (N)	27
	Coefficient of determination, (R2)	0.802
	Adjusted coefficient of determination, (R2adj)	0.795
Adequacy	Coefficient of determination - leave one out, (Q2)	N/A
	Sum of squared residuals, (SSR)	2.29
Cumulative frequency	Standard deviation of residuals, (sN)	0.291
	Sample standard deviation of residuals, (s)	0.303
Residuals	Fisher function, (F)	102
Statistics	Fisher threshold for statistical significance, (Fa)	5.69 (95.0%)
	b0	
	- model descriptor	Intercept
	- coeff. value	2.12
	- coeff. range	±0.256
	- significance	No
	- max covariation	0.249 vs log Kow
	b1	
	- model descriptor	log Kow
	- coeff. value	0.520
	- coeff. range	±0.106
	- significance	

At the bottom of the interface, a blue box contains the instruction: **1. Click "Statistics"**

Data Gap Filling (IGC 50 48h of *T. pyriformis*) Results after subcategorisation

The screenshot shows the QSAR Toolbox interface during a Data Gap Filling workflow. The main window displays a table of results for various chemical structures across 11 target endpoints. The 'IGC50' row is highlighted in yellow, and the cell for the first target (M: 145 mg/L, T: 268 (60.2+1.2E+03) mg/L) is circled in red. The left sidebar shows a filter endpoint tree with 'IGC50' selected under 'Aquatic Toxicity'.

Structure	1 [target]	2	3	4	5	6	7	8	9	10	11
Structure											
Structure info											
Parameters											
Physical Chemical Properties											
Environmental Fate and Transport											
Ecotoxicological Information											
Aquatic Toxicity											
Growth											
48 h											
Protozoa											
Ciliophora											
Ciliata											
Tetrahymena pyriformis											
IGC50	M: 145 mg/L T: 268 (60.2+1.2E+03) mg/L	M: 31.7 mg/L	M: 112 mg/L	M: 3.9 mg/L	M: 14 mg/L	M: 7.96 mg/L	M: 8.2 mg/L	M: 937 mg/L	M: 191 mg/L		M: 167 mg/L
Intoxication	1/1										
Mortality	60/80	M: 10.5 mg/L	M: 6.62 mg/L	M: 7.77 mg/L			M: 3.19 mg/L		M: 20 mg/L	M: 5.01 mg/L	
Physiology	19/22				M: 1.66 mg/L	M: 14.6 mg/L	M: 5.64 mg/L				
Sediment Toxicity											
Terrestrial Toxicity											
Human Health Hazards											
Profiling											

Data Gap Filling (IGC 50 48h of *T. pyriformis*) Save the derived QSAR model

- To save the new regression model follow these steps:
 - Go to the last row on the Document tree
 - Click on "Model/QSAR"
 - Select Save model
 - Enter the model name and fill editable fields if necessary
 - Click on OK

Data Gap Filling (IGC 50 48h of *T. pyriformis*) Save the derived QSAR model

The screenshot shows the 'Customize model content' wizard window. The 'Wizard pages' list on the left includes 'QSAR Identity', 'General information', 'Defining the endpoint - OECD Principle 1', 'Defining the algorithm - OECD Principle 2', 'Applicability domain - OECD Principle 3', 'Training set and statistics - OECD Principle 4', 'External validation and predictivity - OECD Principle 4', and 'Mechanistic interpretation - OECD Principle 5'. The 'QSAR Identity' page is active, showing fields for 'QSAR Title/Caption' (IGC50 *T. pyriformis*, Growth 48h) and 'Version' (1.0). The 'Save model' button is highlighted with callout 3. An 'Information' dialog box with the message 'The model was saved successfully!' and an 'OK' button is shown with callout 4. In the bottom right, a sidebar menu has 'Model/QSAR' highlighted with callout 1. Below the wizard, a table of 'All descriptors' is visible, listing various parameters like 'Acidic pKa' and 'BAF' with their units.

Active descriptors		Correlation		Information	
Data points					
27		0.896			

All descriptors		Unit		Information	
Name					
(Q) Acidic pKa (Chemaxon)					
(Q) Basic pKa (Chemaxon)					
Acidic pKa (OASIS Consensus)					
Acidic pKa (OASIS Electric)					
Acidic pKa (OASIS Regression)					
Amino acids pKa (OASIS Regression)					
BAF		log(L/kg)			
BAF (lower trophic)		log(L/kg)			
BAF (mid trophic)		log(L/kg)			
BAF (upper trophic)		log(L/kg)			
BAF (upper trophic, biotransformation rate is zero)		log(L/kg)			

1. Click **"Model/QSAR"**, then **"Save model"**; 2. Type name of the model and fill the fields in the wizard if necessary (Use Next/Back buttons to navigate within it); 3. Click **"Save model"**; 4. Click **OK**.

Outlook

- Background
- Keywords
- Objectives
- The exercise
- **Workflow of the exercise**
 - Input
 - Profiling
 - Data
 - Category definition
 - Data gap filling
 - **QSAR model**

Data Gap Filling

How to see the derived QSAR?

The screenshot displays the QSAR Toolbox interface with several key components:

- Workflow Panel (Top Left):** Shows a sequence of steps: Input, Profiling, Data, Category definition, Data Gap Filling, and Reporting. Step 3 is highlighted on the 'Data Gap Filling' step.
- Document Tree (Middle Left):** A hierarchical tree of chemical categories. Step 1 points to the 'Aldehydes (Acute toxicity) Strict (US-EPA N...)' category.
- Structure and Parameters (Center):** Displays the chemical structure and associated parameters for the selected category. Step 2 points to the 'IC50' parameter.
- Details for 23 (Q)SAR models (Right):** A table listing various QSAR models. Step 4 points to the 'IC50 T.pyriformis, Growth 48h (1.0)' model.
- Data Matrix (Bottom):** A table showing predicted values for various models. The 'IC50' row is highlighted in yellow.

QSAR name	#	Predicted	Class	Domain	Duration	Effect	Endpoint	Fisher	Kingdom
Fathead minnow 96h LC50 - Danish QSAR DB battery model (1.0)	14	Out of Domain	Actinopterygii (ray-finned fishes spiny rayed)	Out of domain	96 h	Mortality	LC50		Animalia (anim)
IC50 T.pyriformis, Growth 48h (1.0)	15	268 mg/L	Ciliatea	In domain	48 h	Growth	IGC50	102	Protozoa
M1 - LC50 - Pimephales promelas (fathead minnow) (1.0)	16	1.6 mg/L		Object reference not set to an instance of an object.	96 h	Mortality	LC50	192	
M2 - LC50 - Pimephales promelas (fathead minnow) (1.0)	17			Object reference not set to an instance of an object.	96 h	Mortality	LC50	998	
M3 - LC50 - Pimephales promelas (fathead minnow) (1.0)	18			Object reference not set to an instance of an object.	96 h	Mortality	LC50	661	
M4 - LC50 - Pimephales promelas (fathead minnow) (1.0)	19	167 mg/L		Object reference not set to an instance of an object.	96 h	Mortality	LC50	762	
Photoinduced toxicity of PAHs (1.0)	20	Not Phototoxic		Object reference not set to an instance of an object.		Photoinduced Toxicity			Toxicity on Daphnia magna
Pseudokirchneriella s. 72h EC50 - Danish QSAR DB battery model (1.0)	21	Out of Domain		Out of domain	72 h	Growth Inhibition	EC50		
Pseudokirchneriella s. 72h EC50 - Danish QSAR DB Leadscope model (1.0)	22	Out of Domain		Out of domain	72 h	Growth Inhibition	EC50		

1. Select a non-Gap filling list from the documented tree; 2. Note the accepted prediction will be inserted into data matrix 3. Click "(Q)SAR"; 4. The derived QSAR is listed in the panel with Relevant (Q)SAR models.

Data Gap Filling

How to see the derived QSAR?

As seen in the next five screen shots the derived model can be used to:

- Visualize training set of the model;
- Visualize the domain of the model;
- Visualize whether a chemical is in the domain of the model;
- Enter in Data Gap filling;
- Perform predictions for:
 - Selected chemical
 - All chemicals (in the matrix)
 - Chemicals in domain.

Data Gap Filling

Visualisation of the training set

Details for 23 (Q)SAR models

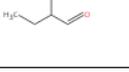
QSAR name	Predicted	Class	Domain	Duration	Effect
Fathead minnow 96h LC50 - Danish QSAR DB SciQSAR model (1.0)	Out of Domain	Actinopterygii (ray-finned fishes, spiny rayed fishes)	Out of domain	96 h	Mortality
IGC50 T.pyriformis, Growth 48h (1.0)	15 268 mg/L	Ciliatea	In domain	48 h	Growth
M1 - LC50 - Pimephales promelas (fathead minnow) (1.0)			Object reference not set to an instance of an object.	96 h	Mortality
M2 - LC50 - Pimephales promelas (fathead minnow) (1.0)			Object reference not set to an instance of an object.	96 h	Mortality
M3 - LC50 - Pimephales promelas (fathead minnow) (1.0)			Object reference not set to an instance of an object.	96 h	Mortality
M4 - LC50 - Pimephales promelas (fathead minnow) (1.0)			Object reference not set to an instance of an object.	96 h	Mortality
Photoinduced toxicity of PAHs (1.0)	20 Not Phototoxic		Object reference not set to an instance of an object.		Photoinduced Toxicity
Pseudokirchneriella s. 72h EC50 - Danish QSAR DB battery model (1.0)	21 Out of Domain		Out of domain	72 h	Growth Inhibition
Pseudokirchneriella s. 72h EC50 - Danish QSAR DB Leadscope model (1.0)	22 Out of Domain		Out of domain	72 h	Growth Inhibition
Pseudokirchneriella s. 72h EC50 - Danish QSAR DB Leadscope model (1.0)					

Find Show only chemical relevant (Q)SARs

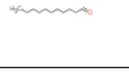
Training IGC50 T.pyriformis, Growth 48h" (27 chemicals)

File

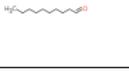
1
97-96-1
IGC50: 112 mg/L



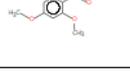
2
112-44-7
IGC50: 3.90 mg/L



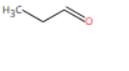
3
112-31-2
IGC50: 8.20 mg/L



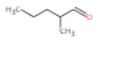
4
613-45-6
IGC50: 191 mg/L



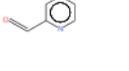
5
123-38-6
IGC50: 216 mg/L



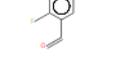
6
123-15-9
IGC50: 296 mg/L



7
1121-60-4
IGC50: 148 mg/L



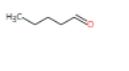
8
446-52-6
IGC50: 103 mg/L



9
66-25-1
IGC50: 152 mg/L



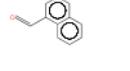
10
110-62-3
IGC50: 104 mg/L



11
2987-16-8
IGC50: 235 mg/L



12
66-77-3
IGC50: 59.4 mg/L



13 15 16

Save to smi OK

1. Right click on the derived **QSAR model**;
2. Select **Show training set**;
3. Note the experimental data is displayed under CAS# of each chemical;
4. The training set can be saved as *.smi file.

Data Gap Filling

Visualisation of model domain

QSAR name	Predicted	Class	Domain	Duration
Fathead minnow 96h LC50 - Danish QSAR DB SciQSAR model (1.0)	Out of Domain	Actinopterygii (ray-finned fishes, spiny rayed fishes)	Out of domain	96 h
IGC50 T.pyriformis, Growth 48h (1.0)	268 mg/L	Ciliata	In domain	48 h
M1 - LC50 - Pimephales promelas (fathead minnow) (1.0)			Object reference not set to an instance of an object.	96 h
M2 - LC50 - Pimephales promelas (fathead minnow) (1.0)			Object reference not set to an instance of an object.	96 h
M3 - LC50 - Pimephales promelas (fathead minnow) (1.0)			Object reference not set to an instance of an object.	96 h
M4 - LC50 - Pimephales promelas (fathead minnow) (1.0)			Object reference not set to an instance of an object.	96 h
Photoinduced toxicity of PAHs (1.0)	Not Phototoxic		Object reference not set to an instance of an object.	
Pseudokirchneriella s. 72h EC50 - Danish QSAR DB battery model (1.0)	Out of Domain		Out of domain	72 h
Pseudokirchneriella s. 72h EC50 - Danish QSAR DB Leadscope model (1.0)	Out of Domain		Out of domain	72 h
Pseudokirchneriella s. 72h EC50 - Danish QSAR DB Leadscope model (1.0)			Object reference not set to an instance of an object.	

Explanation for Domain -> Domain

Filter:

Categories

- Domain

Domain

Explanation

Profiler: US-EPA New Chemical Categories

- Acid Chlorides
- Acrylamides
- Acrylates/Methacrylates (Acute toxicity)
- Aldehydes (Acute toxicity)**
- Aliphatic Amines
- Aluminum Compounds
- Anilines (Acute toxicity)
- Azides (Acute toxicity)
- Benzotriazoles (Acute toxicity)
- Benzotriazole-hindered phenols
- Boron Compounds
- Cationic (quaternary ammonium) surfactants
- Cobalt
- Diazoniums (Acute toxicity)
- Epoxides
- Esters (Acute toxicity)
- Hydrazines and Related Compounds
- Hindered Amines
- Imides (Acute toxicity)
- Lanthanides or Rare Earth Metals

Query details

[1] Reference Query | Metabolism

Profiling schemes

- Custom
- Empiric
- Endpoint Specific
- General Mechanistic
- Predefined
 - Database Affiliation
 - Inventory Affiliation
 - OECD HPV Chemical Categories
 - Substance type
 - US-EPA New Chemical Categories
 - Toxicological

Selected categories

Aldehydes (Acute toxicity)

Available categories

(N/A)

- Acid Chlorides
- Acrylamides
- Acrylates/Methacrylates (Acute toxicity)
- Acrylates/Methacrylates (Chronic toxicity)

Multiple categories

Strict OR-ed AND-ed

1. Right click on the derived **QSAR model**; 2. Select **"Display Domain"**; 3. Note the boundaries of the domain are combined logically; 4. If the chemical answers the query of the domain then the current query is labelled with **GREEN** tick; 5. Otherwise is labelled with **RED** cross.

Data Gap Filling

Visualisation of whether a chemical is in the domain of the model

The screenshot displays the QSAR Toolbox software interface during a Data Gap Filling workflow. The top menu bar includes 'Data Gap Filling', which is currently active. The main workspace shows a data matrix with columns for chemical identifiers (e.g., C6H12O, C11H22O, C4H6O, C8H14O, C10H20O, C5H6N2O, C9H10O3) and rows for various QSAR models. A 'Confirm' dialog box is open, asking 'The defined target chemical is not active. Do you want to continue with a different...'. A context menu is also visible over a model entry, with 'Display Domain' selected. Blue callouts 1-4 indicate the sequence of actions: 1. Highlighting a cell in the data matrix; 2. Clicking the '(Q)SAR' button; 3. Clicking 'Yes' in the confirmation dialog; 4. Clicking 'Display Domain' in the context menu.

Q SAR name	#	Predicted	Class	Domain	Duration	Effect	Endpoint
Fathead minnow 96h LC50 - Danish QSAR DB Leadscope model (1.0)	11	13.8 mg/L	Actinopterygii (ray-finned fishes, spiny rayed fishes)	In domain	96 h	Mortality	LC50
Fathead minnow 96h LC50 - Danish QSAR DB SciQSAR model (1.0)	12	13.3 mg/L	Actinopterygii (ray-finned fishes, spiny rayed fishes)	In domain	96 h	Mortality	LC50
IGC50 T.pyriformis, Growth 48h (1.0)	13	12.1 mg/L	Actinopterygii (ray-finned fishes, spiny rayed fishes)	Out of domain	48 h	Growth	IGC50
M1 - LC50 - Pimephales promelas (fathead minnow) (1.0)	14	12.1 mg/L	Actinopterygii (ray-finned fishes, spiny rayed fishes)	Object reference not set to an instance of an object.	96 h	Mortality	LC50
M2 - LC50 - Pimephales promelas (fathead minnow) (1.0)	15	12.1 mg/L	Actinopterygii (ray-finned fishes, spiny rayed fishes)	Object reference not set to an instance of an object.	96 h	Mortality	LC50
M3 - LC50 - Pimephales promelas (fathead minnow) (1.0)	16	12.1 mg/L	Actinopterygii (ray-finned fishes, spiny rayed fishes)	Object reference not set to an instance of an object.	96 h	Mortality	LC50
M4 - LC50 - Pimephales promelas (fathead minnow) (1.0)	17	12.1 mg/L	Actinopterygii (ray-finned fishes, spiny rayed fishes)	Object reference not set to an instance of an object.	96 h	Mortality	LC50
Photoinduced toxicity of PAHs (1.0)	18	Not Phototoxic	Actinopterygii (ray-finned fishes, spiny rayed fishes)	Object reference not set to an instance of an object.		Photoinduced	Toxicity on Danubia ma

1. Highlight the cell of one of the analogues (e.g., chemical # 6 in the data matrix; 2. Click on "(Q)SAR"; 3. A message informs you that the QSAR is applied not on the target chemical. Click Yes; 4. Right click above the model and Left click on Display domain (see next screen shot).

Data Gap Filling

Visualisation of whether a chemical is in the domain of the model

- The chemical is an “aldehyde” as required by US-EPA categorization group (boundary 1 on next screen shot).
- The chemical is an “aldehyde” as required by Acute aquatic toxicity MOA by OASIS group (boundary 2) and to be not “reactive unspecified” (boundary 3)
- It can react with protein by Schiff-base formation (boundary 4) and should not belong to any of the eliminated mechanistic domains according to Protein binding by OASIS (boundary 5):
 - Michael addition (α,β -Aldehydes, Conjugated systems with electron withdrawing groups) (boundary 5)
 - SNAr (Activated aryl and heteroaryl compounds) (boundary 5)
 - Schiff base formation (Bis aldehydes, Di-substituted α,β -unsaturated aldehydes and Aromatic carbonyl compounds) (boundary 5)
- The chemical should be an “aldehyde” as required by Aquatic toxicity classification by ECOSAR (boundary 6) and not to be “imidazoles” (boundary 7).
- Another requirement is Log Kow to be ≥ 0.308 and ≤ 4.77 (boundary 8):

Data Gap Filling

Visualisation of whether a chemical is in the domain of the model

The image displays two screenshots of the QSAR Toolbox software interface, illustrating the domain classification process for a chemical. The left screenshot shows the 'Protein binding by OASIS' profiler, and the right screenshot shows the 'Aquatic toxicity classification by ECOSAR' profiler. Both screenshots feature a category tree with nodes containing icons with green checkmarks (indicating 'In domain') or red X marks (indicating 'Out of domain').

Key elements in the screenshots include:

- 1:** A yellow box highlights a node in the category tree, representing a boundary where a chemical is excluded from the domain.
- 2:** A yellow box highlights a node in the category tree, representing another boundary where a chemical is excluded from the domain.
- 3:** A yellow box highlights a node in the category tree, representing a boundary where a chemical is included in the domain.

The target chemical is out of the model domain due to:

- 1) Belonging to "Michael addition" mechanism by "Protein binding by OASIS" profiler, which have been eliminated from the domain (negated by logical "NOT") (boundary 5)
- 2) The chemical is not an "aldehyde" as requested by ECOSAR profiler (boundary 6).

⚠ The definitive designation for belonging or not to the domain is the collectible boundary (3) which is red crossed in case of "Out of domain" (green checked in case of "In domain")

Data Gap Filling

Enter Gap filling

1 Select the model

QSAR name	#	Predicted	Domain	Class	Database
Fathead minnow 96h LC50	3	No prediction	Out of domain		
QSAR DB Leadscope model					
Fathead minnow 96h LC50	14	No prediction	Out of domain		
QSAR DB SciQSAR model (1.0)					
IGC50 T. pyriformis Growth 48 h (1.0)	15	268 mg/L	In domain	Ciliatea	Aquatic OASIS
M1 - LC50 - Pimephales promelas (fathead minnow) (1.0)	16	71.6 mg/L	In domain		
M2 - LC50 - Pimephales promelas (fathead minnow) (1.0)	17	372 mg/L	In domain		
M3 - LC50 - Pimephales promelas (fathead minnow) (1.0)	18	865 mg/L	In domain		
M4 - LC50 - Pimephales promelas (fathead minnow) (1.0)	19	167 mg/L	In domain		

2 Click Run

3 Select Enter Gap filling

4 Click OK

Data Gap Filling Settings

- Only endpoint relevant

At this position:

- Select a cell with a rigid (bold) path
- Automated workflows 0
- Standardized workflows 0

Select QSAR method

- Enter Gap filling
- Predict selected chemical
- Predict all chemicals
- Predict chemicals in domain

Go to target chemical and call (Q)SAR;
 1. Select the model; 2. Click **Run**; 3. Select **Enter Gap filling**; 4. Click **OK**; Then you will be transferred automatically to **Gap filling** and can operate (not shown);

Data Gap Filling

Perform prediction for chemicals in domain (for selected chemical and all chemicals - analogically)

The screenshot displays the 'Details for 23 (Q)SAR models' dialog box with the following data:

QSAR name	#	Predicted	Domain	Class name	Database
Fathead minnow 96h LC	3	No prediction	Out of domain		
QSAR DB Leadscope model	4	No prediction	Out of domain		
Fathead minnow 96h LC	4	No prediction	Out of domain		
QSAR DB SciQSAR model	4	No prediction	Out of domain		
IGC50 T. pyriformis Growth 48 h (1.0)	15	268 mg/L	In domain	Ciliatea	Aquatic OASIS
M1 - LC50 - Pimephales promelas (fathead minnow) (1.0)	16	71.6 mg/L	In domain		
M2 - LC50 - Pimephales promelas (fathead minnow) (1.0)	17	372 mg/L	In domain		
M3 - LC50 - Pimephales promelas (fathead minnow) (1.0)	18	865 mg/L	In domain		
M4 - LC50 - Pimephales promelas (fathead minnow) (1.0)	19	167 mg/L	In domain		

The 'Select QSAR method' dialog box shows the following options:

- Enter Gap filling
- Predict selected chemical
- Predict all chemicals
- Predict chemicals in domain

At the bottom of the main window, the 'Data Gap Filling Settings' are shown:

- Only endpoint relevant
- At this position:**
 - Select a cell with a rigid (bold) path
 - Automated workflows: 0
 - Standardized workflows: 0

The 'Run' button is highlighted with a red callout box labeled '2'. The 'Predict chemicals in domain' radio button is highlighted with a red callout box labeled '3'. The 'OK' button is highlighted with a red callout box labeled '4'. The 'IGC50 T. pyriformis Growth 48 h (1.0)' model is highlighted with a red callout box labeled '1'.

1. Select the **QSAR model**; 2. Click **Run**; 3. Select **Predict Chemicals in domain**; 4. Click **OK**;

Data Gap Filling

Perform prediction for chemicals in domain

The screenshot displays the QSAR Toolbox interface during a Data Gap Filling workflow. The main workspace is a grid where each column represents a different chemical and each row represents a different endpoint. The endpoints are listed in the left sidebar under 'Ecotoxicological Information'.

Endpoint	1	2	3	4	5	6	7	8	9	10	11	
ICG50	79/100	M: 145 mg/L T: 268 (60.2+1.2E+03) mg/L Q: 268 (60.2+1.2E+03) mg/L	M: 31.7 mg/L	Q: 95.3 (22+412)...	M: 112 mg/L	M: 3.9 mg/L Q: 7.94 (1.68+37...	M: 14 mg/L	M: 7.96 mg/L	M: 8.2 mg/L Q: 13.1 (2.88+59...	M: 937 mg/L	Q: 134 (31+578)...	Q: 8.35 (1.75+39...
Intoxication	1/1											
Mortality	60/80	M: 10.5 mg/L	M: 6.62 mg/L	M: 7.77 mg/L					M: 3.19 mg/L		M: 20 mg/L	M: 5.01 mg/L
Physiology	19/22				M: 1.66 mg/L	M: 14.6 mg/L	M: 5.64 mg/L					

Outlook

- Background
- Keywords
- Objectives
- The exercise
- **Workflow of the exercise**
 - Input
 - Profiling
 - Data
 - Category definition
 - Data gap filling
 - QSAR model
 - **Export QSAR prediction**

Export QSAR results

- The QSAR predictions for the chemicals in the matrix can be exported into a file
- In the Endpoint tree **right click** on Tetrahymena pyriformis (for the endpoint IGC50 48h for Tetrahymena pyriformis) and **select** Export Data matrix from the context menu (see next three screen shots).

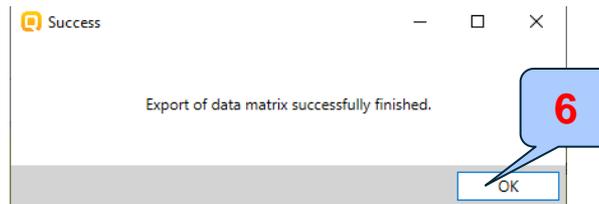
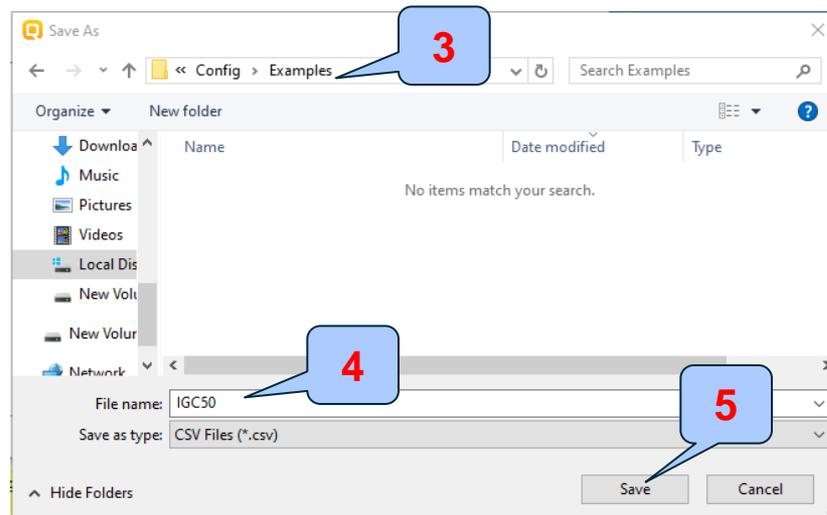
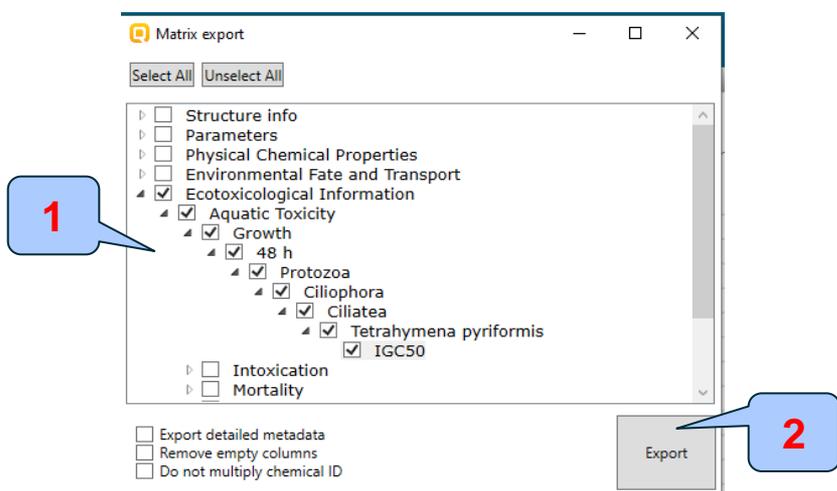
Export QSAR results

The screenshot displays the QSAR Toolbox interface. On the left, the 'Documents' panel shows a tree structure for 'Document 1' with various endpoints. The 'Data Gap Filling Settings' panel is also visible. The main workspace shows a 'Filter endpoint tree...' on the left and a grid of chemical structures and their corresponding data on the right. A context menu is open over a row in the endpoint tree, with 'Export Data matrix' selected. Callout boxes 1 and 2 highlight the right-click action and the menu selection respectively.

Endpoint	Value	Endpoint	Value	Endpoint	Value	Endpoint	Value	Endpoint	Value	Endpoint	Value	Endpoint	Value	Endpoint	Value
IGC50	79/108	M: 145 mg/L	T: 268 (60.2=1...	Q: 268 (60.2=1...	M: 7.96 mg/L	M: 8.2 mg/L	Q: 13.1 (2.88=59...	M: 937 mg/L	Q: 134 (31+578)...	Q: 8.35 (1.75+39...	M: 167 mg/L	M: 167 mg/L	M: 167 mg/L	M: 167 mg/L	M: 167 mg/L
Intoxication	171	M: 10.5 mg/L			56 mg/L	M: 14.6 mg/L	M: 5.64 mg/L	M: 3.19 mg/L		M: 20 mg/L	M: 5.01 mg/L				

1. Right click on the row of endpoint tree associated with predictions from the QSAR model; 2. Select **Export Data matrix** (see next screen shot).

Export QSAR results



1. The nodes from the tree associated with QSAR predictions which will be exported are selected with check marks; 2. Click **Export**; 3. Browse to save the file on your PC; 4. Give a name of the file; 5. Click **Save**; 6. Click **OK** when the file is exported.

Outlook

- Background
- Keywords
- Objectives
- The exercise
- **Workflow of the exercise**
 - Input
 - Profiling
 - Data
 - Category definition
 - Data gap filling
 - **Report**

Report

The screenshot displays the QSAR Toolbox software interface. The top menu bar includes 'Reports', 'Profiling', 'Data', 'Category definition', 'Data Gap Filling', and 'Report'. The 'Report' menu item is highlighted with a red box and labeled '1'. Below the menu bar, the 'Reports' sub-menu is open, showing 'Prediction Data Matrix', 'Category', 'QMRF', and 'SMI File'. The 'QMRF' option is highlighted with a blue box and labeled '2'. On the left side, the 'Documents' panel shows a tree view of chemical models, with 'Tetrahymena pyriformis' selected and highlighted in yellow, labeled '3'. The main window displays a list of QSAR models, with '[115] ECOSAR: GREEN ALGAE 96 h EC50 Growth Schiff Bases-Azomethine (1.0)' selected and highlighted in blue. The 'OK' button at the bottom of the model list is highlighted with a blue box and labeled '4'. The background shows a chemical structure and a table of results.

1. Go to **Report** module; 2. Click **QMRF**;
 3. Select the name of the user-defined QSAR model; 4. Click **OK**;

Report

The image illustrates the process of generating a report in the QSAR Toolbox. It shows the 'Customize report content and appearance' wizard with various customization options. The 'Generated report files' window displays the output files, including the QMRF report and the training set data file. The steps are numbered 1 through 6, corresponding to the instructions in the text box below.

1. Navigate through the Wizard to customize the report; 2. Select **Create report**; 3. Choose **QMRF report** and then **Open (4)** to create a PDF format of the report or click **Save as** if you want to save the file; 5. Choose **Training set** in order to create a MS Excel file (training set of the QSAR along with their data) or 6. Click **Save as**;

Report

QMRF report

IGC50 new

1 / 4

IGC50 new

A (Q)SAR model

1. (Q)SAR Identifier

- 1.1. (Q)SAR Identifier (title):
IGC50 new (v.1.0)
- 1.2. Other related models:
Not available
- 1.3. Software coding the model:
QSAR Toolbox 4.4.1

2. General information

- 2.1. Date of QMRF:
10-April-2020
- 2.2. QMRF author(s) and contact details:
Not available
- 2.3. QMRF update(s):
Not available
- 2.4. Date of the QMRF update(s):
Not available
- 2.5. Model developer(s) and contact details:
Not available
- 2.6. Date of model development and/or publication:
Not available
- 2.7. Reference(s) to main scientific papers and/or software package:
Not available
- 2.8. Availability of information about the model:
Not available
- 2.9. Availability of another QMRF for exactly the same model:
Not available

3. Defining the endpoint (OECD Principle 1)

IGC50 new

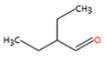
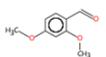
2 / 4

- 3.1. Species:
Tetrahymena pyriformis
- 3.2. Endpoint:
IGC50
- 3.3. Comment on the endpoint:
Not available
- 3.4. Endpoint units:
Not available
- 3.5. Dependent variable:
Not available
- 3.6. Experimental protocol:
Not available
- 3.7. Endpoint data quality and variability:
Not available

Training set

4. Defining the algorithm (OECD Principle 2)

4.1. Type of model:

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	
1			Training set #1			Training set #2			Training set #3			Training set #4			
2	Substance identity														
	Structure														
															
3															
4	CAS number			97-96-1			112-44-7			112-31-2			613-45-6		
5	Chemical name			Ethylbutanal			C11-H22-O			Decanal			2,4-DIMETHOXYBENZALDEHYD		
6	Other identifier														
7	SMILES			CCC(CC)C=O			CCCCCCCCC=O			CCCCCCCCC=O			COc1ccc(C=O)c(OC)c1		
8	Parameters			unit											
9															
10															
11	Profilers														
12															
13	Training set data and user gathered														
14	Training set data														
	sublevel	endpoint	value	unit	species, duration, test type, type of method, assay, strain, test guideline, year, reference	value	unit	species, duration, test type, type of method, assay, strain, test guideline, year, reference	value	unit	species, duration, test type, type of method, assay, strain, test guideline, year, reference	value	unit	species, duration, test type, type of method, assay, strain, test guideline, year, reference	
15					Tetrahymena pyriformis IGC50			Tetrahymena pyriformis IGC50			Tetrahymena pyriformis IGC50			Tetrahymena pyriformis IGC50	
16	Aquatic Toxicity	IGC50	112	mg/L		3.9	mg/L		8.2	mg/L		191	mg/L		
17															
18															

Congratulations!

- You have used the Toolbox to build a user-defined QSAR model.
- You now know another useful tool in the Toolbox.
- Continue to practice with this and other tools. Soon you will be comfortable dealing with many situations where the Toolbox is useful.