

OECD QSAR Toolbox v.3.4

Illustrating functionalities of
Query tool

Outlook

- **Background**
- Objectives
- Overview of Query tool
- Query tool window
- The exercise
- Workflow process
- Save QT searches

Background

- This is a step-by-step presentation designed to take the user through the functionalities of Query tool (QT) engine implemented in Toolbox

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Objectives

This presentation demonstrates a number of functionalities of the Query tool (QT):

- Identifying chemicals with specified structural fragments
- Identifying chemicals answering specific structural fragment criteria combined with parametric ranges
- Identifying chemicals answering specific combination of data, structural fragments and parametric data

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Overview of Query tool

Goal: Searching for chemicals by structure, sub fragments, phys-chem properties and experimental data

- **Chemical identifier search**

- CAS
- Name
- Molecular structures
- Tautomeric number

- **Parameter search**

- Calculated 2D parameters
- Calculated 3D parameters

- **Data search**

- Search for data and metadata within imported databases

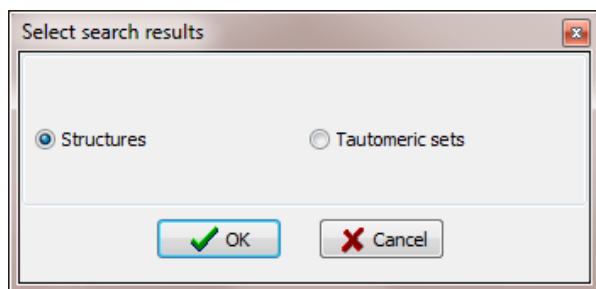
- **Extended search**

- Profiling
- Substructure
- Similarity

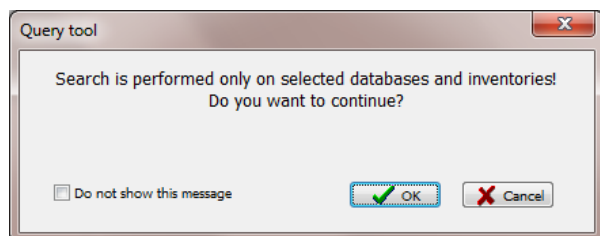
Overview of Query tool

Prerequisites

- The Query tool functionality search for single structures or tautomeric sets matching desired criteria. The user should select one of the proposed options



- The Query tool functionality search for chemicals within the selected databases and inventories only



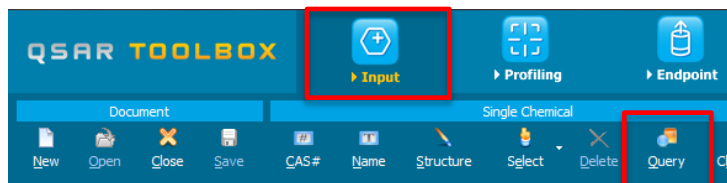
Overview of Query tool

Procedure for defining query

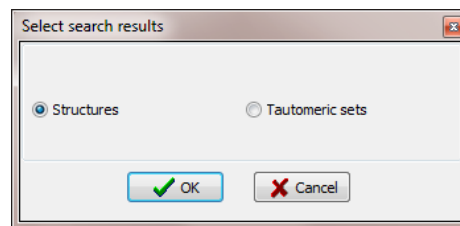
Step 1: Select databases/inventories of interest



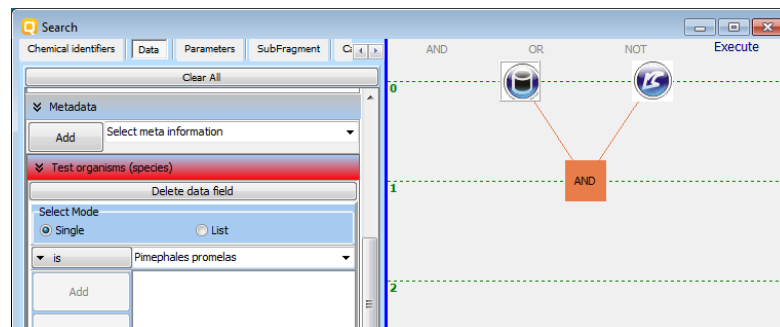
Step 2: Click on Query button



Step 3: Select structures/tautomeric sets



Step 4: Specify criteria for searching structures

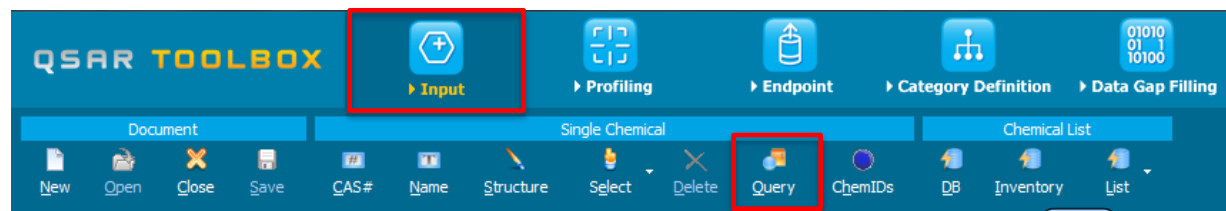


Outlook

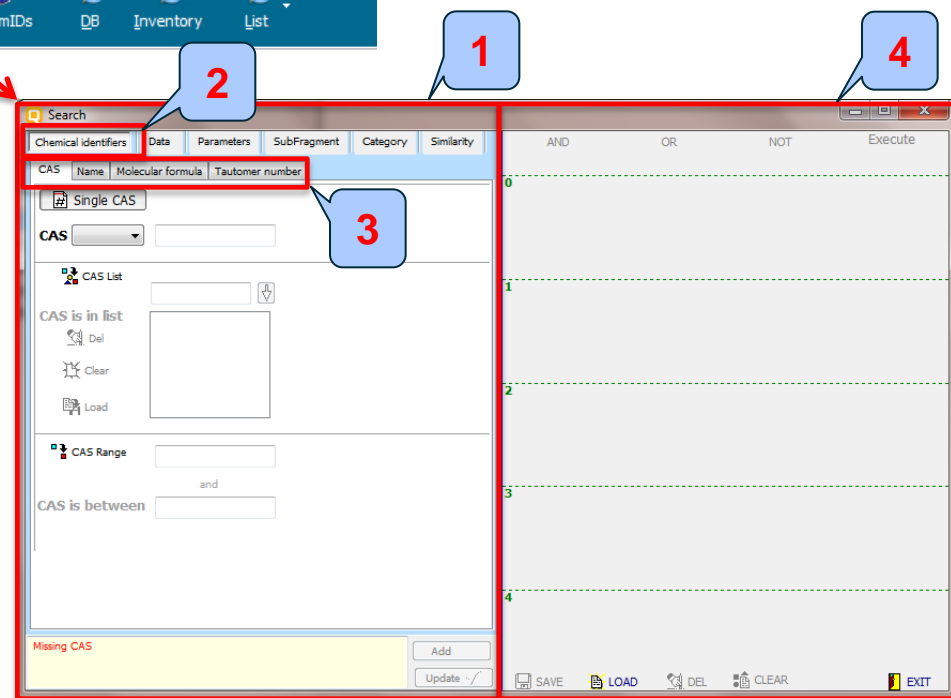
- Background
- Objectives
- Overview of Query tool
- **Query tool window**
- The exercise
- Workflow process
- Save QT searches

Query tool window

- The Query tool is easily accessible on the Toolbox input panel



- Query tool main components
 - Query edit panel (1)
 - search group panel (2)
 - available searches for selected group (3)
 - Query tree logic panel (4)



Outlook

- Background
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- Overview of Query tool
- Query tool window
- **The exercise**
- Workflow process
- Save QT searches

The Exercise

- In this exercise we will demonstrate the following queries:
 - Sub fragment search for:
 - *Substituted diphenyl amine (Example 1)*
 - *Aliphatic halogens (Example 2)*
 - Combination of Environmental Data (BCF) and 3D parameters (*Dmax*) (*Example 3*)
 - Combination of predefined category (Aldehydes) and ecotox data ($LC_{50} < 1\text{mg/l}$) (*Example 4*)
 - Combination of positive Ames; positive Carcinogenicity data and sub fragment search (*Epoxides*) (*Example 5*)
 - Combination of Skin sensitization data (EC 3) and predefined category (*Aldehydes*) (*Example 6*)

Outlook

- Background
- Objectives
- Overview of Query tool
- Query tool window
- The exercise
- **Workflow process**
- Save QT searches

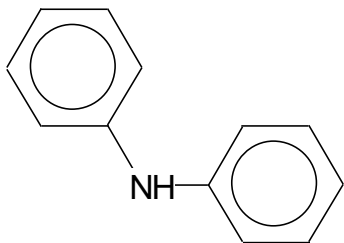
Sub fragment search for identifying chemicals

Substituted diphenyl amine

Example 1

Search for structures that meet the structural requirements:

- *Substituted diphenyl amine*



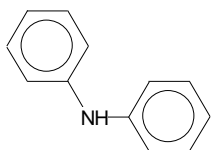
c1ccc(Nc2ccccc2)cc1

Sub fragment search for identifying chemicals

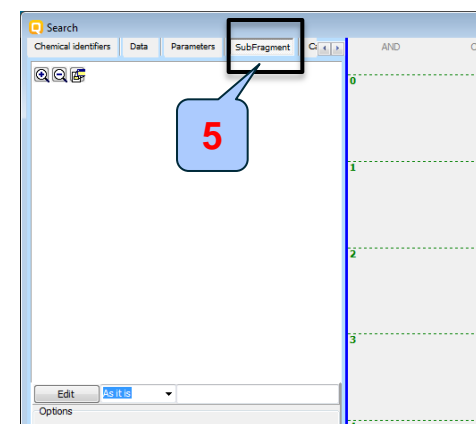
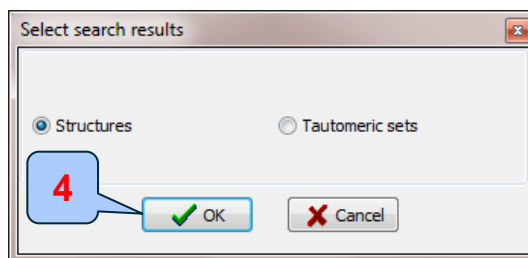
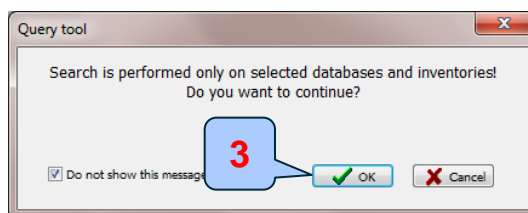
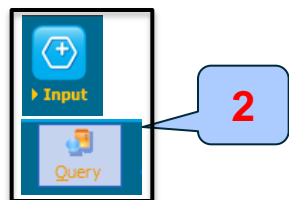
Procedure for defining

Example 1

- Substituted diphenyl amine



c1ccc(Nc2ccccc2)cc1



QT procedure starts with selecting databases/inventories used for searching the desired criteria:

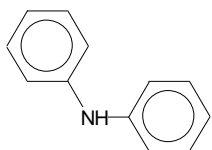
- Select** HPVC OECD inventory located under **Endpoint section**. No databases have been selected in this excirsize; 2. **Click** on Query button located under **Input** section; The message informs the user that search will be performed on selected databases or inventories only 3. **Click** OK. The window proposing two different options for searching (discrete or tautomeric sets) appears. By default "structures" is selected. In our case we are searching for single structures 4. **Click** OK 5. Query panel appears; 6. **Select** "Sub Fragment" panel

Sub fragment search for identifying chemicals

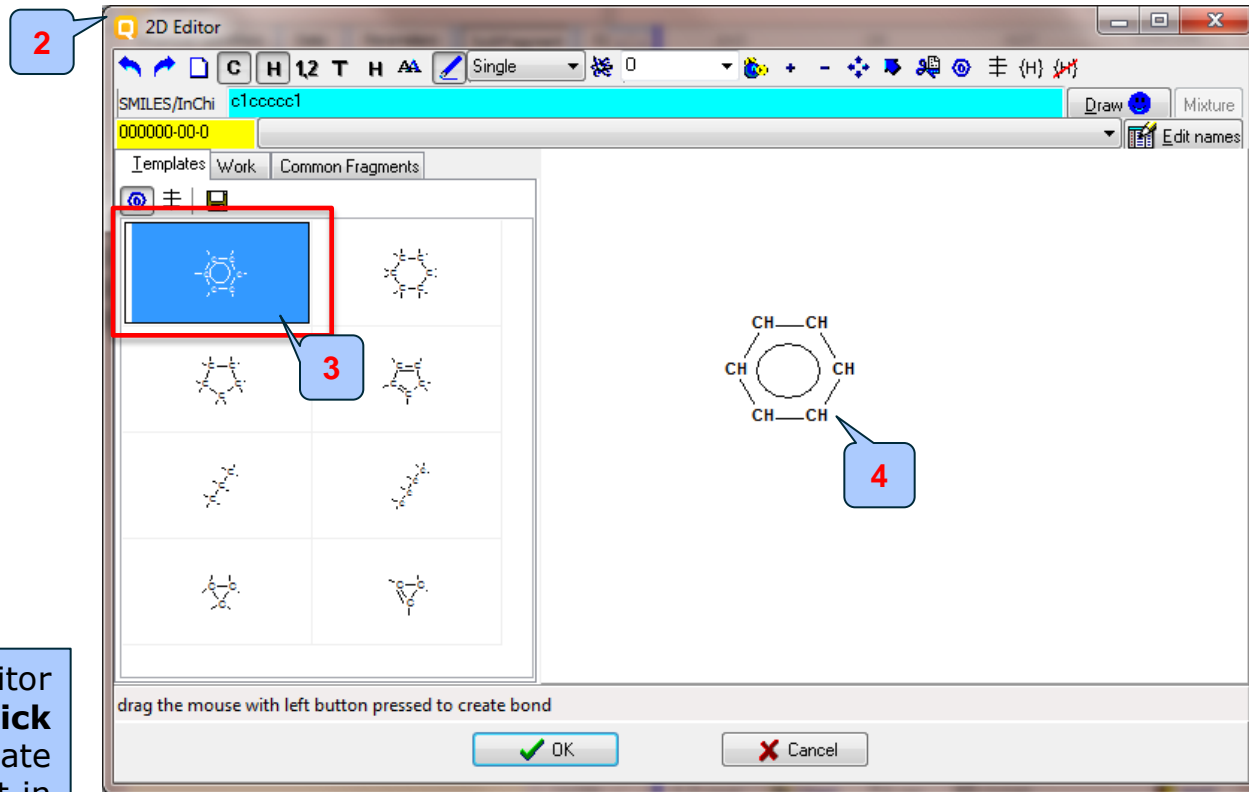
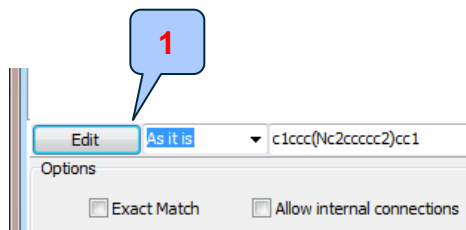
Procedure for defining

Example 1

- Substituted diphenyl amine



c1ccc(Nc2ccccc2)cc1



1. **Click** Edit button; 2. The 2D editor window appears; 3. Perform **left click** on the benzene ring from the Template panel 4. **Left click** on the blank plot in order to generate benzene fragment;

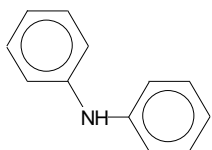
Continued on the next slide

Sub fragment search for identifying chemicals

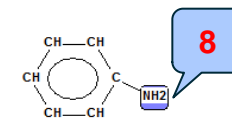
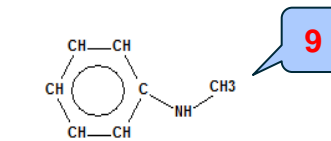
Procedure for defining

Example 1

- Substituted diphenyl amine



c1ccc(Nc2ccccc2)cc1

5. **Click** on the button of Single bond; 6. **Highlight** one of the C atom from the benzene ring and **drag** to generate single bond; 7. **Select** N atom from the list; 8. **Put** the selected N atom over the C atom from the single bond; 9. **Repeat** step 5 and **Draw** single bond to the N atom from NH2 group;

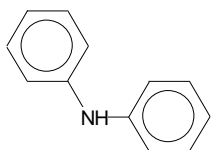
Continued on the next slide

Sub fragment search for identifying chemicals

Procedure for defining

Example 1

- Substituted diphenyl amine



c1ccc(Nc2ccccc2)cc1

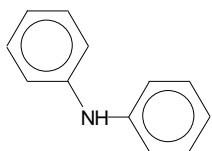
10. **Left click** over benzene ring from the template in order to take benzene ring 11. **Left click** over the C atom in order to define second benzene ring to the NH group 12. **Click Draw**; 13. **Click OK**

Sub fragment search for identifying chemicals

Procedure for defining

Example 1

- Substituted diphenyl amine



c1ccc(Nc2ccccc2)cc1

1. **Click** Add button; 2. The defined query appears on logic panel; 3. **Double click** over the query to execute it or **click** Execute button.

The screenshot shows the 'Search' window with the 'SubFragment' tab selected. The 'Edit' field contains the SMILES string c1ccc(Nc2ccccc2)cc1. The 'Options' section has 'Exact Match' and 'Allow internal connections' checked. The 'Add' button is highlighted with a red box and a callout '1'. The logic panel on the right shows the query added as a single condition, highlighted with a red box and a callout '2'. The 'Execute' button is highlighted with a red box and a callout '3'.

Sub fragment search for identifying chemicals

Procedure for defining

Example 1

- Substituted diphenyl amine

1

Structure

1 [target] 2 [target] 3 [target] 4 [target] 5 [target] 6 [target] 7 [target] 8 [target]

Substance Identity
Physical Chemical Properties
Environmental Fate and Transport
Ecotoxicological Information
Human Health Hazards

Structural criteria

1. The Query tool (QT) identified 26 chemicals matching the desired criteria

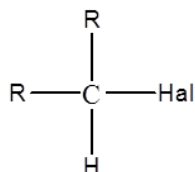
Sub fragment search for identifying chemicals

Aliphatic halogens

Example 2

Search for structures that meet the structural requirements:

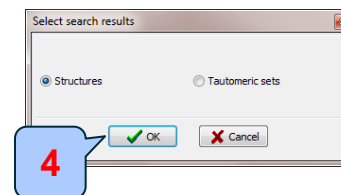
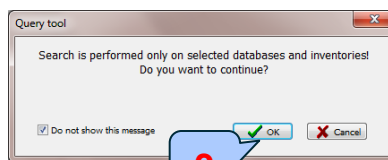
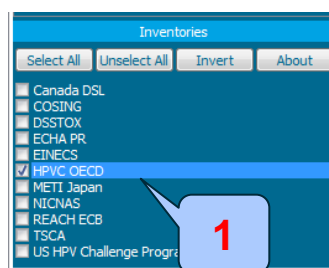
- *Aliphatic halogens*



R – Any atom except H

Hal – Cl, Br, I

- **HPVC OECD** inventory has been selected
- Search for discrete chemicals



1. **Select** the HPVC OECD inventory (no database has been selected in this case, only HPVC OECD) located under Endpoint section; 2. **Click** on Query button under Input section; 3. **Click** OK 4. **Click** OK in order to search for discrete chemicals

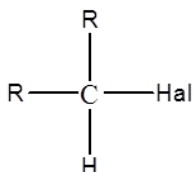
Sub fragment search for identifying chemicals

Aliphatic halogens

Example 2

Search for structures that meet the structural requirements:

- *Aliphatic halogens*



R – Any atom except H

Hal – Cl, Br, I

- **HPVC OECD** inventory has been selected
- Search for discrete chemicals

1. Query panel appears; 2. **Go** to SubFragment panel; 3. **Click** Edit button; 4. 2D Editor window appears

The screenshot shows the QSAR Toolbox interface. The 'Search' window is active, with the 'SubFragment' tab selected. The '2D Editor' window is open, showing a grid of chemical fragments. Callout boxes 1, 2, 3, and 4 indicate the sequence of actions: 1. Query panel appears; 2. Go to SubFragment panel; 3. Click Edit button; 4. 2D Editor window appears.

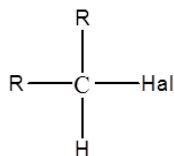
Sub fragment search for identifying chemicals

Aliphatic halogens

Example 2

Search for structures that meet the structural requirements:

- *Aliphatic halogens*

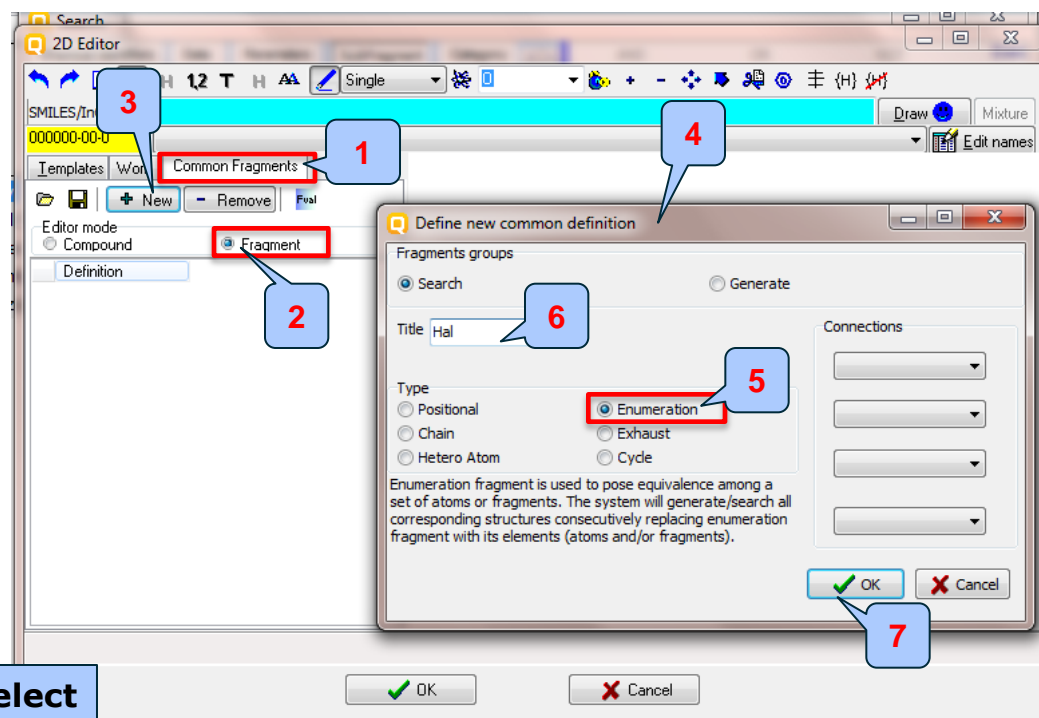


R – Any atom except H

Hal – Cl, Br, I

- Define common fragment Hal with three members (halogen atoms)

1. **Click** on Common fragments panel; 2. **Select** Fragment radio button; 3. **Click** New; 4. Additional window appears; 5. **Select** Enumeration type fragment; 6. **Define name** of the fragment (e.g. Hal); 7. **Click** OK



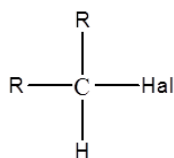
Sub fragment search for identifying chemicals

Aliphatic halogens

Example 2

Search for structures that meet the structural requirements:

- Aliphatic halogens



R – Any atom except H

Hal – Cl, Br, I

- Define common fragment Hal with three members (halogen atoms)

- The common fragment definition appears in the library with fragments;
- Click** on button with periodic table;
- Select** Cl atom;
- Click** Yes

The screenshot shows the '2D Editor' window. In the top toolbar, a button labeled 'Select atom from periodic table' is highlighted with a blue callout '2'. Below the toolbar, the 'Common Fragments' panel shows a definition for 'Hal' with a blue square icon, highlighted with a blue callout '1'. An inset window titled 'Periodic Table' is open, showing the periodic table with Chlorine (Cl) highlighted in red and a blue callout '3' pointing to it. At the bottom of the periodic table window, a red box highlights 'Selected element: Cl', and a blue callout '4' points to the 'Yes' button in the dialog box.

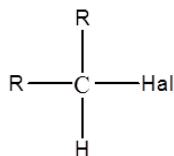
Sub fragment search for identifying chemicals

Aliphatic halogens

Example 2

Search for structures that meet the structural requirements:

- *Aliphatic halogens*

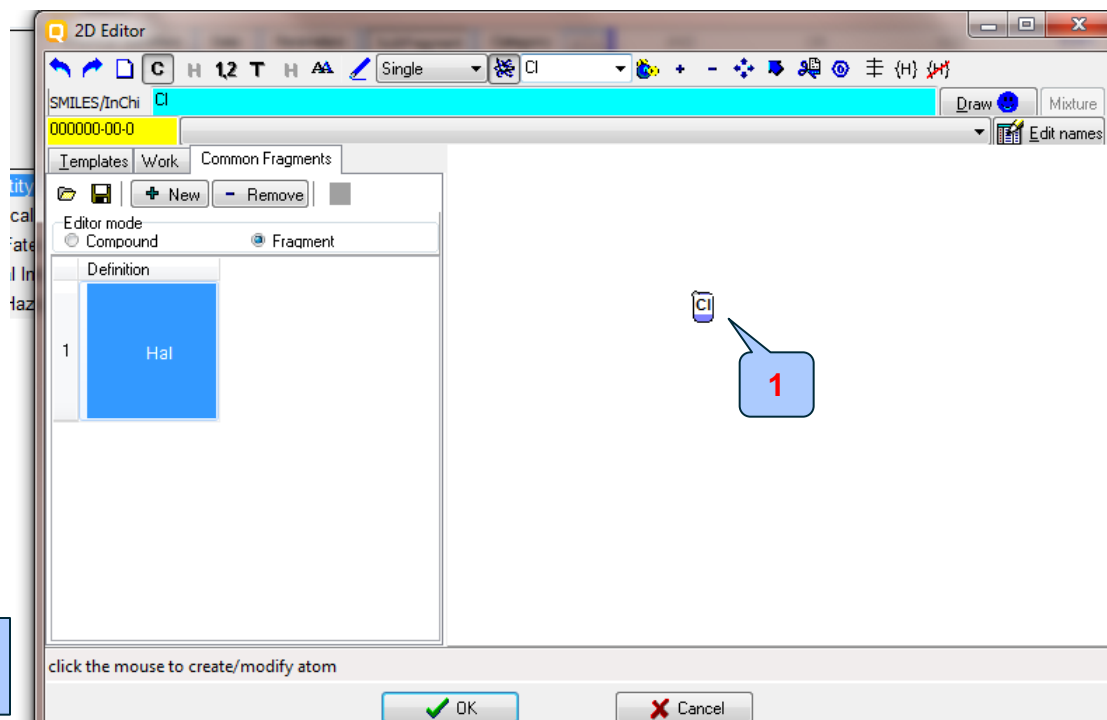


R – Any atom except H

Hal – Cl, Br, I

- Define common fragment Hal with three members (halogen atoms)

1. **Click** on the plot area in order to create Cl atom



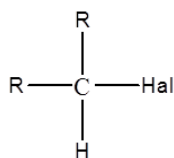
Sub fragment search for identifying chemicals

Aliphatic halogens

Example 2

Search for structures that meet the structural requirements:

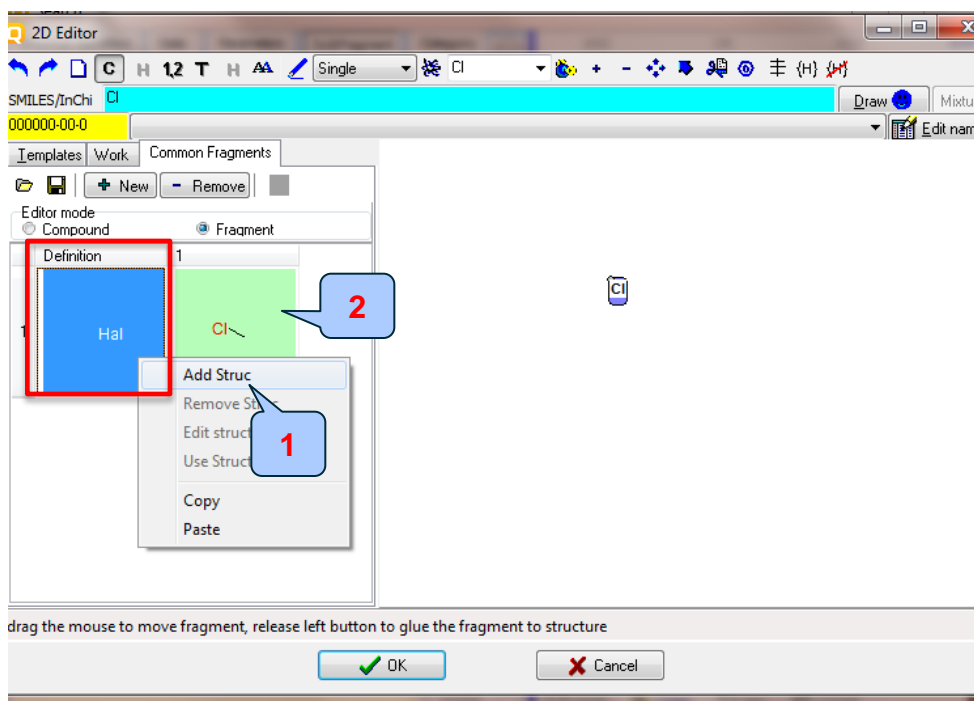
- *Aliphatic halogens*



R – Any atom except H

Hal – Cl, Br, I

- Define common fragment Hal with three members (halogen atoms)



1. **Right click** over the library with fragments and select "Add Struc"
2. The Cl atom appears on the right

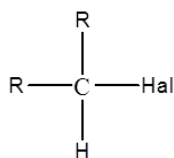
Sub fragment search for identifying chemicals

Aliphatic halogens

Example 2

Search for structures that meet the structural requirements:

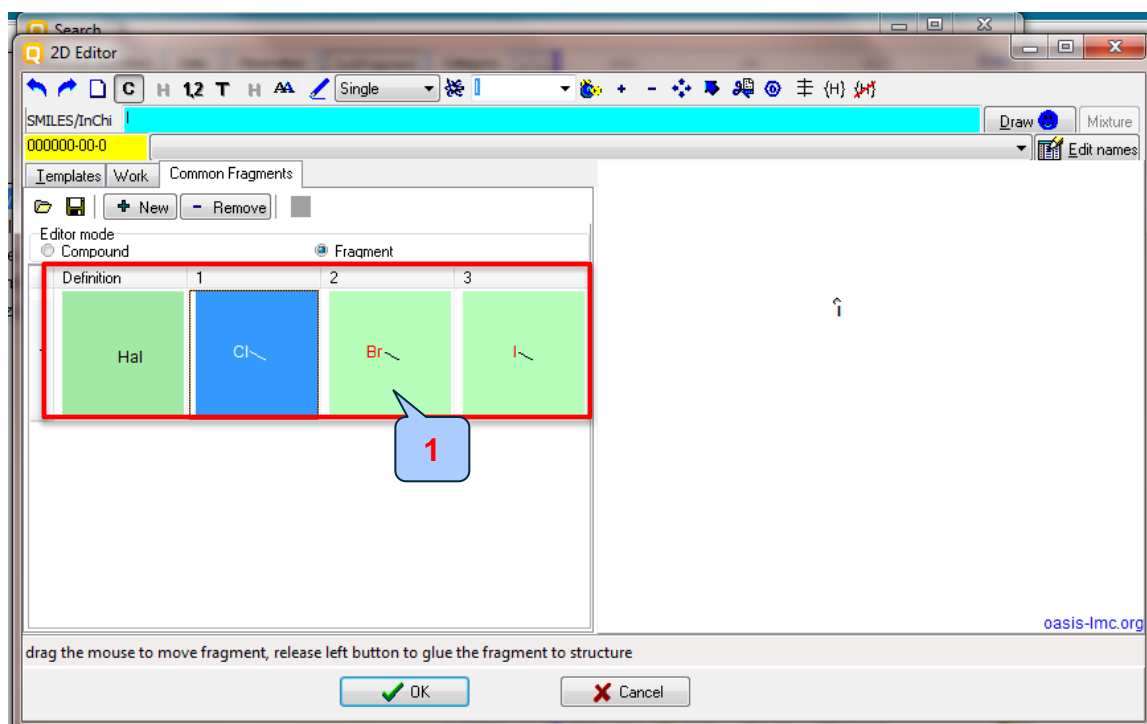
- Aliphatic halogens*



R – Any atom except H

Hal – Cl, Br, I

- Define common fragment Hal with three members (halogen atoms)



1. Add the other two halogen atoms (Br and I) following steps shown on slides (#25-27)

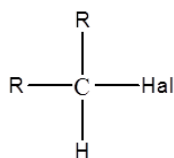
Sub fragment search for identifying chemicals

Aliphatic halogens

Example 2

Search for structures that meet the structural requirements:

- Aliphatic halogens



R – Any atom except H

Hal – Cl, Br, I

- Define fragment R including any type atom except H atom

The screenshot shows the '2D Editor' window with the 'Common Fragments' table. The table has three columns: 'Definition', '2', and '3'. The first row contains 'Hal', 'Cl', and 'Br'. A red callout box '1' points to the '+ New' button. A second dialog box, 'Define new common definition', is open. It has a 'Title' field containing 'Anyatom' (callout '3'), a 'Type' section with 'Enumeration' selected (callout '2'), and 'OK' and 'Cancel' buttons (callout '4').

1. **Click** New; 2. **Select** Enumeration type fragment; 3. **Define name** of the fragment (e.g. Any atom); 4. **Click** OK

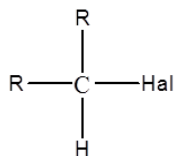
Sub fragment search for identifying chemicals

Aliphatic halogens

Example 2

Search for structures that meet the structural requirements:

- Aliphatic halogens



R – Any atom except H

Hal – Cl, Br, I

- Define fragment R including any type atom except H atom

1

2

3

4

- The definition appears in list with fragments
- Click on the periodic table button
- Select "Any Atom" from the pop-up list
- Click Yes

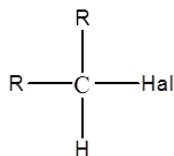
Sub fragment search for identifying chemicals

Aliphatic halogens

Example 2

Search for structures that meet the structural requirements:

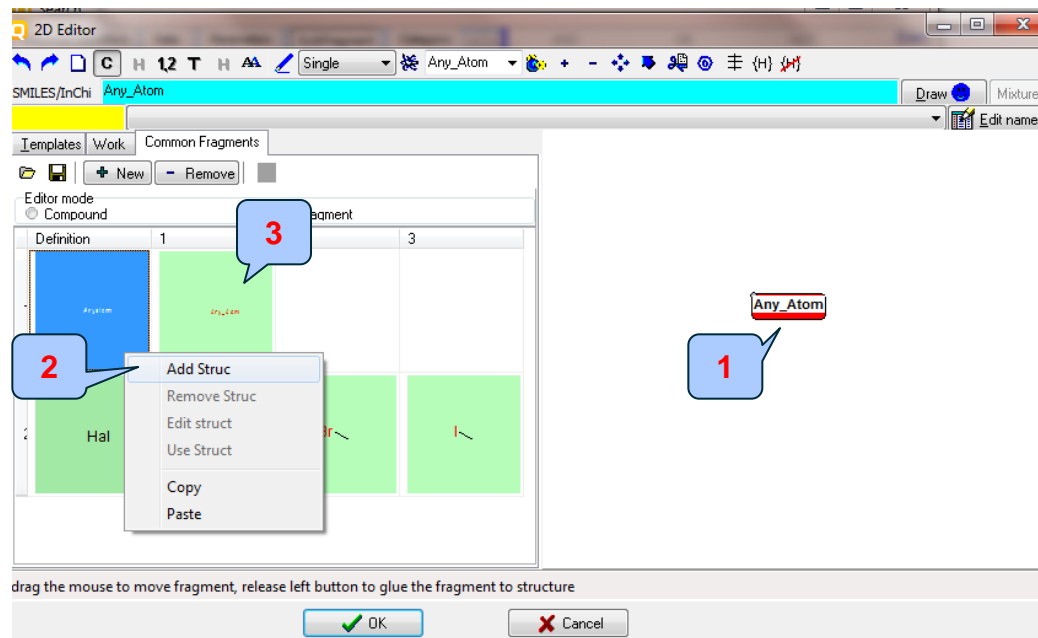
- Aliphatic halogens*



R – Any atom except H

Hal – Cl, Br, I

- Define fragment R including any type atom except H atom



- 1. Click** on the plot in order to create the fragment
- 2. Right click** over the definition and select "Add Struc"
- The fragment appears on the right

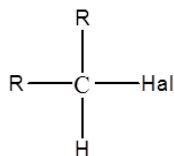
Sub fragment search for identifying chemicals

Aliphatic halogens

Example 2

Search for structures that meet the structural requirements:

- Aliphatic halogens



R – Any atom except H
Hal – Cl, Br, I

- Define skeleton of target compound

| Definition | 1 | 2 | 3 |
|------------|----------|---|---|
| Any atom | Any atom | | |
| Hal | | | |
| Cl | | | |
| Br | | | |
| I | | | |

- Click on Compound radio button
- Define the carbon skeleton of the defined query
- Use single bond button (help explanation is provided on slide #18)

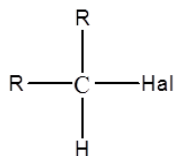
Sub fragment search for identifying chemicals

Aliphatic halogens

Example 2

Search for structures that meet the structural requirements:

- *Aliphatic halogens*



R – Any atom except H

Hal – Cl, Br, I

- Define skeleton of target compound

The screenshot shows the 2D Editor window with the following elements:

- SMILES/InChI field:** C[*Anyatom;Any_Atom][*Anyatom;Any_Atom][C]C
- Common Fragments panel:** A table with columns for Definition, 1, 2, and 3. The 'Any atom' fragment is selected in column 1.
- Chemical Structure:** A central carbon atom bonded to two methyl groups (CH3) and one 'Anyatom' group. Callout boxes 1, 2, and 3 indicate the selection and placement of fragments.

- 1. Left click** over the definition of Any atom fragment (the fragment is selected)
- 2. Put** it over CH₃ group
- 3. Repeat** again for the second CH₃ group

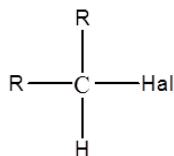
Sub fragment search for identifying chemicals

Aliphatic halogens

Example 2

Search for structures that meet the structural requirements:

- Aliphatic halogens



R – Any atom except H

Hal – Cl, Br, I

- Define skeleton of target compound

2D Editor

SMILES/InChI Cl[*Anyatom:Any_Atom][*Anyatom:Any_Atom][*Hal:Cl.Br]C

| Definition | 1 | 2 | 3 |
|------------|---------|----|---|
| Anyatom | Anyatom | | |
| Hal | Cl | Br | I |

Editor mode: Compound Fragment

drag the mouse with left button pressed to create bond

OK Cancel

1. **Left click** over the Hal fragment
2. **Put** it over CH₃ group in order to replace CH₃ group with Hal atoms

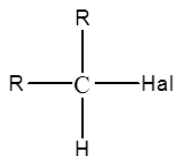
Sub fragment search for identifying chemicals

Aliphatic halogens

Example 2

Search for structures that meet the structural requirements:

- *Aliphatic halogens*



R – Any atom except H

Hal – Cl, Br, I

- Define skeleton of target compound

2D Editor

SMILES/InChI C[*Anyatom,Any_Atom][*!Anyatom,Any_Atom][*!Hal,Cl,Br,I]C

Common Fragments

| Definition | 1 | 2 | 3 |
|------------|---------|----|---|
| Anyatom | Anyatom | | |
| Hal | Cl | Br | I |

click/drag with: left button to select; right button to move

OK Cancel

1. **Click** on the scissors button
2. **Erase** the free CH₃ group (by left button and drag)

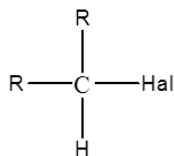
Sub fragment search for identifying chemicals

Aliphatic halogens

Example 2

Search for structures that meet the structural requirements:

- Aliphatic halogens



R – Any atom except H

Hal – Cl, Br, I

- Define skeleton of target compound

- Click on the {H} button in order to make the H atom connected to C-atom explicit
- Click over the C atom
- Click OK

The screenshot shows the 2D Editor interface. At the top, the SMILES/InChi string is C(H)('Anyatom:Any_Atom')['Anyatom:Any_Atom']Hal,Cl,Br,I. Below this, there is a table of fragments:

| Definition | 1 | 2 | 3 |
|------------|---------|----|---|
| Anyatom | Anyatom | | |
| Hal | Cl | Br | I |

The 'Hal' fragment is highlighted in blue. The 'OK' button at the bottom is also highlighted. Three callout boxes with numbers 1, 2, and 3 point to the {H} button, the C atom, and the OK button respectively.

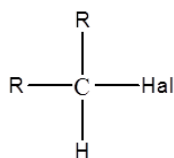
Sub fragment search for identifying chemicals

Aliphatic halogens

Example 2

Search for structures that meet the structural requirements:

- *Aliphatic halogens*



R – Any atom except H

Hal – Cl, Br, I

- Define skeleton of target compound

The screenshot shows the 'Search' window in the QSAR Toolbox. The 'SubFragment' tab is active, displaying a chemical structure of an aliphatic halogen (a carbon atom bonded to a hydrogen atom, another carbon atom, and a halogen atom). A blue callout box labeled '1' points to this structure. Below the structure, the search query is defined as: C(H)(*!Anyatom;Any_Atom)(*!Anyatom;Anyatom;Any_Atom)!Hal;Cl,Br,I. A blue callout box labeled '2' points to the 'Add' button. The search results pane on the right shows a single result, with a blue callout box labeled '3' pointing to the search icon.

1. The definition of aliphatic halogens appears on the blank plot
2. **Click** Add button
3. **Double click** on the query to execute it

Sub fragment search for identifying chemicals

Aliphatic halogens

Example 2

- Aliphatic halogens

The screenshot shows the QSAR Toolbox software interface. On the left, a document list shows a query result of 44 chemicals. The central workspace displays a table with 8 columns, each labeled '1 [target]' through '8 [target]'. Below the table, a chemical structure diagram shows a central carbon atom bonded to R, Hal, and H, with another R group attached. A red box highlights this diagram, and a red arrow points from it to a specific chemical structure in the table, which is also highlighted with a red box. A callout box with the number '1' points to the document list.

1. The Query tool (QT) identified 44 chemicals matching the desired criteria

Sub fragment search for identifying chemicals

BCF and (Dmax)

Example 3

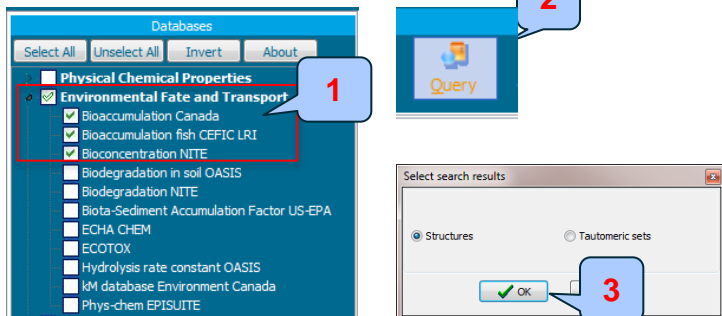
- Structures search criteria
 - Endpoint is BCF
 - 3D parameter – minimum value of Diameter maximum $>15 \text{ \AA}$

Sub fragment search for identifying chemicals

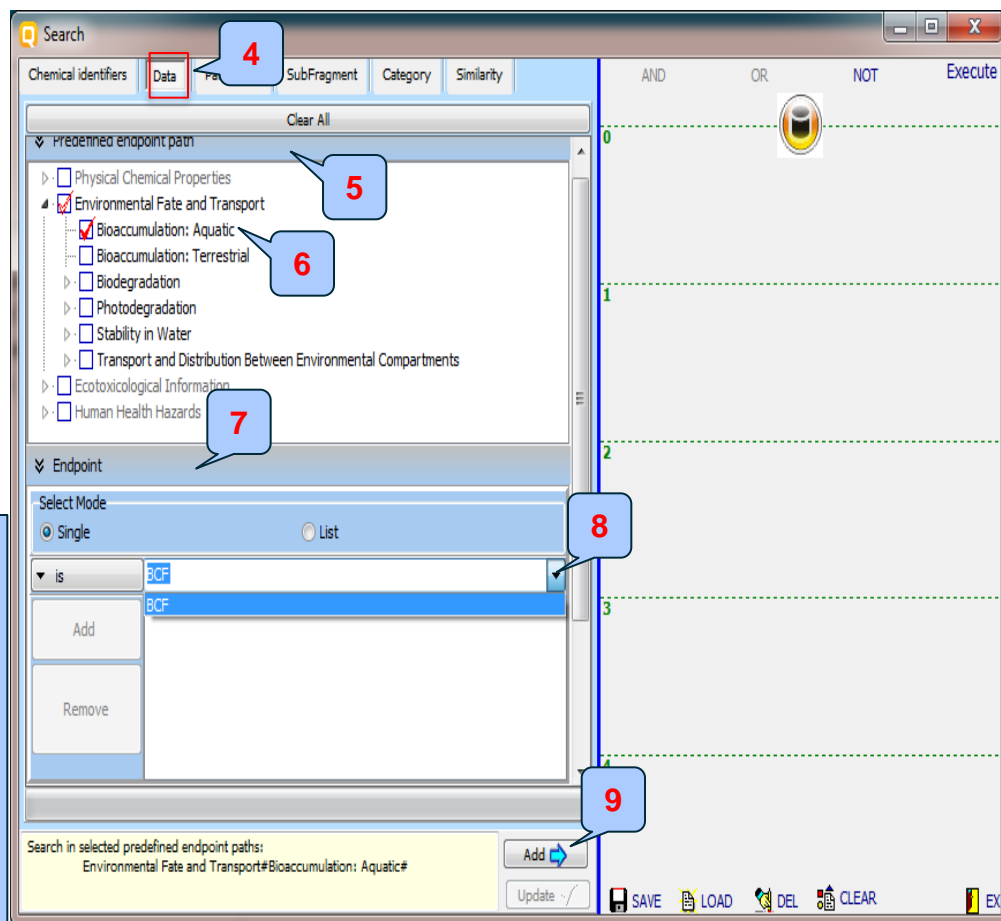
BCF and (D_{max})

Example 3

- Structures search criteria
 - Endpoint is BCF
 - 3D parameter – minimum value of Diameter maximum $> 15 \text{ \AA}$



- Select** databases including BCF data (Bioaccumulation Canada; Bioaccumulation fish CEFIC LRI and Bioconcentration NITE). No inventory has been selected in this exercise
- Click** on Query button
- Select** Structures
- Go** to Data panel
- Click on** Predefined endpoint path in order to expand it
- Select** Bioaccumulation: Aquatic
- Click** Endpoint tab in order to expand it
- Select** BCF from the appeared popup menu
- Click** Add button



Sub fragment search for identifying chemicals

BCF and (Dmax)

Example 3

- Structures search criteria
 - Endpoint is BCF
 - 3D parameter – minimum value of Diameter maximum $>15 \text{ \AA}$

The screenshot shows the 'Parameters' panel in the QSAR Toolbox. The 'Parameters' tab is selected, and the 'Diameter maximum' parameter is configured with a mean value of ≥ 15 Å. The 'Add' button is highlighted with a callout, indicating the next step in the process.

- Open Parameters panel
- Select Diameter maximum from the po-up list
- Specify qualifier " \geq " 15 in the Mean value field
- Click Add button

Sub fragment search for identifying chemicals

BCF and (D_{max})

Example 3

- Structures search criteria
 - Endpoint is BCF
 - 3D parameter – minimum value of Diameter maximum $>15 \text{ \AA}$

Both queries should be linked together by logical AND. For this purpose both queries should be selected first. How to do this:

1. Right click over the first query to select it (the selected boundary should become orange colored)



Selected query

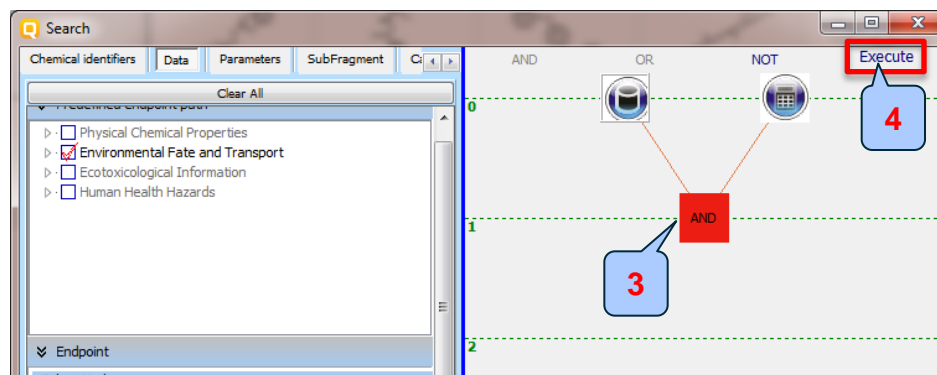
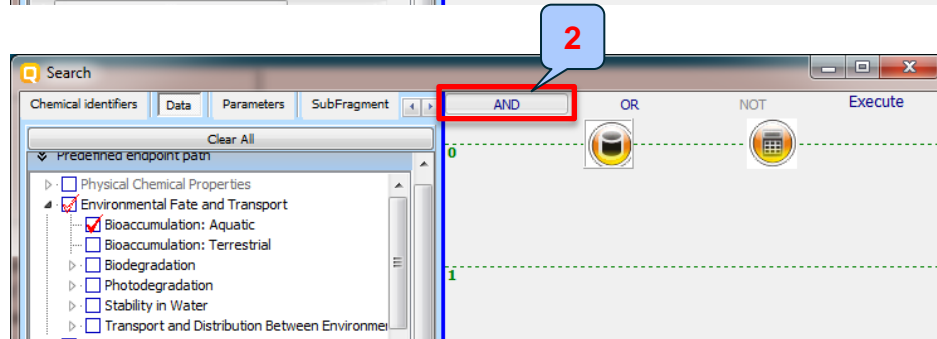
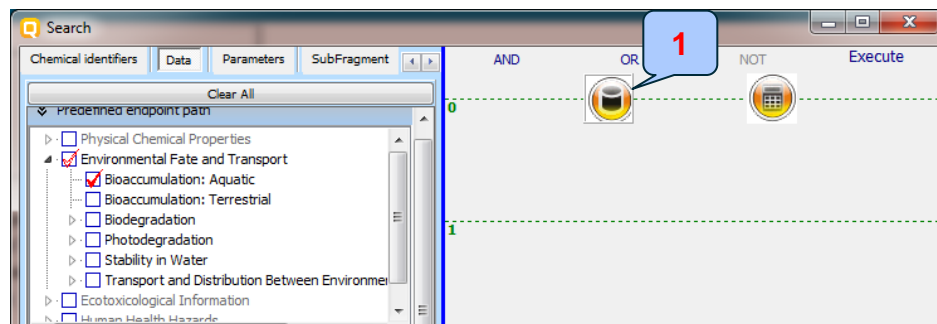


Not selected query

2. When the both queries are selected, **click AND** button

3. The two queries are combined by logical AND

4. Execute the AND query



Sub fragment search for identifying chemicals

BCF and (D_{max})

Example 3

The screenshot displays the QSAR Toolbox software interface. The top menu bar includes options like Input, Profiling, Endpoint, Category Definition, Data Gap Filling, and Report. Below the menu, there are tabs for Document, Single Chemical, and Chemical List. The main window is divided into several sections:

- Documents:** A list of 126 chemicals identified by a query. The first chemical is highlighted with a blue box and a red callout containing the number '1'. Below the list, the chemical structure of the first entry is shown.
- Filter endpoint tree...:** A tree view showing various endpoints such as Substance Identity, Physical Chemical Properties, Environmental Fate and Transport, Ecotoxicological Information, Human Health Hazards, and Profile.
- Data Matrix:** A table with 5 columns labeled '1 [target]', '2 [target]', '3 [target]', '4 [target]', and '5 [target]'. Each column contains a chemical structure. A red box highlights these five structures.

The Query tool (QT) identified 127 chemicals matching the desired criteria. The list of identified chemicals appear automatically on data matrix. Number of found chemicals is marked in the name of the document (1). In order to check the correctness of the performed query search, the user should calculate D_{\max} for the list of chemicals and to gather BCF data for them. The last two steps are presented on the next two slides

Sub fragment search for identifying chemicals

BCF and (Dmax)

Example 3

1. Right click over the endpoint tree; **2. Select Show hidden**; **3. Open** the 3D parameters **4. Find** Diameter maximum and right click on it; **5. Select "Calculate Diameter maximum for all chemicals"** from the appeared menu; **6. Right click** over the Diameter maximum row and select **Sort values by Ascending** order.

The 3D parameters table shows the following data for Diameter maximum:

| | | | | | |
|------------------|-------------------|-----------------|---------------|-----------------|-----------------|
| Diameter maximum | 15.2(14.7;15.7) Å | 16.3(13;20.3) Å | 16(14;16.8) Å | 19(14.5;27.1) Å | 16.9(14;21.3) Å |
|------------------|-------------------|-----------------|---------------|-----------------|-----------------|

The context menu for sorting values is shown with the following options:

- Sort (targets priority)
- Sort
- Sort
- Function...
- Export CAS list
- Export
- Copy path

The 'Sort' option is selected, and the 'Ascending' order is chosen.

Sub fragment search for identifying chemicals

BCF and (Dmax)

Example 3

The screenshot displays the QSAR Toolbox interface. The top menu bar includes 'Input', 'Profiling', 'Endpoint', 'Category Definition', 'Data Gap Filling', and 'Report'. The toolbar below the menu has sections for 'Document', 'Single Chemical', and 'Chemical List'. The 'Documents' pane on the left shows a tree view with 'Query result' entries. The 'Filter endpoint tree...' pane in the middle shows a list of parameters, including 'Substance Identity', 'Parameters' (with sub-items '2D' and '3D'), 'Calculated heat of formation', 'Diameter effective', 'Diameter maximum', 'Diameter minimum', 'Dipole moment', 'Electronegativity', and 'GAP Energy'. The results table on the right shows a single entry for a target chemical with a chemical structure and a list of SMILES strings. A red box highlights one of the SMILES strings, and a red arrow points from a text box below to this string.

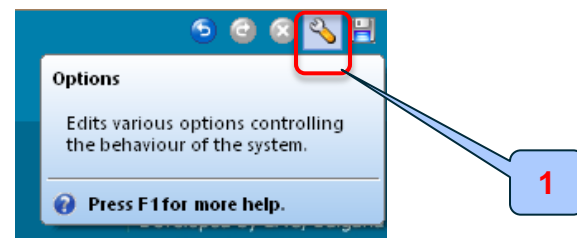
The following message could be displayed if the SMILES of a chemical has length higher than 60 symbols. This could be resolved by changing the Calculation options (see next slide)

Sub fragment search for identifying chemicals

BCF and (Dmax)

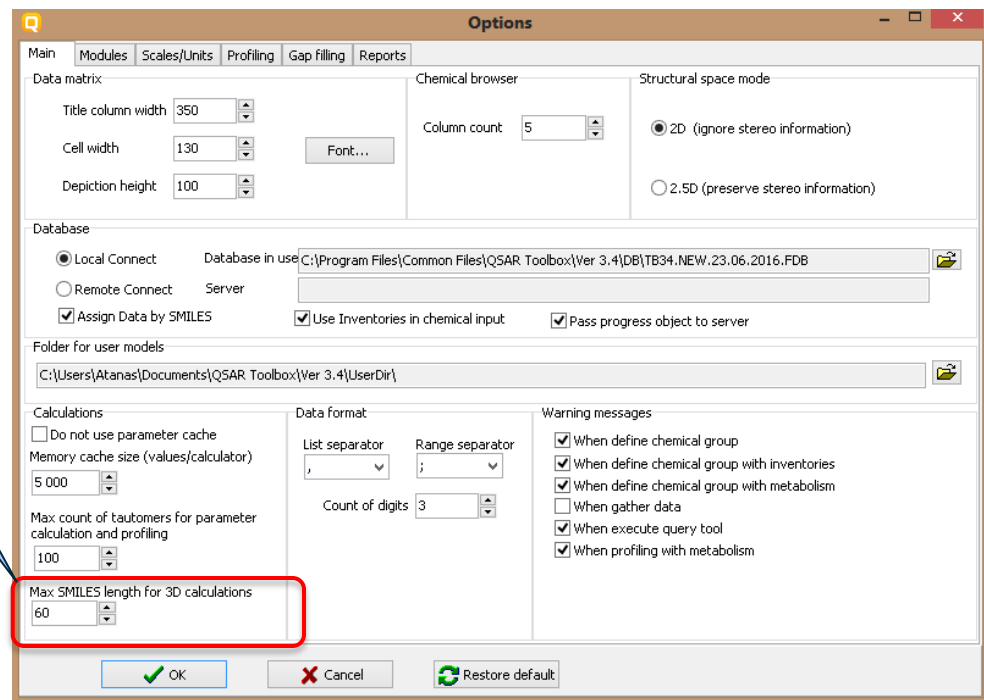
Example 3

1. Press **Options** button.



2

2. Change the **max SMILES length for 3D calculations** from 60 to 100.



Sub fragment search for identifying chemicals

BCF and (Dmax)

Example 3

The screenshot shows the QSAR Toolbox interface with the 'Filter endpoint tree...' window open. The 'Parameters' section is expanded to show 'Diameter maximum' selected. The results table below shows values for five targets:

| Parameter | 1 [target] | 2 [target] | 3 [target] | 4 [target] | 5 [target] |
|------------------|---------------|-----------------|-----------------|-------------------|-------------------|
| Diameter maximum | 15(12.5;17) Å | 15(14.3;16.2) Å | 15.1(14.5;16) Å | 15.1(12.1;18.1) Å | 15.2(14.7;15.7) Å |

Recalculate **the diameter maximum** as done in the previous slides.

Sub fragment search for identifying chemicals

BCF and (Dmax)

Example 3

| Endpoint | CAS | Structure | Value | Author |
|-------------------------------------|-----|-----------|--------------|--------|
| <input checked="" type="checkbox"/> | BCF | 120-78-5 | 7.2 L/kg wet | |
| <input checked="" type="checkbox"/> | BCF | 120-78-5 | 7.2 L/kg wet | |
| <input checked="" type="checkbox"/> | BCF | 78-42-2 | 6.5 L/kg wet | |
| <input checked="" type="checkbox"/> | BCF | 78-42-2 | 6.5 L/kg wet | |
| <input checked="" type="checkbox"/> | BCF | 78-42-2 | 22 L/kg wet | |
| <input checked="" type="checkbox"/> | BCF | 78-42-2 | 22 L/kg wet | |
| <input checked="" type="checkbox"/> | BCF | 298-07-7 | 2.4 L/kg wet | |
| <input checked="" type="checkbox"/> | BCF | 298-07-7 | 2.4 L/kg wet | |

1. Databases are already selected, **Click** gather data
2. **Click** OK
3. **Click** Select one
4. **Click** OK
5. Data appear on data matrix
6. All 127 chemicals have BCF data

Sub fragment search for identifying chemicals

LC 50 and predefined category (Aldehydes)

Example 4

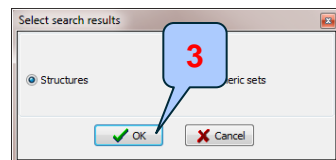
- Structures search criteria
 - Endpoint: LC 50 <1 mg/l
 - Fish: *P.promelas*
 - Effect: *Mortality*
 - Predefined category:
aldehydes

Sub fragment search for identifying chemicals

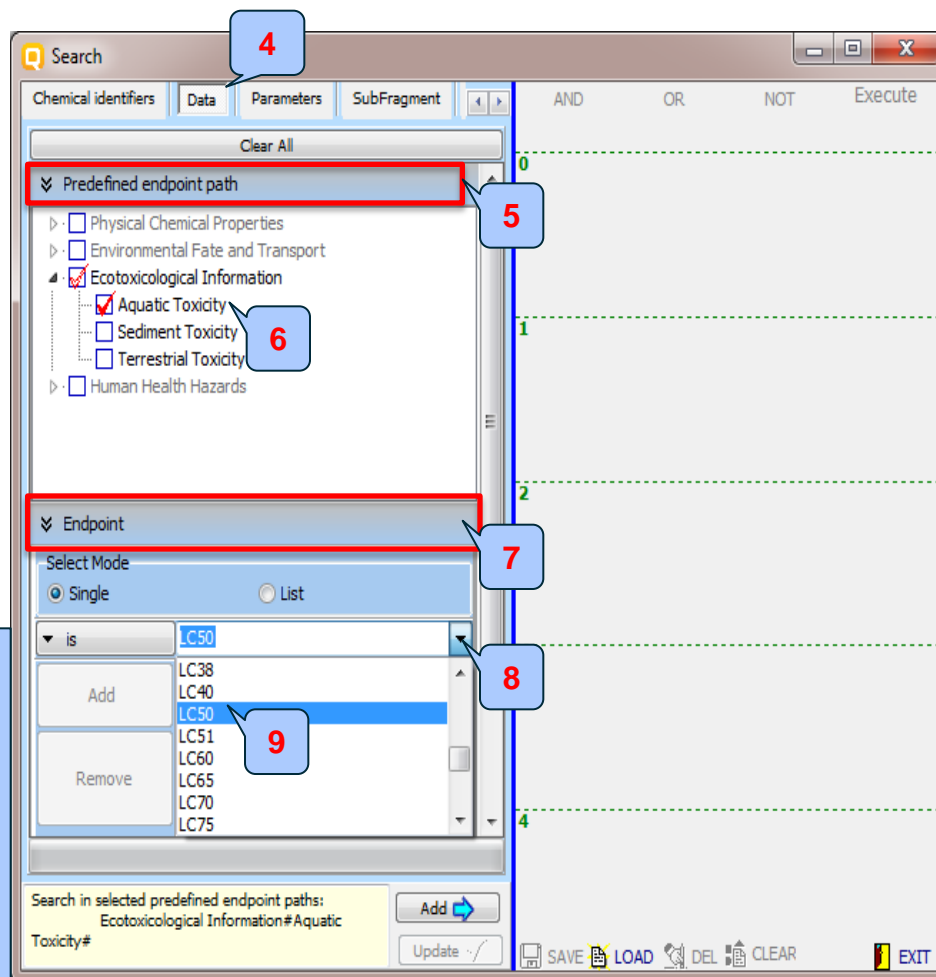
LC 50 and predefined category (Aldehydes)

Example 4

- Structures search criteria
 - Endpoint: LC 50 < 1 mg/l
 - Fish: *P.promelas*
 - Effect: *Mortality*
 - Predefined category: *aldehydes*



- Select** databases related to LC50 data (Aquatic ECETOC; aquatic Japan MoE; Aquatic OASIS; ECOTOX). No inventories has been selected in this case.
- Click** on Query tool button
- Select** Structures
- Go** to Data panel
- Open** Predefined endpoint path in order to expand it
- Open** Ecotoxicological Information and **select** Aquatic Toxicity
- Open** Endpoint tab
- Open** pop-up menu
- Select** LC50



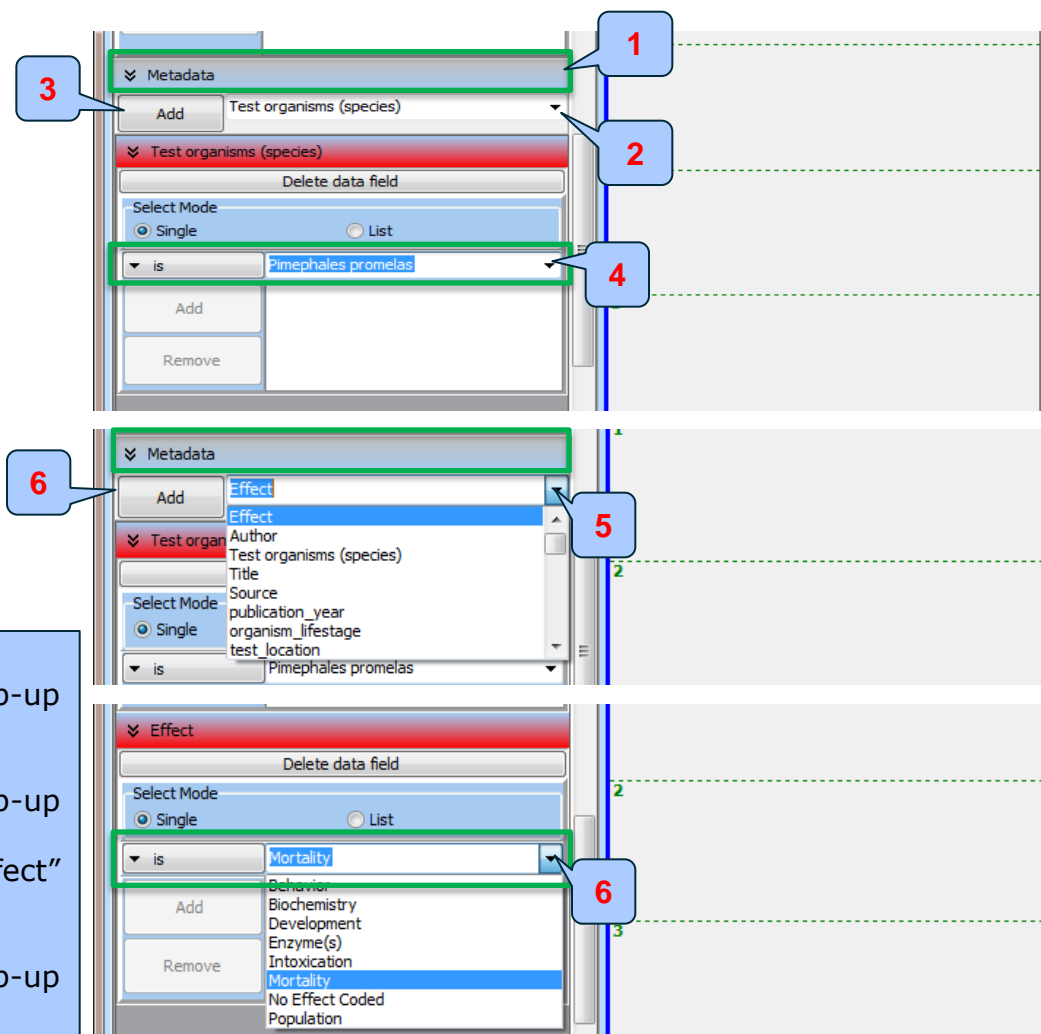
Continued on next slide

Sub fragment search for identifying chemicals

LC 50 and predefined category (Aldehydes)

Example 4

- Structures search criteria
 - Endpoint: LC 50 <1 mg/l
 - Fish: *P.promelas*
 - Effect: *Mortality*
 - Predefined category: *aldehydes*



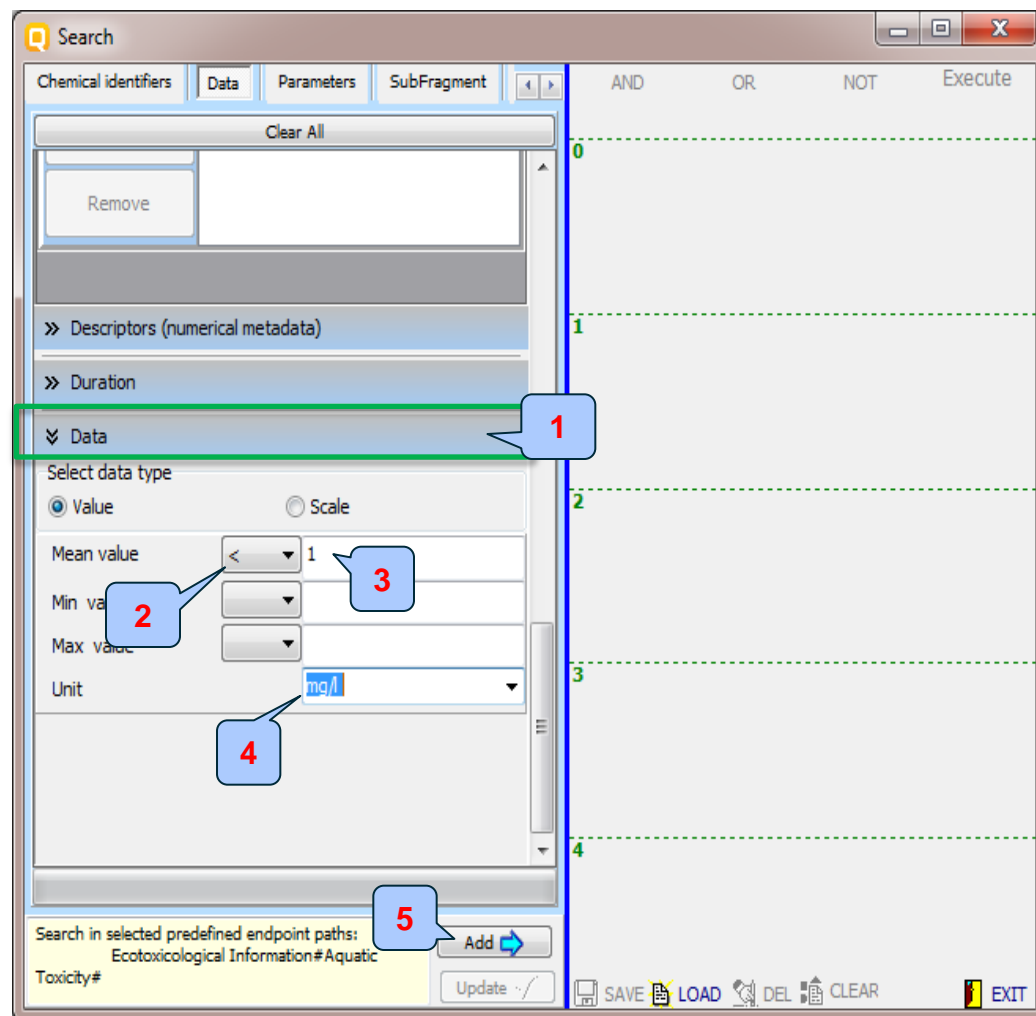
- 1. Open** Metadata field
- 2. Select** "Test organism (species)" from pop-up menu
- 3. Click** Add
- 4. Select** *Pimephales promelas* from pop-up menu
- 5. Go back** to Metadata field and select "Effect" from the pop-up menu
- 6. Click** Add
- 7. Select** Mortality from the appeared pop-up menu

Sub fragment search for identifying chemicals

LC 50 and predefined category (Aldehydes)

Example 4

- Structures search criteria
 - Endpoint: LC 50 <1 mg/l
 - Fish: *P.promelas*
 - Effect: *Mortality*
 - Predefined category: *aldehydes*



- 1. Open** Data panel
- 2. Open** qualifiers from Mean value and select <
- 3. Type** 1 in the blank field
- 4. Select** mg/l from the list with units
- 5. Click** Add

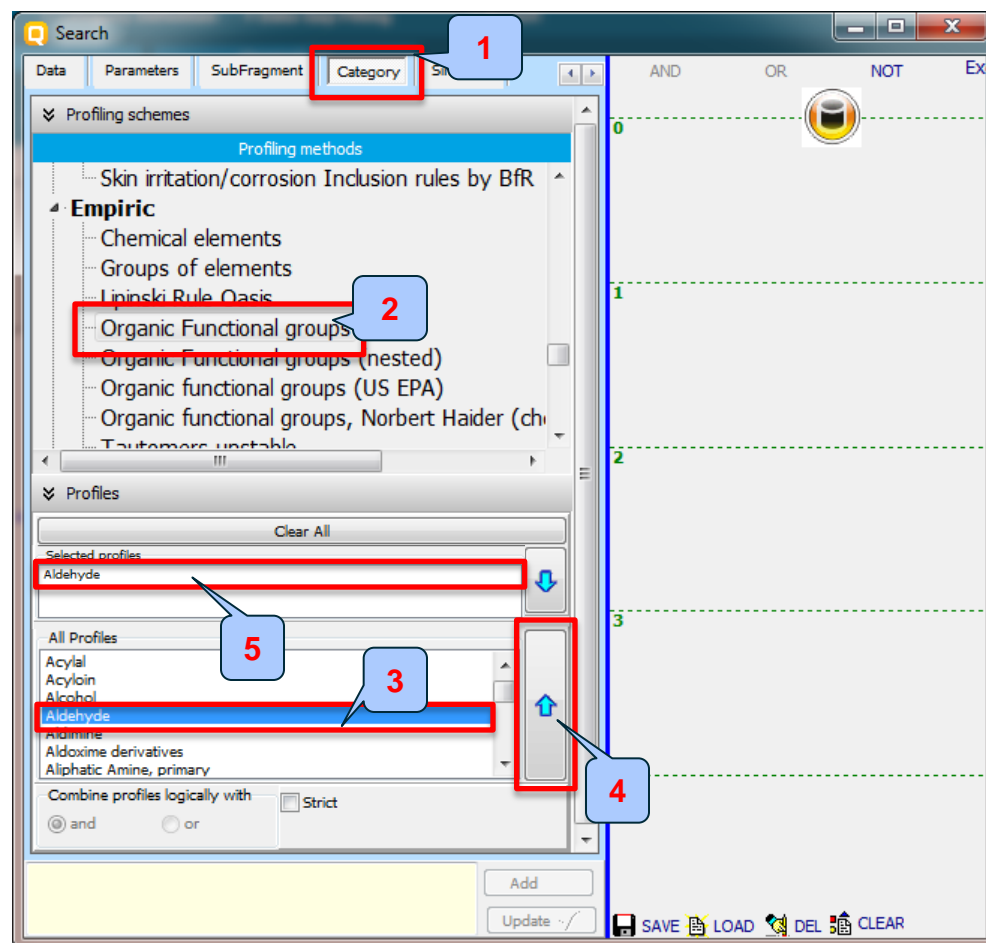
Sub fragment search for identifying chemicals

LC 50 and predefined category (Aldehydes)

Example 4

- Structures search criteria
 - Endpoint: LC 50 <1 mg/l
 - Fish: *P.promelas*
 - Effect: *Mortality*
 - Predefined category: *aldehydes*

- Open** Category panel
- Find** Organic functional groups profiler from the list with profilers
- Find** Aldehyde
- Move** the selected category from panel "All profilers" to the panel "Selected profiles"
- The selected category appears in the panel "Selected profiles"



Sub fragment search for identifying chemicals

LC 50 and predefined category (Aldehydes)

Example 4

- Structures search criteria
 - Endpoint: LC 50 <1 mg/l
 - Fish: *P.promelas*
 - Effect: *Mortality*
 - Predefined category: *aldehydes*

- Click Add button.
 - The query with predefined category appears on the logic panel.
- The both queries should be combined by logical AND. Follow the steps explained on slide # 44
- Right click over first query to select it (slide # 42)
 - Click AND button
 - The two queries are combined by logical AND
 - Click Execute button in order to execute the query

The screenshot displays the QSAR Toolbox software interface. The top menu bar includes 'Data', 'Parameters', 'SubFragment', 'Category', and 'Similarity'. The main window is divided into several sections:

- Profiling schemes:** A tree view showing 'Profiling methods' and 'Empiric' categories. Under 'Empiric', there are sub-categories like 'Chemical elements', 'Groups of elements', 'Lipinski Rule Oasis', and 'Organic Functional groups'.
- Profiles:** A list of predefined profiles, including 'Aldehyde', 'Acetal', 'Acetoxy', 'Acid anhydride', 'Acid anhydride, mixed phosphonic', 'Acridine', 'Acridone/ Acridinimine', and 'Acrylamide'. The 'Aldehyde' profile is selected.
- Logic Panel:** A central area showing a logical query tree. It features nodes for 'AND', 'OR', and 'NOT'. A callout '4' points to the 'AND' button. A callout '3' points to the first query node. A callout '5' points to the combined 'AND' node. A callout '6' points to the 'Execute' button.
- Buttons:** At the bottom, there are buttons for 'Add', 'Update', 'SAVE', 'LOAD', 'DEL', 'CLEAR', and 'EXIT'. The 'Add' button is highlighted with a red box and a callout '1'.

Sub fragment search for identifying chemicals

LC 50 and predefined category (Aldehydes)

Example 4

The screenshot displays the QSAR Toolbox interface. The top menu bar includes 'Input', 'Profiling', 'Endpoint', 'Category Definition', 'Data Gap Filling', and 'Report'. The toolbar below contains icons for 'New', 'Open', 'Close', 'Save', 'CAS#', 'Name', 'Structure', 'Select', 'Delete', 'Query', 'ChemIDs', 'DB', 'Inventory', and 'List'. The main workspace is divided into several panels. On the left, the 'Documents' panel shows a tree view with 'Query result 7 chemicals' highlighted by a blue callout box with the number '1'. The middle panel shows the 'Filter endpoint tree...' and 'Structure' options. The right panel displays a 'Chemical List' with 7 columns, each labeled '[target]'. Each column contains a chemical structure and a corresponding LC50 value. The values are: M: 0.845 mg/L, 6.2...; M: 0.935 mg/L, 1.1...; M: 0.767 mg/L, 15...; M: 0.368 mg/L, 0.3...; M: 0.3 mg/L, 0.3(0...; M: 0.465 mg/L, >0...; M: <5 mg/L, 1.5(0...

The Query tool (QT) identified 7 chemicals matching the desired criteria. The list of identified chemicals appear automatically on the data matrix. Number of found chemicals is marked in the name of the document (1). In order to check the correctness of the performed query search the user should gather ecotox data and profile according to OFG Profiler. The last two steps are presented on the next two slides

Sub fragment search for identifying chemicals

LC 50 and predefined category (Aldehydes)

Example 4

The screenshot shows the QSAR Toolbox interface. On the left, the 'Databases' sidebar is expanded to 'Ecotoxicological Information', with 'Aquatic ECETOC' and 'Aquatic Japan MoE' selected. The 'Structure' viewer shows a chemical structure. The 'Data matrix' table has 7 columns labeled '1 [target]' through '7 [target]'. A red box highlights a row for 'Pimephales promelas' with values: (7/15), M: 0.845 mg/L, 0.8...; M: 0.935 mg/L, 0.9...; M: 0.767 mg/L, 0.7...; M: 0.368 mg/L, 0.3...; M: 0.3 mg/L, 0.3(0...; M: 0.465 mg/L; M: <5 mg/L, 1(0.9;... .

Numbered callouts indicate the steps:

1. Databases are already selected, **Click** gather data
2. **Click** OK
3. **Click** Select one
4. **Click** OK
5. Data appear on data matrix answering the following criterias:
 LC50 < 1mg/l
 Effect: Mortality
 Test species: *P.promelas*
 Aldehydes by OFG

Sub fragment search for identifying chemicals LC 50 and predefined category (Aldehydes)

Example 4

The screenshot displays the QSAR Toolbox interface during the Profiling step. The top navigation bar includes 'Input', 'Profiling', 'Category Definition', 'Data Gap Filling', and 'Report'. The left sidebar shows 'Profiling methods' and 'Empiric' options. The main area shows a table of 7 target chemicals with their structures and profiles. A red box highlights the 'Organic Functional groups' section of the profiles, which lists 'Aldehyde' for all 7 targets. Numbered callouts 1-5 indicate key actions: 1. Click 'Profiling' in the top bar; 2. Click 'Unselect All' in the 'Profiling methods' section; 3. Check 'Organic Functional groups' in the 'Empiric' section; 4. Click 'Apply' in the 'Profiling methods' section; 5. Point to the 'Aldehyde' category in the profile table.

| | 1 [target] | 2 [target] | 3 [target] | 4 [target] | 5 [target] | 6 [target] | 7 [target] |
|------------------------------|---|----------------------------------|---|---|--|---------------------------|----------------------------------|
| Structure | | | | | | | |
| Substance Identity | | | | | | | |
| Ecotoxicological Information | (7/29) M: 0.845 mg/L, 0.8... | M: 0.935 mg/L, 1.1... | M: 0.767 mg/L, 0.7... | M: 0.368 mg/L, 0.3... | M: 0.3 mg/L, 0.3(0... | M: 0.465 mg/L | M: <5 mg/L, 1(0.9;... |
| Profile | | | | | | | |
| Empiric | | | | | | | |
| Organic Functional groups | Aldehyde Aryl Aryl halide Phenol | Aldehyde Alkyl halide Aryl | Aldehyde Aryl Aryl halide Phenol | Aldehyde Alkyl arenes Aryl Ether tert-Butyl | Aldehyde Aryl Aryl halide Ether | Aldehyde Aryl Ether | Aldehyde Aryl Nitrobenzene |

1. Go to Profiling
2. Unselect All
3. Select Organic functional group
4. Click Apply
5. All 7 chemicals have "Aldehyde" fragment within its structure

Sub fragment search for identifying chemicals

Chemicals with Ames and Carcinogenicity positive data including Epoxide fragment

Example 5

- Structures search criteria
 - Endpoint: Gene mutation
 - Species: *S.thyphimurium*
 - Data: *Positive*

AND

- Endpoint: *Summary carcinogenicity*
- Species: *Rat*
- Route: *gavage*
- Data: *Positive*
- Predefined category: *Epoxides*

Sub fragment search for identifying chemicals

Chemicals with Ames and Carcinogenicity positive data including Epoxide fragment

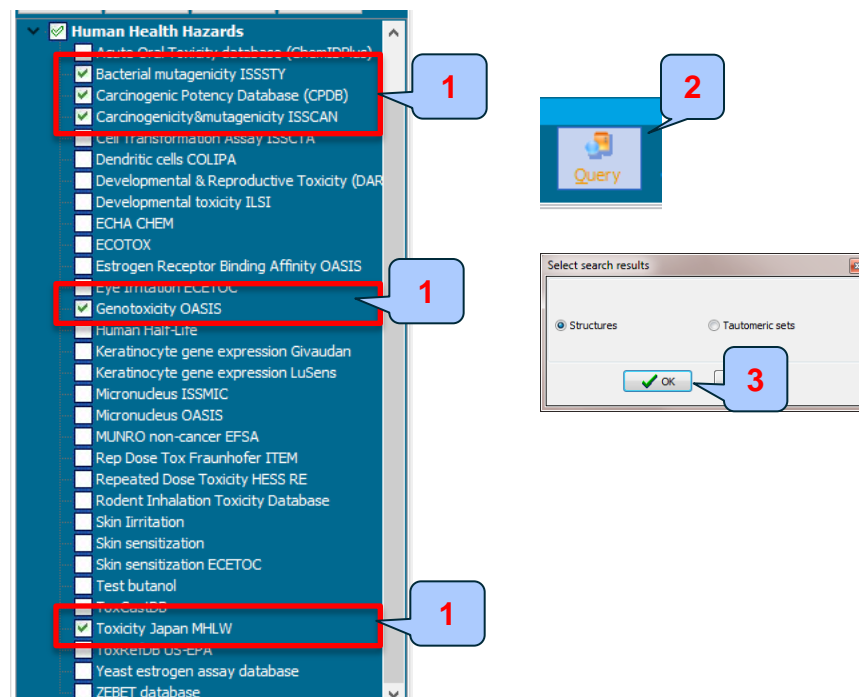
Example 5

• Structures search criteria

- Endpoint: Gene mutation
- Species: *S.thyphimurium*
- Data: *Positive*

AND

- Endpoint: *Summary carcinogenicity*
- Species: *Rat*
- Route: *gavage*
- Data: *Positive*
- Predefined category: *Epoxides*



Before application of Query tool, the user should select databases which includes required data. Inventories are not selected in this particular case.

1. Select the following databases:

- Bacterial mutagenicity ISSSTY
- Carcinogenicity potency Database (CPDB)
- Carcinogenicity&mutagenicity ISSCAN
- Genotoxicity OASIS
- Toxicity Japan MHLW

2. Click on Query button

3. Select Structures

Sub fragment search for identifying chemicals

Chemicals with Ames and Carcinogenicity positive data including Epoxide fragment

Example 5

•Structures search criteria

- Endpoint: Gene mutation
- Species: *S.thyphimurium*
- Data: *Positive*

AND

- Endpoint: *Summary carcinogenicity*
- Species: *Rat*
- Route: *gavage*
- Data: *Positive*
- Predefined category: *Epoxides*

1. Click on Data panel

2. Open Predefined endpoint path panel

3. Select "Genetic Toxicity"

4. Open Endpoint panel

5. Select Gene mutation

Sub fragment search for identifying chemicals

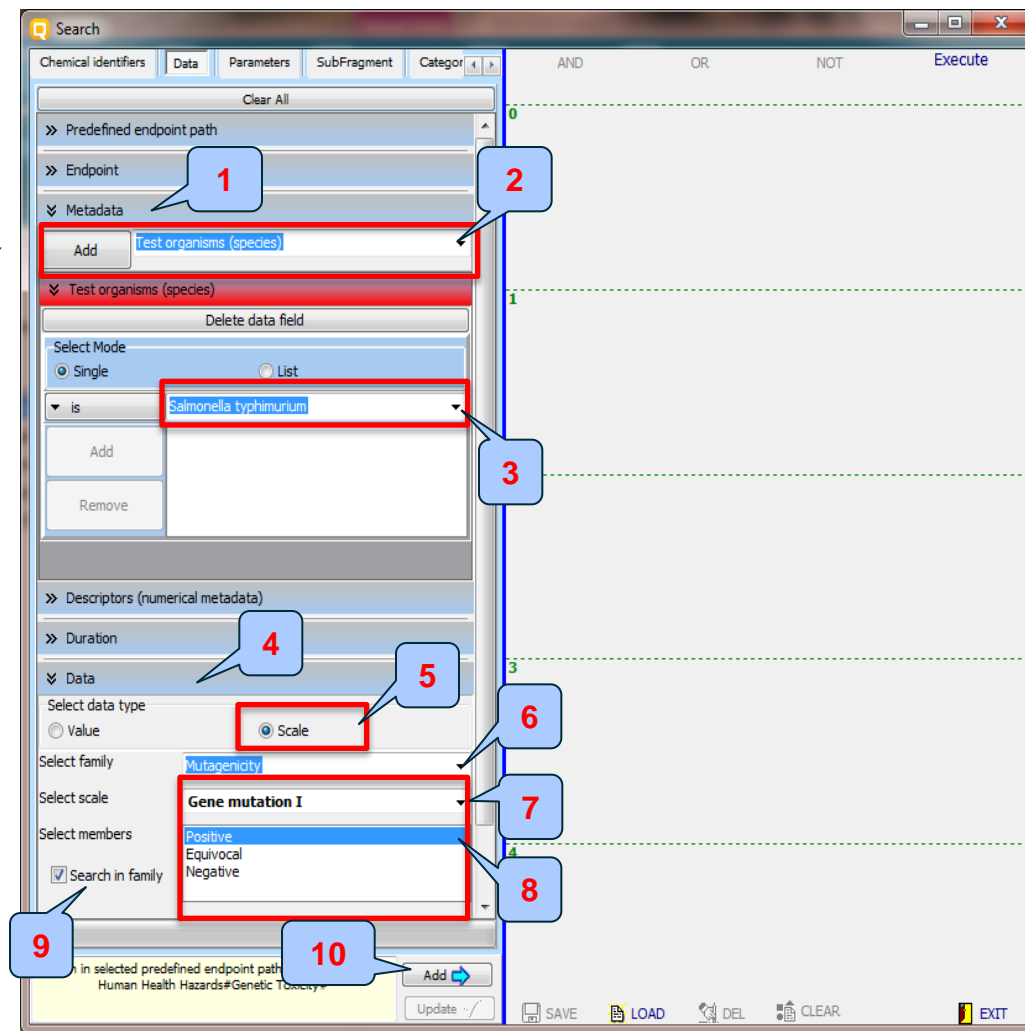
Chemicals with Ames and Carcinogenicity positive data including Epoxide fragment

Example 5

- Structures search criteria
 - Endpoint: Gene mutation
 - Species: *S.thyphimurium*
 - Data: Positive
 - Endpoint: Summary carcinogenicity
 - Species: Rat
 - Route: gavage
 - Predefined category: Epoxides

1. Open Metadata panel
2. Select Test organism (species) from the pop-up menu
3. Click Add
4. Select S.thyhimurium from the pop-up-menu
5. Open Data panel
6. Select Scale radio button
7. Select Mutagenicity family
8. Select scale Gene mutation I
9. Select Positive from the list with scale members
10. Search in family* option is selected by default (remain it as it is)
11. Click Add button

• Search in family option allows to find data pertaining to different scales within one family (e.g. find positive data belonging to scale Gene mutation I and Chromosomal aberration I (OASIS) part of family Mutagenicity). The latter is possible due to the implemented scale conversions.



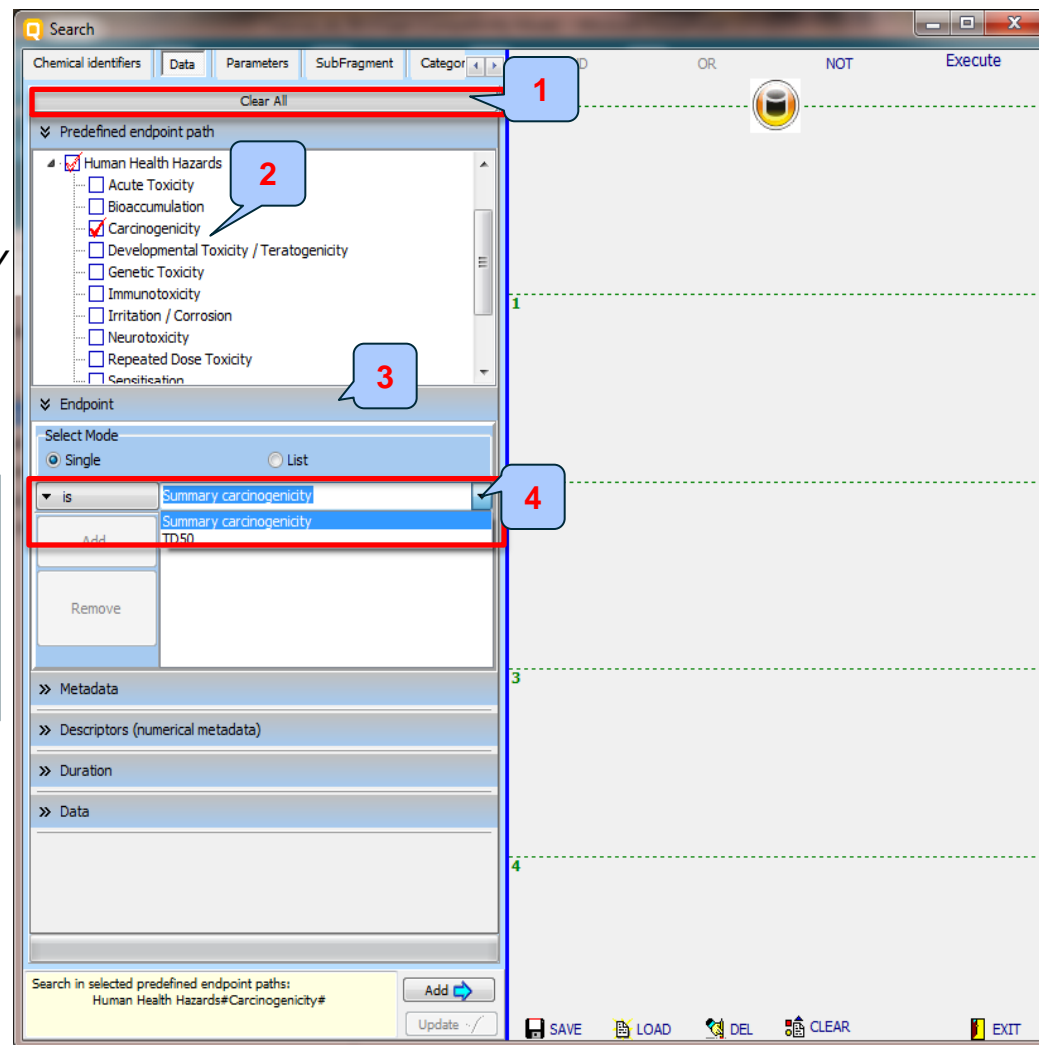
Sub fragment search for identifying chemicals

Chemicals with Ames and Carcinogenicity positive data including Epoxide fragment

Example 5

- Structures search criteria
 - Endpoint: Gene mutation
 - Species: *S.thyphimurium*
 - Data: *Positive*
 - Endpoint: *Summary carcinogenicity*
 - Species: *Rat*
 - Route: gavage
 - Predefined category: *Epoxides*

1. Before defining the second query **click** on Clear All button
2. **Open** Predefined endpoint path and select "Carcinogenicity" node
3. **Open** Endpoint tab
4. **Select** Summary carcinogenicity from the appeared pop-up list



Sub fragment search for identifying chemicals

Chemicals with Ames and Carcinogenicity positive data including Epoxide fragment

Example 5

- Structures search criteria
 - Endpoint: Gene mutation
 - Species: *S.thyphimurium*
 - Data: *Positive*
 - Endpoint: *Summary carcinogenicity*
 - Species: *Rat*
 - Route: *gavage*
 - Predefined category: *Epoxides*

1. **Open** Metadata panel
2. **Select** Route of administration from pop-up menu
3. **Click** Add button
4. **Select** Gavage from the list
5. **Go back** to Metadata panel and select Test organism (species) from the pop-up menu. Click Add button
6. **Select** Rat from the list
7. **Open** Data panel
8. **Select** Scale
9. **Select** Carcinogenicity family
10. **Select** scale Carcinogenicity I (ISSCAN)
11. **Select** Positive
12. **Click** Add button
13. The query appears on the logic panel

The screenshot shows the 'Search' window in the QSAR Toolbox. The interface is divided into several panels: 'Metadata', 'Route of administration', 'Test organisms (species)', and 'Data'. The 'Route of administration' and 'Test organisms (species)' panels are currently open, showing dropdown menus for 'Gavage' and 'Rat' respectively. The 'Data' panel is also open, showing 'Scale' selected and 'Carcinogenicity I (ISSCAN)' as the selected family and scale. The 'Positive' option is selected under 'Select members'. The 'Add' button is visible at the bottom of the 'Data' panel. The logic panel on the right shows the resulting query structure, with a callout 13 pointing to it.

Sub fragment search for identifying chemicals

Chemicals with Ames and Carcinogenicity positive data including Epoxide fragment

Example 5

•Structures search criteria

- Endpoint: Gene mutation
- Species: *S.thyphimurium*
- Data: *Positive*
- Endpoint: *Summary carcinogenicity*
- Species: *Rat*
- Route: gavage
- Predefined category: *Epoxides*

1. Click on Category panel
2. Select Carcinogenicity alerts by ISS
3. Select category Epoxides and aziridines (Genotox)
4. Move the selected category to the panel Selected profiles
5. Click Add button
6. The query appears on the logic panel

The screenshot shows the QSAR Toolbox software interface. The 'Category' panel is selected, and 'Carcinogenicity (genotox and nongenotox) alerts by ISS' is chosen. 'Epoxides and aziridines (Genotox)' is moved to the 'Selected profiles' panel. The 'Add' button is clicked, and the query appears on the logic panel.

Sub fragment search for identifying chemicals

Chemicals with Ames and Carcinogenicity positive data including Epoxide fragment

Example 5

- Structures search criteria
 - Endpoint: Gene mutation
 - Species: *S.thyphimurium*
 - Data: Positive
 - Endpoint: Summary carcinogenicity
 - Species: Rat
 - Route: gavage
 - Predefined category: Epoxides

The screenshot displays the 'Search' window in the QSAR Toolbox. The left sidebar contains the following settings:

- Predefined endpoint path:**
 - Human Health Hazards
 - Acute Toxicity
 - Bioaccumulation
 - Carcinogenicity
 - Developmental Toxicity / Teratogenicity
 - Genetic Toxicity
 - Immunotoxicity
 - Irritation / Corrosion
 - Neurotoxicity
 - Repeated Dose Toxicity
 - Sensitization
- Endpoint:**
 - Select Mode: Single
 - is: Gene mutation
- Test organisms (species):**
 - is: Salmonella typhimurium

The right workspace shows a query diagram with three query nodes (beaker icons) connected to a central 'AND' node. Numbered callouts indicate the steps: 1. Right-click on a query node, 2. Click the 'AND' button, 3. The resulting 'AND' node, and 4. Click the 'Execute' button.

- Right click over the first two queries (see slide # 42)
- Click AND button
- The three queries are combined by logical AND
- Click on Execute button

Sub fragment search for identifying chemicals

Chemicals with Ames and Carcinogenicity positive data including Epoxide fragment

Example 5

The Query tool (QT) identified 6 chemicals matching the desired criteria. In order to check the correctness of the query the user should gather experimental data for Ames and Carcinogenicity and profile the identified chemicals according to applied Carcinogenicity profiler. The last two steps are presented on the next two slides

Sub fragment search for identifying chemicals

Chemicals with Ames and Carcinogenicity positive data including Epoxide fragment

Example 5

| Structure | 1 [target] | 2 [target] | 3 [target] | 4 [target] | 5 [target] | 6 [target] |
|---|-------------------------|-------------------------|-------------------------|-------------------------|-------------------------|-------------------------|
| Bioaccumulation | | | | | | |
| Carcinogenicity | | | | | | |
| Hamster (1/2) | | | | M: Positive, 56.1 ... | | |
| Mouse (6/22) | M: Positive, 24.3 ... | M: Negative, Negative | M: Positive, 63.7 ... | M: Positive, 34.7 ... | M: Positive, 912 m... | M: Positive, 118 m... |
| Rat | | | | | | |
| Carcinogenicity | | | | | | |
| Summary Carcinogenicity | | | | | | |
| Gavage (6/10) | M: Positive, Positive | M: Positive | M: Positive, Positive | M: Positive, Positive | M: Positive | M: Positive, Positive |
| Inhalation (3/4) | | M: Positive, Negative | M: Positive | | M: Positive | |
| Undefined Route of Administration | | | | | | |
| TD50 (6/12) | M: 3.78 mg/kg/day... | M: 2.96 mg/kg/day... | M: 21.3 mg/kg/day... | M: 4.28 mg/kg/day... | M: 74.4 mg/kg/day... | M: 55.4 mg/kg/day... |
| Developmental Toxicity / Teratogenicity | | | | | | |
| Genetic Toxicity | | | | | | |
| In Vitro | | | | | | |
| Bacterial Reverse Mutation Assay (...) | | | | | | |
| Gene Mutation | | | | | | |
| Salmonella typhimurium (6/84) | M: Positive, Positiv... | M: Positive, Positiv... | M: Positive, Positiv... | M: Positive, Positiv... | M: Positive, Positiv... | M: Positive, Positiv... |
| DNA Damage and Repair Assay, U... | | | | | | |

| Endpoint | CAS | Structure | Value | Author |
|-------------------------|----------|--------------------------|----------|------------------|
| Summary carcinogenicity | 101-90-6 | <chem>c1ccc(cc1)O</chem> | Positive | Romualdo Benigni |
| Summary carcinogenicity | 101-90-6 | <chem>c1ccc(cc1)O</chem> | Positive | Romualdo Benigni |
| Summary carcinogenicity | 106-89-8 | <chem>c1ccc(cc1)O</chem> | Positive | Romualdo Benigni |
| Summary carcinogenicity | 106-89-8 | <chem>c1ccc(cc1)O</chem> | Positive | Romualdo Benigni |
| Summary carcinogenicity | 556-52-5 | <chem>c1ccc(cc1)O</chem> | Positive | Romualdo Benigni |
| Summary carcinogenicity | 556-52-5 | <chem>c1ccc(cc1)O</chem> | Positive | Romualdo Benigni |
| Summary carcinogenicity | 96-09-3 | <chem>c1ccc(cc1)O</chem> | Positive | Romualdo Benigni |
| Summary carcinogenicity | 96-09-3 | <chem>c1ccc(cc1)O</chem> | Positive | Romualdo Benigni |

1. Databases are already selected, **Click** gather data
2. **Click** OK
3. **Click** Select one
4. **Click** OK
5. Data appear on data matrix answering the following criteria:
Ames mutagenicity (S. thuphimurium): Positive
Summary carcinogenicity (gavage, rat): Positive

Sub fragment search for identifying chemicals

Chemicals with Ames and Carcinogenicity positive data including Epoxide fragment

Example 5

The screenshot shows the QSAR Toolbox software interface. The top menu bar includes 'Input', 'Profiling', 'point', 'Category Definition', 'Data Gap Filling', and 'Report'. The 'Profiling' menu is open, showing various endpoints. The 'Carcinogenicity (genotox and nongenotox) alerts by ISS' option is selected. The main window displays a table of search results for six different target structures. The table has columns for 'Structure', '1 [target]', '2 [target]', '3 [target]', '4 [target]', '5 [target]', and '6 [target]'. The 'Structure' column shows chemical structures of various epoxide-containing molecules. The '1 [target]' column shows the search results for the first target, which is an epoxide fragment. The 'Human Health Hazards' row is highlighted in red, and the 'Profile' section is also highlighted in red. The 'Profile' section shows 'Endpoint Specific' and 'Carcinogenicity (genotox and nongenotox) alerts by ISS' with a count of 6/137. The 'Carcinogenicity (genotox and nongenotox) alerts by ISS' row is also highlighted in red, and the text 'Epoxides and aziri... Structural alert for ...' is visible in the cells for targets 1 through 6.

1. Go to Profiling
2. Unselect All
3. Select Carcinogenicity (genotox and nongenotox) alerts by ISS
4. Click Apply
5. All 6 chemicals have "Epoxides and Aziridines" fragment within its structure

Sub fragment search for identifying chemicals

Chemicals with Skin sensitization positive data including Aldehyde fragment

Example 6

- Structures search criteria
 - Endpoint: *EC3*
 - Data: *Positive*
 - Predefined category: alpha, beta-unsaturated aldehydes

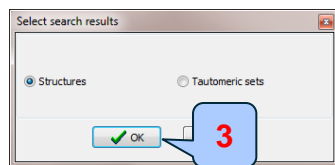
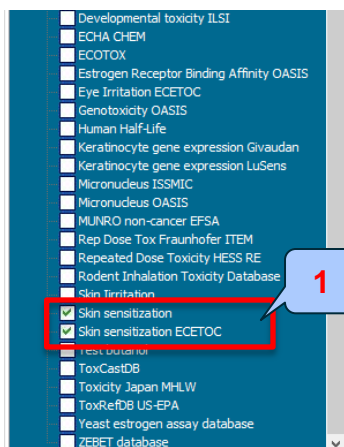
Sub fragment search for identifying chemicals

Chemicals with Skin sensitization positive data including Aldehyde fragment

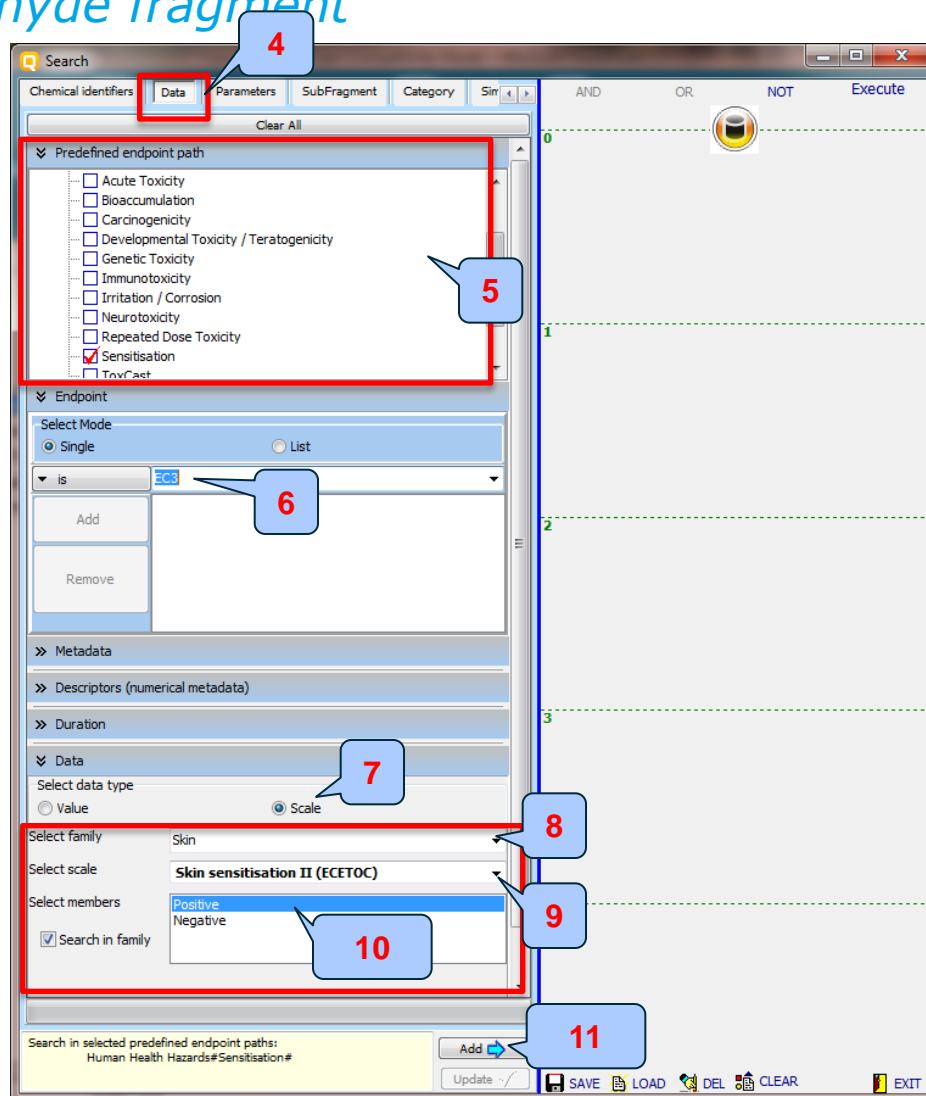
Example 6

• Structures search criteria

- Endpoint: EC3
- Data: Positive
- Predefined category: alpha, beta-unsaturated aldehydes



1. Select databases including skin sensitization data. No inventories has been selected in this case
2. Click on Query tool button
3. Select Structures
4. Click on Data panel
5. Open Predefined endpoint path and select Sensitization
6. Open Endpoint panel and select EC3
7. Open Data panel and Select Scale
8. Select family Skin
9. Scale Skin sensitization II (ECETOC)
10. Select Positive
11. Click Add button



Sub fragment search for identifying chemicals

Chemicals with Skin sensitization positive data including Aldehyde fragment

Example 6

- Structures search criteria
 - Endpoint: *EC3*
 - Data: *Positive*
 - Predefined category: alpha, beta-unsaturated aldehydes

- Click on Category panel
- Select Protein binding alerts for skin sensitization by OASIS v1.4
- Select category Michael addition >>alpha, beta-Unsaturated carbonyl compounds>>alpha, beta-Aldehydes and Move the selected category to the panel Selected profiles
- Click Add button
- The query appears on the logic panel

The screenshot shows the QSAR Toolbox interface with several callouts:

- 1**: Points to the 'Category' tab in the search panel.
- 2**: Points to the 'Protein binding alerts for skin sensitization by OASIS v1.4' profile in the 'Profiling methods' list.
- 3**: Points to the 'Selected profiles' section where the chosen category is listed.
- 4**: Points to the 'Add' button at the bottom of the search panel.
- 5**: Points to the logic panel on the right, where the query is displayed.

Sub fragment search for identifying chemicals

Chemicals with Skin sensitization positive data including Aldehyde fragment

Example 6

- Structures search criteria
 - Endpoint: *EC3*
 - Data: *Positive*
 - Predefined category: alpha, beta-unsaturated aldehydes

The screenshot displays the QSAR Toolbox search interface. The left pane shows the search configuration for the 'Data' tab, with 'EC3' selected as the endpoint and 'Positive' as the data type. The 'SubFragment' tab is also visible. The right pane shows a query tree with two search criteria connected by an 'AND' operator. The 'Execute' button is highlighted.

- Right click** over the query in order to select it
- Click** AND button
- The two queries are combined together by logical AND
- Click** on Execute button

Sub fragment search for identifying chemicals

Chemicals with Skin sensitization positive data including Aldehyde fragment

Example 6

The Query tool (QT) identified **13** chemicals matching the desired criteria. In order to check the correctness of the query the user should gather experimental data for skin sensitization and profile the identified chemicals according to the "Protein binding alerts for skin by OASIS v1.4" profiler used in the query boundary. The last two steps are presented on the next two slides.

Sub fragment search for identifying chemicals

Chemicals with Skin sensitization positive data including Aldehyde fragment

Example 6

1 Gather

2 Read data?

3 EC3

| Endpoint | 1 [target] | 2 [target] | 3 [target] | 4 [target] | 5 [target] | 6 [target] | 7 [target] | 8 [target] |
|-----------------------------------|-------------------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|
| Structure | | | | | | | | |
| Bioaccumulation | | | | | | | | |
| Carcinogenicity | | | | | | | | |
| Developmental Toxicity / Terat... | | | | | | | | |
| Genetic Toxicity | | | | | | | | |
| Immunotoxicity | | | | | | | | |
| Irritation / Corrosion | | | | | | | | |
| Neurotoxicity | | | | | | | | |
| Photoinduced Toxicity | | | | | | | | |
| Repeated Dose Toxicity | | | | | | | | |
| Sensitisation | | | | | | | | |
| Skin | | | | | | | | |
| In Chemico | | | | | | | | |
| In Vitro | | | | | | | | |
| In Vivo | | | | | | | | |
| GPMT (2/2) | M: Positive | M: Positive | | | | | | |
| HRIPT (4/6) | M: Positive, Positiv... | | M: Negative | | | | | M: Positive |
| LLNA | | | | | | | | |
| EC3 (13/14) | M: Positive, Positive | M: Positive | M: Positive | M: Positive | M: Positive | M: Positive | M: Positive | M: Positive |
| Miscellaneous (3/3) | M: Positive | M: Positive | M: Negative | | | | | |
| Undefined Assay (2/2) | M: Positive | M: Positive | | | | | | |
| ToxCast | | | | | | | | |
| Toxicity to Reproduction | | | | | | | | |
| Toxicokinetics, Metabolism an... | | | | | | | | |
| Profile | | | | | | | | |
| General Mec... | | | | | | | | |

1. Databases are already selected, **Click** gather data

2. **Click** OK

3. Data appear on data matrix answering the following criteria:
EC3: Positive

Sub fragment search for identifying chemicals

Chemicals with Skin sensitization positive data including Aldehyde fragment

Example 6

1. Go to Profiling

2. Unselect All

3. Select Protein binding alerts for skin sensitization by OASIS v1.4

4. Click Apply

5. Perform right click over the Protein binding alerts and select Profile statistic

6. All 13 chemicals are alpha-beta aldehydes according to Protein binding alerts for skin sensitization profiler

| Category | Count | % |
|---|-------|--------|
| 1 Michael Addition | 13 | 100.00 |
| 2 Michael Addition >> Michael addition on alpha,beta-unsaturated carbonyl compounds | 13 | 100.00 |
| 3 Michael Addition >> Michael addition on conjugated systems with electron withdrawing gro... | 2 | 15.38 |
| 4 Michael Addition >> Michael addition on conjugated systems with electron withdrawing gro... | 2 | 15.38 |
| 5 Schiff base formation | 1 | 7.69 |

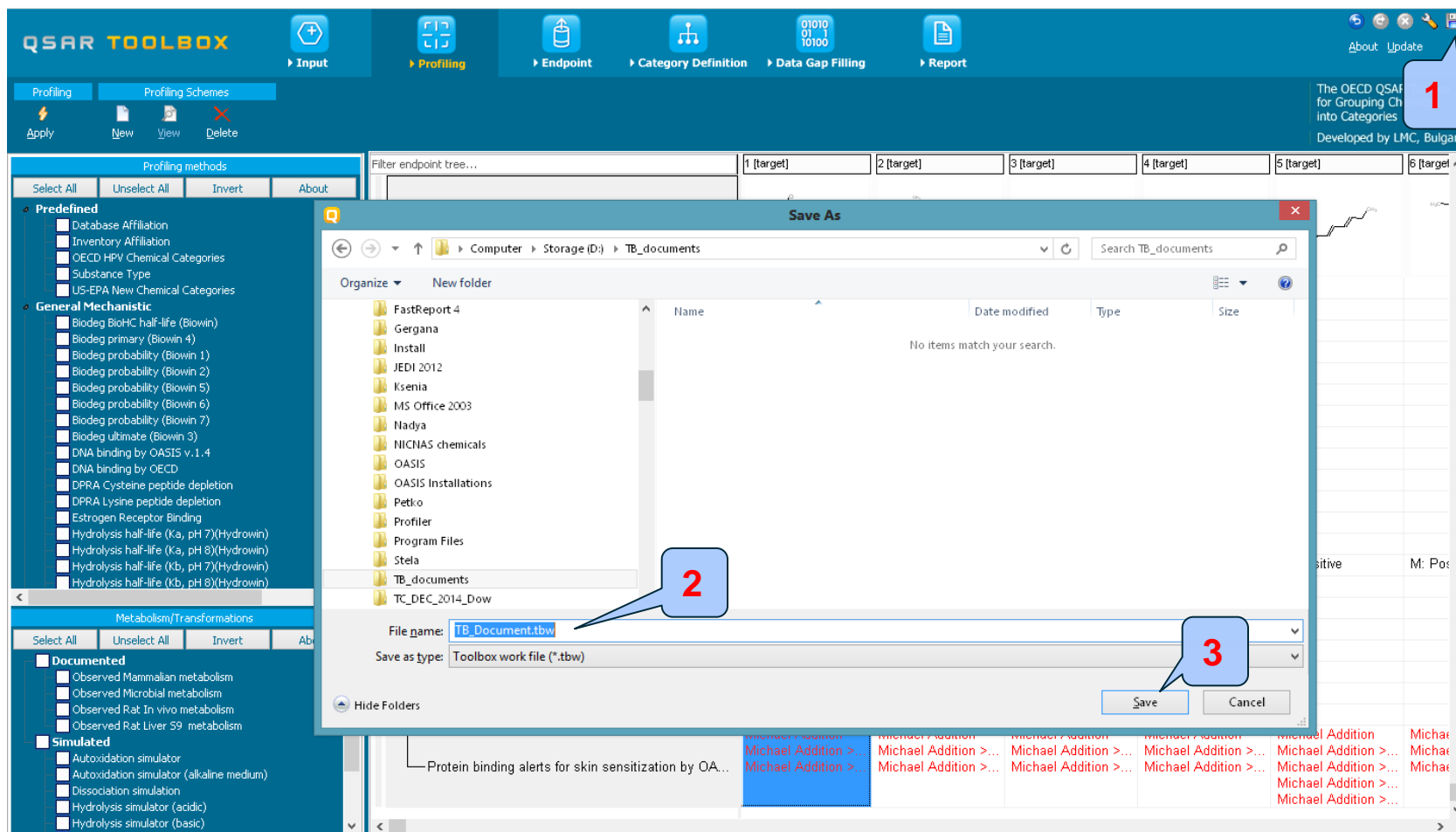
Outlook

- Background
- Objectives
- Overview of Query tool
- Query tool window
- The exercise
- Workflow process
- **Save QT searches**

Saving the prediction result

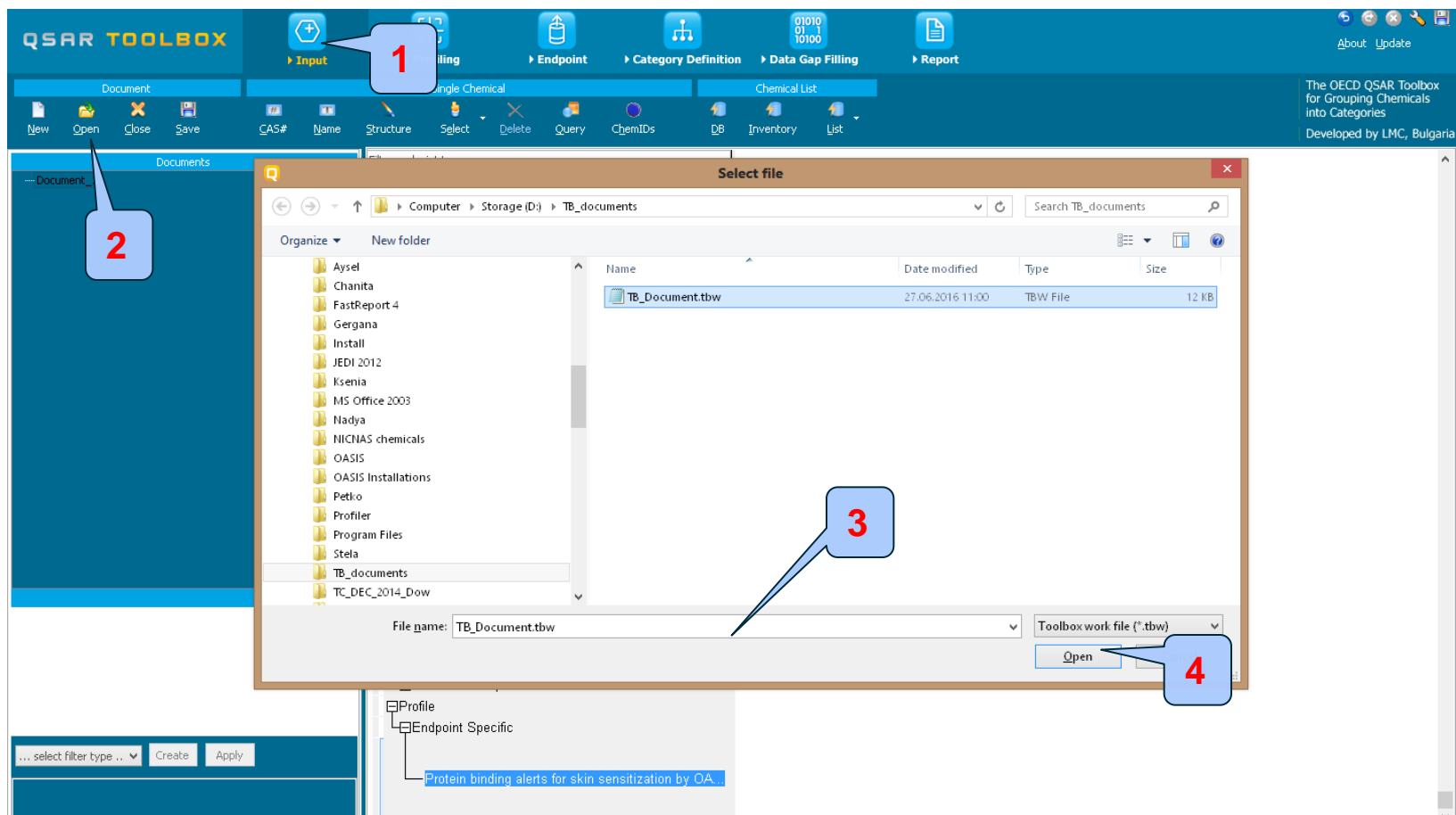
- This functionality allows storing/restoring the current state of Toolbox documents including loaded chemicals, experimental data, profiles, predictions etc., on the same computer. The functionality is implemented based on saving the sequence of actions that led to the current state of the Toolbox document 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 the next screenshots

Saving the QT requests



1. Click on Save button; **2. Define** name of the file; **3. Click** Save button

Open saved file



Once the file has been saved **1. Go** to Input; **2. Click** Open; **3. Find** and **select file**; **4. Click** Open