## QSAR TOOLEOX

The OECD QSAR Toolbox for Grouping Chemicals into Categories

## OECD (Q)SAR Toolbox v.4.4.1

Example illustrating RAAF Scenario 2 and related assessment elements

#### **Outlook**

- Background
- Keywords
- Objectives
- Specific Aims
- Read Across Assessment Framework (RAAF)
- The exercise
- Workflow

### Background

- This is a step-by-step presentation designed to take the Toolbox user through the workflow of a data gap filling exercise and justification of the outcome.
- The read-across prediction will be justified by fulfilling all information requirements according to the Read Across Assessment Framework (RAAF).

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#### **Keywords**

**TARGET CHEMICAL -** chemical of interest

**MODULE –** a Toolbox module is a section dedicated to specific actions and options

**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

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### **Objectives**

# This presentation demonstrates a number of functionalities of the Toolbox:

- Define target endpoint;
- Calculation of alert performance (AP) accounting for metabolism;
- Searching of analogues accounting for metabolism;
- Category consistency check;
- Selection of RAAF scenario;
- Filling in the report sections related to each read-across assessment element.

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### **Specific Aims**

- To familiarize the user with the Read-Across Assessment Framework (RAAF) and more specifically with Scenario 2;
- To introduce to the user the read across assessment elements;
- To introduce to the user the report basket;
- To provide sufficient information to the user allowing for scientific assessment of the outcome;
- To explain to the Toolbox user the rationale behind each step of the exercise.

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## Read-Across Assessment Framework (RAAF) Overview

- RAAF was developed by ECHA as an internal tool which provides a framework for a consistent and structured assessment of grouping and read across approaches under REACH.
- The outcome of the assessment is a conclusion on whether the read across is scientifically acceptable or not.
- The RAAF defines different scenarios for different read-across approaches.
- Each scenario is associated with particular aspects (assessment elements, AEs).
- Total six scenarios are available: two for analogue approach and four for category approach.

## Read-Across Assessment Framework (RAAF) Selection of a RAAF scenario

| SCENARIO | APPROACH | READ-ACROSS HYPOTHESIS<br>BASED ON                           | QUANTITATIVE VARIATIONS   |
|----------|----------|--|---|
| 1        | Analogue | (Bio)transformation to common<br>compound(s)                 | Property of the target substance predicted to<br>be quantitatively equal to those of the source<br>substance or prediction based on a worst-case<br>approach.   |
| 2        | Analogue | Different compounds have<br>qualitatively similar properties | Properties of the target substance predicted<br>to be quantitatively equal to those of the<br>source substance or prediction based on a<br>worst-case approach. |
| 3        | Category | (Bio)transformation to common compound(s)                    | Variations in the properties observed among source substances. Prediction based on a regular pattern or on a worst-case approach.                               |
| 4        | Category | Different compounds have<br>qualitatively similar properties | Variations in the properties observed among<br>source substances. Prediction based on a<br>regular pattern or on a worst-case approach.                         |
| 5        | Category | (Bio)transformation to common<br>compound(s)                 | No relevant variations in properties observed<br>among source substances and the same<br>strength predicted for the target substance.                           |
| 6        | Category | Different compounds have<br>qualitatively similar properties | No relevant variations in properties observed<br>among source substances and the same<br>strength predicted for the target substance                            |

\*Read-Across Assessment Framework (RAAF) available at https://echa.europa.eu/documents/10162/13628/raaf en.pdf

## Read-Across Assessment Framework (RAAF) Selection of a RAAF scenario

- Distinguish whether it is an analogue or a category approach\*
- To identify the basis of the read across hypothesis
  - (Bio)transformation to common compound(s) the read across hypothesis is that different substances give rise to (the same) common compounds to which the organism is exposed
  - Different compounds have the same type of effect(s) the read across hypothesis is that the organism is not exposed to common compounds but rather, as a result of similarity, that different compounds have similar (eco)toxicological and fate properties. These compounds may be the source and target substances themselves or one or more of their (bio)transformation products.
- For a category approach there is a need to take further account whether or not quantitative variations in the properties are observed among the category members

## Read-Across Assessment Framework (RAAF) Selection of RAAF scenario

- Each scenario consists of a pre-defined set of assessment elements (AEs) that, when taken together, cover all of the essential scientific aspects that need to be addressed in the read-across approach for a particular scenario.\*
- Each AE reflects a critical scientific aspect of a read-across.
- The AEs could be:
  - common for all scenario within one approach common AEs for Scenario 1 and 2 (analogue approach) and common AEs for Scenario 3, 4, 5 and 6 (category approach)
  - **specific** addressing specific scenario.

\*Read-Across Assessment Framework (RAAF) available at https://echa.europa.eu/documents/10162/13628/raaf\_en.pdf

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#### • The example

• Workflow

#### **The Example**

- In this example we will predict the skin sensitization potential of chemical: 1,3-Propanediamine, N-(3-aminopropyl) - [CAS# 56-18-8], which will be the "target" chemical;
- The category will be defined based on protein binding mechanism identified in the target chemical after skin metabolism is taken into account. The identified protein binding mechanism is common to all the chemicals in the category;
- A read-across approach will be used for the prediction. The readacross will be based on analogue approach expressed as common underlying mechanism for metabolites of source and target substances;
- Read-across assessment elements will be included to the report;
- Examples for the possible content of each of AEs will be provided.

### The Example Sidebar On Skin Sensitization

- Allergic contact dermatitis that results from skin sensitization is a significant health concern.
- Skin sensitization is a toxicological endpoint that is complex and conceptually difficult.
- However, there is growing agreement that most organic chemicals must react covalently with skin proteins in order to behave as skin sensitizers.
- Therefore, mechanisms by which organic chemicals bind with proteins are relevant to grouping chemicals that may be skin sensitizing agents.

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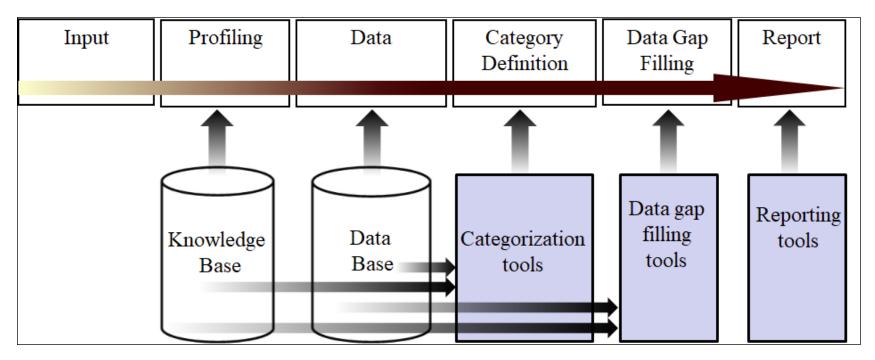
#### Workflow

- The Toolbox has six modules, which are used in a sequential workflow:
  - $\circ$  Input
  - Profiling
  - Data
  - Category Definition
  - Data Gap Filling
  - Report

The modules will be presented in different sequence than the one showed above.

#### Workflow

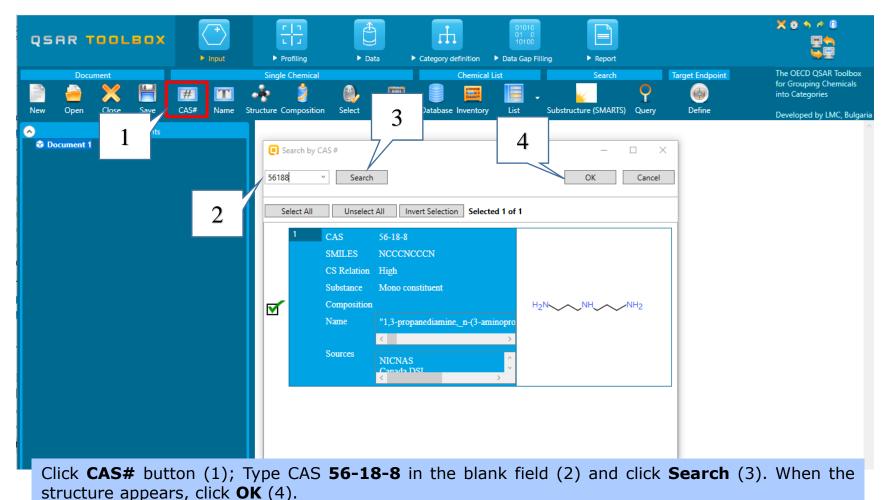
#### Scheme illustrating the Toolbox workflow



#### **Input** Overview

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

#### Input Screen Input target chemical by CAS#



The OECD (Q)SAR Toolbox for Grouping Chemicals into Categories

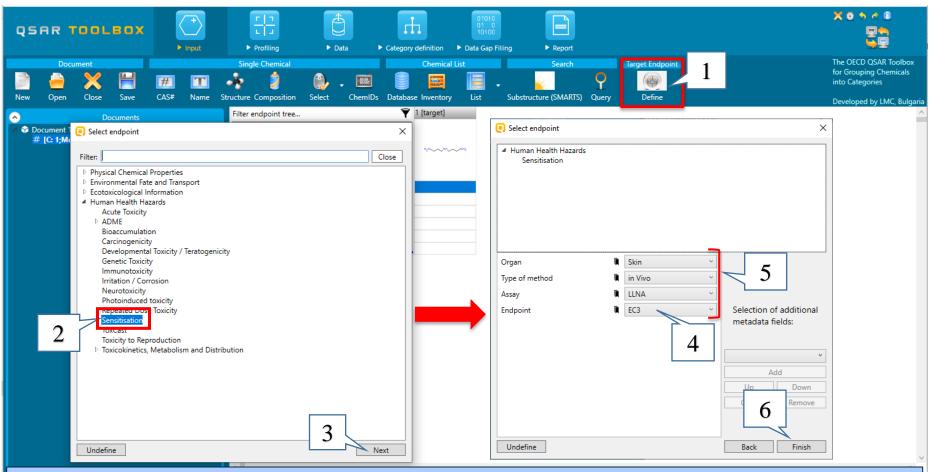
### **Input** Define target endpoint

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 is provided expressed in different highlighting.

Calculation of alert performance (AP) illustrated further is only possible if the target endpoint is preliminary defined.



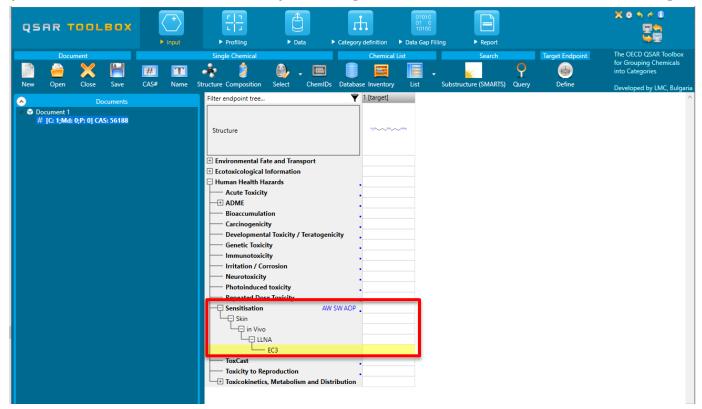
### **Input** Define target endpoint



By clicking **Define** (1) you could select the target endpoint. Select **Sensitisation** in the *Human health hazards* category (2) and click **Next** (3). You need first to select **EC3** endpoint (4) from the drop-down menu and then consecutively the following metadata: *Assay*: **LLNA**, *Organ*: **Skin**, *Type of method*: **In Vivo** (5). Finally click on **Finish** (6).

### **Input** Define target endpoint

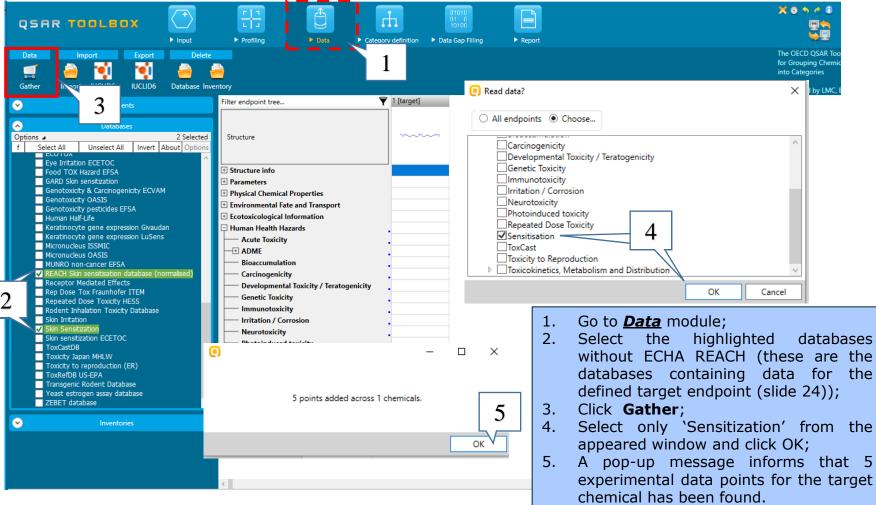
Once the endpoint is defined along with its metadata, they appear in the endpoint tree and the corresponding row of the data matrix is highlighted.



#### **Data** Overview

- "Data" refers to the electronic process of retrieving the environmental fate, ecotoxicity and toxicity data that are stored in the Toolbox.
- Data gathering can be executed in a global fashion (i.e., collecting all data for all endpoints) or on a more narrowly defined basis (e.g., collecting data for a single or limited number of endpoints).

#### **Data** Gather data



The OECD (Q)SAR Toolbox for Grouping Chemicals into Categories

### **Data** Gather data

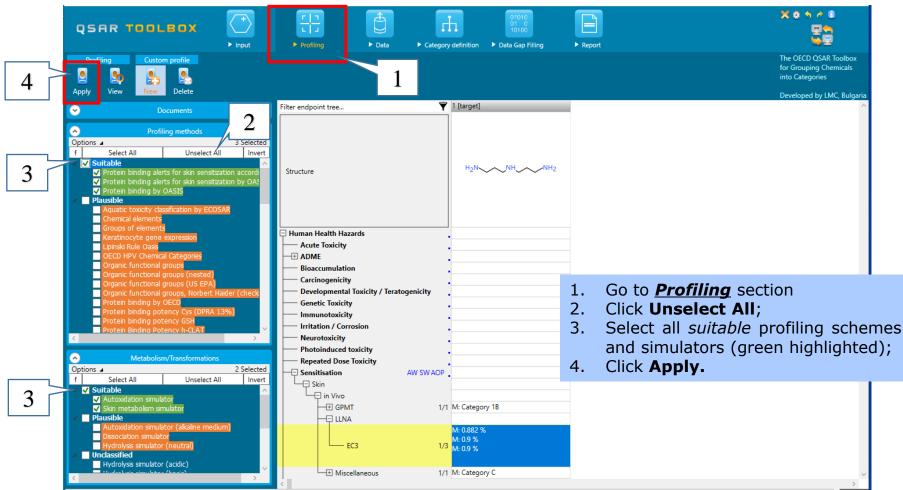
- Toxicity information on the target chemical is electronically collected from the selected dataset(s).
- It should be kept in mind that the search for data and analogues (and further calculation of AP) is performed only among the chemicals which are listed in the selected databases. In this example only the *Skin sensitization database and REACH Skin sensitization database (normalized)* are selected.
- In this example, a pop-up window appears stating there are 5 experimental data points found for the target chemical. There are three out of five ppositive experimental data for the target chemical.
- Go to the *Profiling* module to check for the possible reasons of the positive effect (to check for an alert identified in the target chemical).

#### **Profiling** Overview

- "Profiling" 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;
- "Profiling" module contains all the knowledge in the system coded in profiling schemes (i.e. profilers);
- "Profilers" are a collection of empirical and mechanism knowledge (expertly derived) 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 once are getting colour highlighted\*.

\*For more details regarding relevancy of the profilers see ppt: Example for predicting skin sensitization taking into account alert performance

### **Profiling** Profiling the target chemical



## **Profiling** Profiling results

- 1) No alerts are identified in the target structure as a parent;
- No metabolites are produced as a result of abiotic activation (Autoxidation simulator);
- 3) 5 metabolites are produced as a result of biotic activation (*Skin metabolism simulator*);
- 4) Endpoint specific protein binding alerts are identified in the metabolites produced by the Skin metabolism simulator.

## **Profiling** Profiling results

|  |  | Dry definition    Data Gap Filling     Report   |      |  |
|--|--|---|------|--|
| Profiling     Custom profile       Image: Second sec |  |   |      |  |
| Documents     Document 1   | Filter endpoint tree 🖤   | 1 [target]  |      |  |
| <ul> <li></li></ul>  | Structure  | 11 <sup>5</sup> 21 <sup>7</sup> <sup>1</sup> 21 <sup>1</sup> <sup>1</sup> 2 <sup>1</sup> 21 <sup>1</sup> 2 <sup>1</sup> 21 <sup>1</sup> 2 <sup>1</sup> 2 <sup>1</sup> 2 <sup></sup>   |      |  |
| <ul> <li>✓ ♥ Document 2</li> <li># [C: 1;Md: 0;P: 0] CAS: 56188</li> </ul>   | General Mechanistic<br>Protein binding by OASIS<br>Endpoint Specific | No alert found  | 1    | No alerts are identified in the<br>target structure as a parent;<br>No metabolites are produced          |
| Profiling methods Options      Selected  |  | No alert found No alert found 2   | i    | as a result of abiotic<br>activation (Autoxidation   |
| f         Select All         Unselect All         Invert           ✓         Suitable         ^         ^           ✓         Protein binding alerts for skin sensitization according to the sensitizatio according to the sensitizatio according to the sensitizatio ac  | Autoxidation simulator     General Mechanistic     Fndpoint Specific | 0 metabolite(s)   | 3. 4 | simulator);<br>4 metabolites are produced  |
| <ul> <li>Protein binding alerts for skin sensitization by O/</li> <li>Protein binding by OASIS</li> <li>Plausible</li> </ul>   | Skin metabolism simulator  | 4 metabolite(s)   | i    | as a result of biotic<br>activation (Skin metabolism   |
| Aquatic toxicity classification by ECOSAR Chamical elements C Metabolism/Transformations Options 2 Selected  |  | 3 × Schiff base formation<br>3 × Schiff base formation >> Schiff base formation with carbonyl<br>2 × Schiff base formation >> Schiff base formation with carbonyl<br>1 × Schiff base formation >> Schiff base formation with carbonyl<br>1 × No alert found | 4.   | simulator);<br>Endpoint specific protein<br>binding alerts are identified<br>in the metabolites produced |
| f     Select All     Unselect All     Invert       ∠     Suitable     ^       ∠     Autoxidation simulator   | Endpoint Specific     Protein binding alerts for skin s              | 1 x Skin sensitization Category 1A<br>3 x Schiff base formation   | I    | by the Skin metabolism simulator.  |
| Skin metabolism simulator     Plausible     Autoxidation simulator (alkaline medium)     Dissociation simulator     Hydroksis simulator     Hydroksis simulator (neutral)  |  | 3 x Schiff base formation >> Schiff base formation with carbonyl.<br>2 x Schiff base formation >> Schiff base formation with carbonyl<br>1 x Schiff base formation >> Schiff base formation with carbonyl<br>1 x No alert found                             |      |  |

#### Recap

- In module *Input*, you have entered the target chemical and defined the target endpoint.
- In the *Data* module, you saw the database corresponding to the defined target endpoint. You also found some experimental data for the target chemical available in the selected databases.
- In the *Profiling* module, you profiled the target chemical with profiling schemes and metabolic simulators, suitable for the selected target endpoint.
- Protein binding alerts for skin sensitization were identified for some of the metabolites produced by simulating of biotic activation (skin metabolism).
- Click "Category Definition" to move to the next module.

### Category Definition Overview

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

## **Category Definition** Grouping methods

- The different grouping methods allow the user to group chemicals into chemical categories according to different measures of "similarity" so that within a category data gaps can be filled by read-across.
- For example, starting from a target chemical for which a specific protein binding mechanism is identified, analogues can be found which can bind by the same mechanism and for which experimental results are available.
- If no alert is identified in the target structure, but is identified in its metabolites, analogues can be searched accounting for a metabolism (e.g. metabolites of the analogues to have same metabolic pattern as metabolites of the parent chemical). In this way the target chemical and the identified analogues will have similar metabolic pattern.
- When more than one alert is found in the target structure before or after metabolic activation, 'Alert performance' functionality could help for defining which of them is the most suitable for primary categorization. The latter is shown on the next few slides.

#### QSAR TOOLEOX

## Category Definition Searching for analogues accounting for skin metabolism

|  |  |  |                  | 💽 Grouping options (Skin    | metabolism simulator) |             | - 🗆      |     |
|--|--|--|------------------|-----------------------------|-----------------------|-------------|----------|-----|
| QSAR TOOLBOX   | C  | Ê H  | 01010            | All queries At least        |                       |             |          |     |
|  | ► Input ► Profiling  | Data     Category definition   | Data Gap Filling | Chemical                    | Query                 |             | Criteria |     |
| Define Documents   | Category consist<br>Category consist<br>Combine Clustering Category eleme<br>Filter endpoint tree  |  | – – ×            | Parent<br>Hylix, Jur, Hills | none V                | o criteria. | 4        |     |
| Grouping methods     f     Select All     Unselect All     Im     Protein binding alerts for skin sensitizatio     Protein binding alerts for skin sensitizatio     Protein binding alerts for skin sensitizatio     Protein binding by OASIS     Plausible     Aquatic toxicity classification by ECOSAR     Chemical elements     Groups of elements     Keratinocyte gene expression  | options<br>f Select All<br><b>Documented</b><br>Observed Mammalia<br>Observed Microbial<br>Observed Rat In viv   | netabolism<br>o metabolism<br>netabolism with quantitative data                              |                  | Metabolite 1                | none v Ne             | o criteria. |          |     |
| Lipinski Rule Oasis<br>OECD HPV Chemical Categories<br>Organic functional groups (nested)<br>Organic functional groups (US EPA)<br>Organic functional groups, Norbert Haid<br>Protein binding botency Cys (DPRA 139<br>Protein binding potency GSH<br>Protein Binding Potency GSH  | Autoxidation simula<br>Autoxidation simula<br>Dissociation simulator<br>Hydrolysis simulator<br>Hydrolysis simulator<br>in vivo Rat metabolis<br>Microbial metabolis | tor (alkaline medium)<br>n<br>(acidic)<br>(basic)<br>(neutral)<br>m simulator<br>a simulator |                  | Metabolite 2                | none ~ N              | o criteria. |          |     |
| Protein binding potency Lys (DPRA 13%<br>Respiratory sensitisation   | Rat liver 69 metabo  |  |                  | All chemicals               |                       |             |          |     |
| Structure smallty<br>Substance type<br>US-EPA New Chemical Categories<br>Unclassified<br>Acute aquatic toxicity classificatio<br>Acute aquatic toxicity MOA by OASIS<br>Acute Oral Toxicity<br>Bioaccumulation - metabolism half-lives<br>Biodeg BioHC half-life (Biowin)<br>Biodegradation fragments (BioWIN MITT<br>Biodegradation fragments (BioWIN MITT<br>Biodegradation fragments (Classified Acute)   | 2  |  | 3<br>Cancel      | Parent & Metabolites        | none v N              | o criteria. |          |     |
| Biodegradation probabili<br>Biodegradation probabili<br>Biodegradation probabili<br>Biodegradation probabili<br>Biodegradation untimate<br>Biodegradation untimate<br>Biodegradation untimate<br>Biodegradation untimate<br>Biodegradation untimate<br>Biodegradation untimate<br>Biodegradation probabili<br>Biodegradation untimate<br>Biodegradation untimate<br>B | lick <b>Define w</b> i<br>elect <i>Skin met</i><br>lick <b>OK</b> ;  | i <b>th metabolisr</b><br>abolism simula<br>netabolites proc                                 | tor;             | he selected s               | imulator a            | ppear.      | ОКС      | anc |

April, 2020

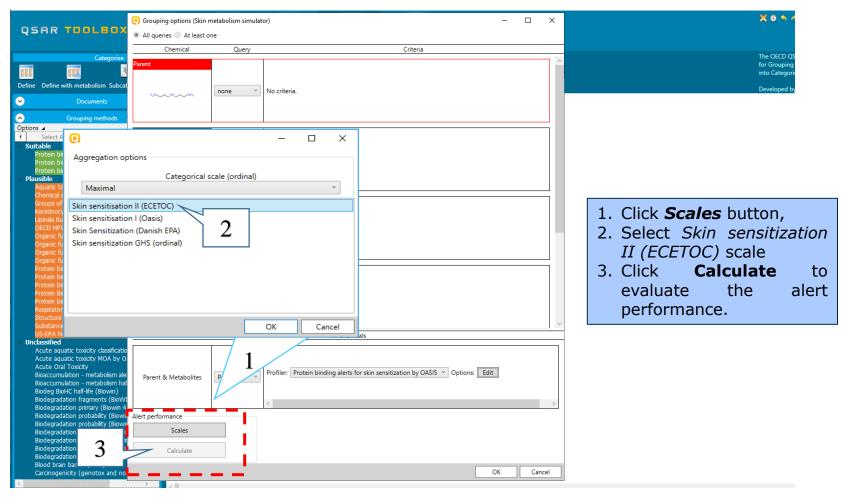
For more details regarding grouping with metabolism see tutorial Tutorial\_20\_TB\_4.4\_New options for grouping with metabolism.pdf

#### QSAR TOOLEOX

## Category Definition Searching for analogues accounting for skin metabolism

|  | Grouping options (Skin)   | metabolism simulato | r) .   | - 🗆 ×          |                    |   | Xo                   | <b>A</b>      |         |      |
|--|---|---------------------|--|----------------|--------------------|---|----------------------|---------------|---------|------|
| QSAR TOO   | All queries At least of the second | one                 |  |                |                    |   | ~ •                  |               |         |      |
|  | Chemical  | Query               | Criteria   |                | -                  |   |                      |               |         | ×    |
| Define Define with metab<br>Composition of the second | Parent<br>nyinggy tergy steep   | none ~              | No criteria.   | ^              | Schiff base format | ion<br>ion >> Schiff base formation<br>ion >> Schiff base formation<br>ion >> Schiff base formation | with carbonyl compou | inds >> Aldeh | lydes   |      |
| f Select All<br>Protein binding alert<br>Protein binding alert<br>Protein binding alert<br>Protein binding alert<br>Protein binding by C<br>Plausible<br>Aquatic toxicity class<br>Chemical elements<br>Groups of elements   | Metabolite 1  | none ~              | No criteria.   |                | Options            |   | with carbony compos  |               | uenyues |      |
| Keratmocyte gene e<br>Lipinski Rule Oasis<br>OECD HPV Chemical<br>Organic functional g<br>Organic functional g<br>Organic functional g<br>Protein binding by C<br>Protein binding pote<br>Protein binding pote   | Metabolite 2  | none ~              | No criteria.   |                | /                  | Up<br>D)carbamoylation of protein n   | Reset                |               | Options | ~ ~  |
| Protein Binding Pote   |   |                     | All chemicals  |                | Combine profiles   | lnvert result   |                      |               |         |      |
| Protein binding pote<br>Respiratory sensitisal<br>Structure similarity<br>Substance type<br>US-EPA New Chemid<br>Udassified  | Parent & Metabolites  | Profile ~           | Profiler: Protein binding alerts for skin sensitization by OASIS Y Op                  | otions: Edit 2 | ● AND ○ OR         | Strict  |                      |               |         |      |
| A cuto countie touis   | Parent & Metabolites  | Profile             |  |                |                    |   | L                    | OK            | Car     | ncel |
| 1<br>Biodegradation frag<br>Biodegradation prim<br>Biodegradation prob<br>Biodegradation prob  | Scales  |                     |  |                |                    |   |                      |               |         |      |
| b  | inding alert  | s for ski           | for the package – "Paren<br>n sensitization by OASIS.<br>dentified alerts in the paren |                |                    |   | elect <i>Pro</i>     | tein          |         |      |

## **Category Definition** Alert performance calculation



## **Category Definition** Alert performance calculation

| Alert performance r  | esults               |                                      |  | - 🗆 X          |   |
|--|----------------------|--------------------------------------|--|----------------|---|
| Using of "Skin met<br>simulator"<br>Combined paren<br>products requirer<br>No al<br>found <and>Schi<br/>formation &gt;&gt; Schi<br/>formation with ca<br/>compounds &gt;&gt;<br/>Aldehydes <and>Sc<br/>formation &gt;&gt; Schi<br/>formation with ca<br/>compounds &gt;&gt; Bis a<br/>(Protein binding aler<br/>sensitization by C</and></and> | Negative             | 80.00%                               | Show chemicals<br>With data(12)<br>Show chemicals<br>With data(3)  | Show all(15)   | Statistic for <b>all</b> alerts<br>identified in the package<br>"Parent & Metabolites"              |
| Using of "Skin met.<br>simulator"<br>Combined paren<br>products requirer<br>No alert<br>(Protein binding aler<br>sensitization by C<br>Using of "Skin met.<br>simulator"<br>Combined paren<br>products requirer<br>Schiff 1  | Negative<br>Positive | 46.22%<br>53.78%<br>51.09%<br>48.91% | Show chemicals<br>With data(611)<br>Show chemicals<br>With data(711)<br>Show chemicals<br>With data(187)<br>Show chemicals | Show all(1322) | Statistic for <b>each</b> of the alerts<br>identified in the package<br>"Parent & Metabolites"      |
| formation >> Schi<br>formation with ca<br>compounds >> Alc<br>(Protein binding aler<br>sensitization by C<br>Using of "Skin met-<br>simulator"<br>Combined paren   |                      | 82.35%                               | With data(179)<br>Show chemicals<br>With data(14)  | Show all(366)  | The alert with the best performance<br>in this case.<br>" <i>Bis aldehydes</i> " alert will be used |
| products requirer<br>Schiff I<br>formation >> Schi<br>formation with ca<br>compounds >> Bis a<br>(Protein binding aler   | Negative             | 17.65%<br>Close                      | Show chemicals<br>With data(3)   | Show all(17)   | for searching for analogues (see next slides).  |

#### L Keep in mind that the statistic is obtained from the chemicals and data, available in the selected databases

#### QSAR TOOLEOX

## Category Definition Searching for analogues accounting for skin metabolism

|                         | Grouping options (Skin metabolism simulator)  | - 0                      | ×      | _ |                     |                                | × (   | ) 🔊 d      |         |     |
|-------------------------|---|--------------------------|--------|---|---------------------|--------------------------------|---|------------|---------|-----|
| Q                       | Il queries At least one   |                          |        |   | 0                   |                                |   | -          |         | ×   |
|                         | Chemical Query C  | riteria                  |        |   | Target categories — |                                |   |            |         |     |
| Defit<br>C<br>Opti<br>f | Parent none No criteria.  |                          | 2      |   |                     | n >> Schiff base formation v   | vith carbonyl compounds                                       | >> Bis alc | dehydes |     |
| ⊿ S<br>⊿ P              | Metabolite 1  |                          |        |   | • Options           |                                |   |            |         |     |
|                         | Metabolite 2  |                          |        |   |                     | Up                             | Reset   | C          | Options | < > |
|                         | All chemicals   |                          | ⊒/ ·   | 1 | Combine profiles    | Invert result                  |   |            |         |     |
|                         | Air criemicais  |                          |        | 1 | AND OR              | Strict                         |   |            |         |     |
| -1                      |   |                          |        |   |                     | Sort results                   |   |            |         |     |
|                         | Click <b>Edit;</b><br>Remove all alerts except this with th   | n by OASIS Y Options: Ed |        |   | . ,                 |                                |   | OK         | Cano    | :el |
|                         | best performance ( <i>Bis aldehydes</i> );<br>Confirm the change by clicking <b>OK</b> ;                      |                          | >      |   | [                   | Grouping with "Protein binding | alerts for skin sensitization by                              | OASIS" —   |         | ×   |
|                         | Confirm that you have selected different<br>from the target categories. This is just a<br>informative message | in 5                     |        |   | 8                   | You have se                    | elected different from target cat<br>Do you want to continue? | tegories!  |         | 4   |
| 5.                      | Click <b>OK</b> in the main window to start th search.  | пе ок с                  | Cancel |   |                     | Do not show this dialog        |   | Yes        |         | lo  |

The OECD (Q)SAR Toolbox for Grouping Chemicals into Categories

## **Category Definition** Summary information for Analogues

17 chemicals with 44 experimental results are found across all 28 analogues related to the defined target endpoint (data for skin sensitization is selected only).

| QSAR TOOLBOX   | ut Profiling Data  | Category definition              | 01010<br>01 0<br>10100<br>Data Gap Filling | ► Report    |             |                |  |          |
|--|--|----------------------------------|--|-------------|-------------|----------------|--|----------|
| Categorize   | Category consistency   |                                  |  |             |             |                | The OECD QSAR<br>for Grouping Che<br>into Categories |          |
| Define Define with metabolism Subcategorize Combi  | 5 5 5  |                                  |  |             | -           |                | Developed by LN                                      |          |
| Documents  | Filter endpoint tree Y   | 1 [target] 2                     | 3  | 4           | 5 6         |                | 7  | 8 ^      |
| Corouping methods Coptions ▲ 0 Selected f Select All Unselect All Invert Suitable  | Structure  | 1/1~~~111                        |  |             | ant.        | 1/2/           | HS<br>HS   | 1/2000   |
| Protein binding alerts for skin sensitization<br>Protein binding alerts for skin sensitization<br>Protein binding by OASIS<br>Plausible<br>Aquatic toxicity classification by ECOSAR<br>Chemical elements<br>Groups of elements<br>Keratinocyte gene expression<br>Lipinski Rule Oasis<br>OECD HPV Chemical Categories | Photoinduced toxicity<br>Repeated Dose Toxicity<br>Sensitisation AW SW AOP<br>Skin<br>GPMT<br>HRIPT<br>LINA<br>Photoinduced toxicity<br>AW SW AOP<br>15/20<br>1/2  |                                  | 1: Positive                                | M: Negative | N           | I: Category 1A |  |          |
| Organic functional groups<br>Organic functional groups (nested)  |  | M: 0.882 %                       | M: 1.68 %                                  | 5           | M: Positive |                | M: Negative  | M: 8.4 % |
| Organic functional groups (US EPA)<br>Organic functional groups, Norbert Haider<br>Protein binding by OECD<br>Protein binding potency Cys (DPRA 13%)<br>Protein binding potency CSH  | Miscellaneous     Miscellaneous     ToxCast     Toxickinetics, Metabolism and Distribution     Profiling     General Mechanistic     Protein binding by OASIS     Endpoint Specific     Protein binding alerts for skin sensitiz | No alert found<br>No alert found | h Category 8                               |             |             |                |  | ~<br>~   |

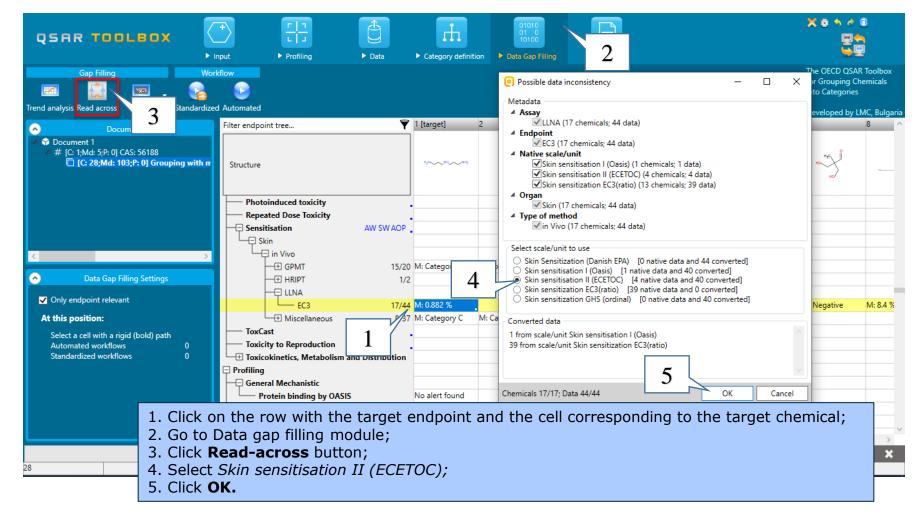
• Chemical statistics representing the number of chemicals and the available experimental data for them.

## Data Gap Filling Overview

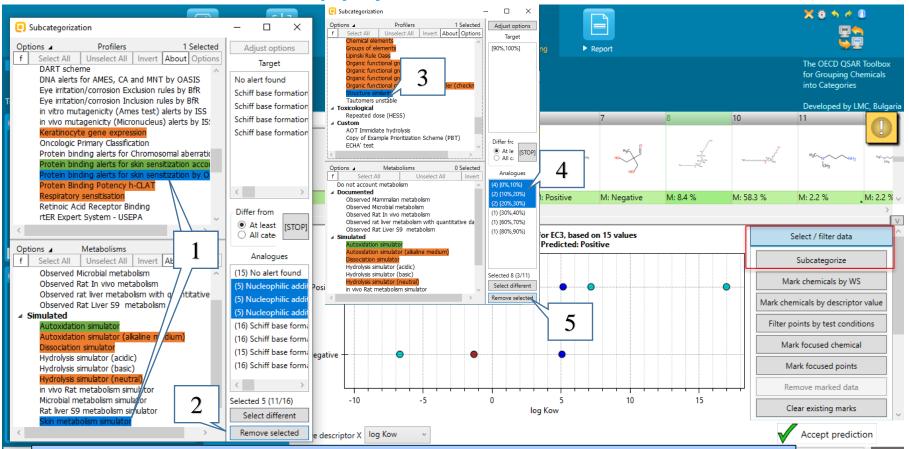
- "Data Gap Filling" module give access to five different data gap filling tools:
  - $\circ$  Read-across
  - Trend analysis
  - (Q)SAR models
  - Standardized workflow
  - Automated workflow
- Depending on the situation, the most relevant data gap mechanism should be chosen, taking into account the 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.

#### In this example we will use the read-across approach.

## **Data Gap Filling** Apply Read-across

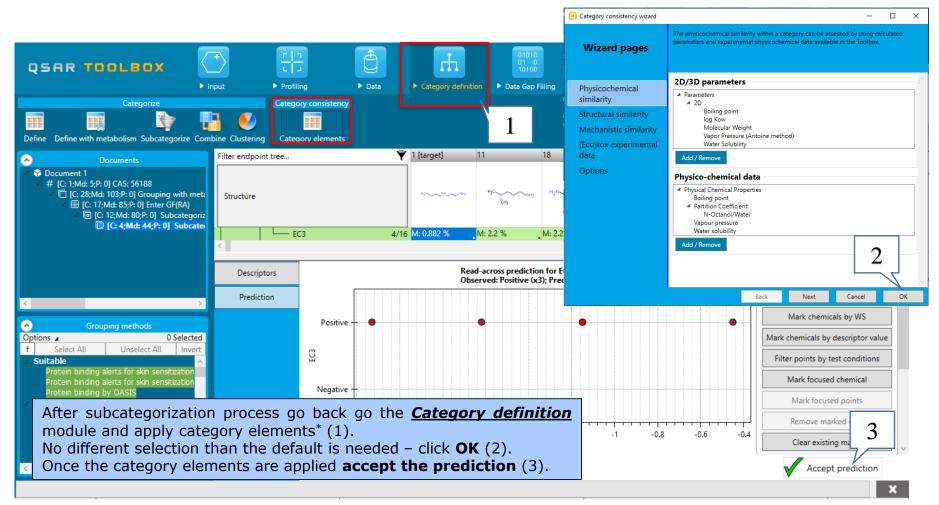


## **Data Gap Filling** Apply Read-across



Open **Select/filter data** and **Subcategorize** by: 1) *Protein binding alerts for skin sensitization by OASIS* profiler in combination with *Autoxidation simulator, 2*) Remove the different analogues; 3) Select *Structural similarity 4*) *Select* all analogues (3) similar less than 30% to the target chemical, by hold Ctrl button; 5) Click *Remove* 

## **Data Gap Filling** Apply Category consistency elements



\*For more information on category elements see Tutorial\_27\_TB 4.4. Category elements for assessing Category consistency.pdf

The OECD (Q)SAR Toolbox for Grouping Chemicals into Categories

#### Recap

- In the *Category definition* module you found analogues based on the alert with the best performance accounting for skin metabolism.
- In Data gap filling module you applied a read-across approach. Readacross is the appropriate data-gap filling method for "qualitative" endpoints like skin sensitisation. Since the most of the analogues and all five neighbouring tested chemicals in the category were positive, it was easy to accept the prediction of positive for the target chemical.
- Category consistency was checked by applying the category elements.
- You are now ready to complete the final module and to create the report.
- Click "Report" to proceed to the last module.

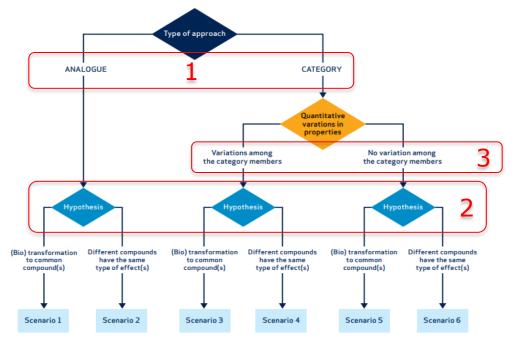
#### **Report** Overview

- The report module generates a report for predictions performed within the Toolbox.
- The report module contains a predefined report template which users can customize.
- Additionally a specific RAAF scenario could be chosen. Selection of one of the scenarios will append automatically the related assessment elements to the corresponding report sections.

## **Report** Selection of RAAF scenario

To select the applicable RAAF scenario for assessment, the following aspect should be identified<sup>\*</sup>:

- 1) the type of approach applied analogue approach or category approach;
- 2) the read-across hypothesis;
- 3) For category approach whether quantitative variations in the properties are observed among the category members must be considered.



\*Read-Across Assessment Framework (RAAF) available at https://echa.europa.eu/documents/10162/13628/raaf\_en.pdf

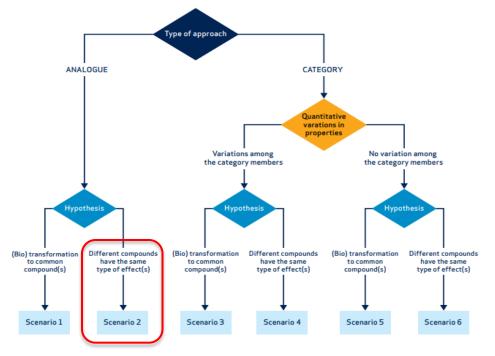
The OECD (Q)SAR Toolbox for Grouping Chemicals into Categories

#### **Report** Selection of RAAF scenario

For the current example:

- the type of approach applied analogue approach is used (threshold of  $\leq 3$  analogues is proposed by LMC for the analogue approach);
- the read-across hypothesis different compounds with common underlying mechanism for metabolites of source and target substances;

Based on that Scenario II was identified as appropriated for the current example.



## Read-Across Assessment Framework (RAAF) Scenario 2

- Scenario 2 covers the analogue approach for which the read-across hypothesis is based on different compounds with qualitatively similar properties.
- For the REACH information requirement under consideration, the property investigated in a study conducted with one source substance is used to predict properties that would be observed in a study with the target substance if it were to be conducted.
- The current case corresponds to Example 2 for Scenario 2 of the RAAF\*. The target (B) and the source chemicals (A) are biotransformed to substances causing the same type of effects through a common mechanism (A1 and B1). The rest of the obtained compounds, non-common for the target and the source substance does not influence the prediction of the property under the consideration.

|        | PARENT SUBSTANCES | (BIO)TRANSFORMATION |    | NON-COMMON<br>COMPOUNDS |
|--------|-------------------|---------------------|----|-------------------------|
| SOURCE | А                 | A → A1+ A2          | A1 | A2                      |
| TARGET | В                 | B→B1                | В1 | -                       |

\*Read-Across Assessment Framework (RAAF) available at https://echa.europa.eu/documents/10162/13628/raaf\_en.pdf

## Report

#### Generation report according to RAAF-Scenario 2

| QSAR TOOLBOX   | Input     Input  | ► Data Category definit      | 01010<br>01 0<br>10100<br>ion Data Gap Filling                      | ► Report  | X & S & B   |
|--|--|------------------------------|---|---|---|
| Reports  | Export   |                              | Customize report content an   | d appearance  | - <u> </u>  |
| Prediction Da 2 egory QMRF   | SMI File SDF File CAS List Data Matr                     | ix                           | Wizard pages  |   | to include into report by checking/unchecking the corresponding section box.<br>der of appearance by using buttons "Move Up" and "Move Down". |
| Documents  | Filter endpoint tree                                     | 1 [target]                   | 2   |   |   |
| 🔺 😪 Document 1   |  |                              | Customization<br>Customize report                                   | Add RAAF  | scenario 2 🗸 🗸  |
| <ul> <li>▲ # [C: 1;Md: 5;P: 1] CAS: 56188</li> <li>▲ □ [C: 28;Md: 103;P: 1] Groupin</li> <li>▲ ⊞ [C: 17;Md: 85;P: 1] Enter G</li> <li>▲ □ [C: 12;Md: 80;P: 1] Sut</li> </ul> | GF(RA)<br>bcategoriz                                     | 1/2~~~11/~~11/2              | Prediction<br>Target and pressummary                                |   | s (l)   |
| @ [C: 4;Md: 138;P: 1]  | Subcateg Photoinduced toxicity<br>Repeated Dose Toxicity | AW SW AOP                    | Prediction detains ()<br>Prediction details (II)<br>Target profiles | Prediction detail     Target profiles     Analogues select            |   |
|  | L <sub>P</sub> Skin                                      |                              | Analogues selection   | Appendix: Specif  | fic report explanations   |
|  |  |                              | details<br>M Category   | Category  |   |
|  | GPMT<br>HRIPT<br>  | 1 3/20 M: Category 1B        | Category definition<br>and members                                  | Category definition Consistency check<br>Consistency check<br>Options |   |
|  |  | R: Positive                  | Consistency check   | ☑ Data matrix   |   |
|  | EC3  | 17/45 M: 0.882 %<br>M: 0.9 % | Options<br>Data matrix  | Options   |   |
|  | → Miscellaneou<br>→ ToxCast                              | us 8/37 M: Category C        | M Options   |   |   |
|  | Toxicity to Reproduction                                 |                              |   |   | Move Up Move Down   |
|  | Profiling  |                              |   |   | word protection of the PDF files.<br>on is removed, this will be specified in the first page of the report                                    |
|  |  |                              |   |   | Back Next Cancel Create report  |
|  | Report module and clip                                   | ck on the cell with the      | e prediction;   |   | v   |

- 2. Click the **Prediction** button;
- 3. Check the box at the top to add RAAF scenario;
- 4. Select **Scenario 2** from the drop-down menu. Section of the report to which the related AE automatically appeared are getting yellow highlighted.

## Report

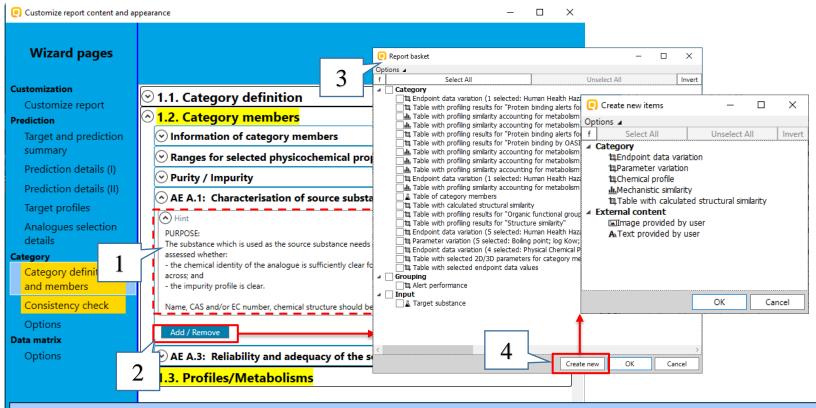
#### Generation report according to RAAF-Scenario 2

| Wizard pages  | Select which sections to include into report by checking/unchecking the com<br>Rearange sections order of appearance by using buttons "Move Up" and "M<br>1   |  |
|---|---|--|
| ustomization  | Add RAAF scenario   | Scenario 2   |
| Customize report  | Customize report content and appearance   | Customize report content and appearance  |
| Target and prediction<br>summary<br>Prediction details (I)  | I I I I I I I I I I I I I I I I I I I   | Wizard pages   |
| Prediction details (II)<br>Target profiles<br>Analogues selection<br>details<br>ategory<br>Category definition<br>and members<br>Consistency check<br>Options<br>Data matrix<br>Options | Customization<br>Customization<br>Customization<br>Customize report<br>Prediction<br>Customize report<br>Customize report<br>Customiz | Target and prediction summary       Structural similarity         Prediction details (I)       Structural similarity         Prediction details (I)       AE A.2: Link of structural similarity         Category       Mechanistic similarity         Category definition and members       Structural similarity         Iconsistency check       Structural similarity |

Each of the AEs will be considered in the next slides.

and members (2) and Consistency check (3).

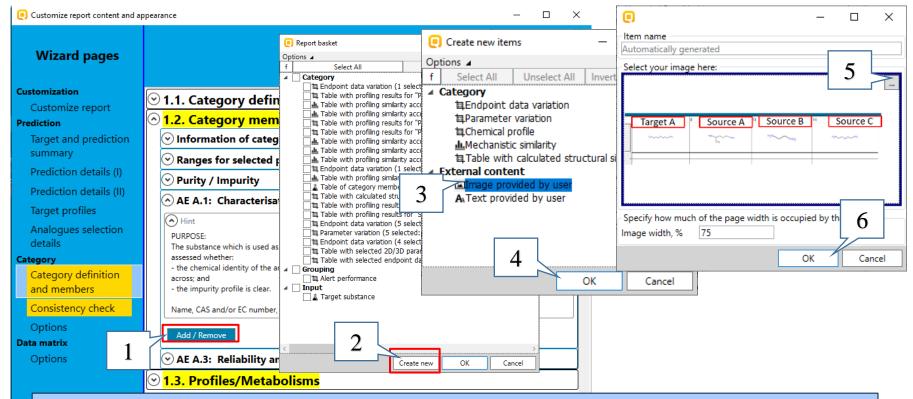
Create report



Hint for each of the assessment elements is available (1). Information can be included by clicking the **Add/Remove** button (2) located below the corresponding AE. The *Add/Remove* button invokes the so-called "*Report basket*" (3). The latter contain different items triggered by the actions of the user during the workflow (e.g. Alert performance calculation, applying of category elements, etc.).

Additionally, new items (including items with external content) can be created (4).

Items with external content (picture and text) will be added for AE 2.1. Compounds the test organism is exposed to



Click the **Add/Remove** button (1) and then **Create new** (2). Select to create an item with external content – *Image provided by user* (3) and click **OK** (4). New window appears where you can add your custom picture by Copy/Paste or browsing (5) to the directory in your PC where the desired picture is saved\*. Finally confirm by **OK** (6).

\*In the current example a picture illustrating the target chemical marked as **Target A** and source chemicals marked as **Source A**, **B** and **C** was prepared in advance.

| Customize report content and appearar   | Report basket     →      →      →      ×      ×       |
|---|---|
|   | Options ∡           f         Select All         Unselect All         Invert  |
| Wizard pages  | Category     Greate new items     Create new items     Create new items     Greate new |
| Customize report  | Image: Chemical profile ("Protein definition of the profile of th                         |
| summary<br>Prediction details (I)   | Information       Profiling similarity account       Image for         Ranges for       Category members       External content         Burnage provided by user       Structural similarity       External content         Purity / Im       Chemical profile (       3  |
| Target profiles   | AE A.1: Ch  |
| Category<br>Category definition<br>and members<br>Consistency check<br>Options<br>Data matrix | he sub<br>seese 1<br>Grouping<br>the ch<br>cross; and<br>he impurity pro-<br>lame, CAS and/c<br>Add / Remove  |

The newly created item appears in the *Report basket* (1). Now text will be also included. Click **Create new** (2), select **Text provided by user** (3) and click **OK** (4). Copy the following example text:

- Source substances (analogues) A, B and C have same primary aliphatic amine as the target substance A;
- The target and source substances are activated as a result of skin metabolism. Two alerting groups are identified: Aldehyde and Bis aldehyde;
- Primary group is defined based on the alert with highest performance: Bis aldehyde according to Protein binding alerts for skin sensitization profiler accounting for SS metabolism;
- Positive experimental data is available for the source substances A, B and C (references for the data could be also included)
- Substances A, B and C are used to predict the toxic effect of target A.

and paste it in the new window (5). Finally confirm by **OK** (6).

| <b>urity</b> manually editable field<br>ed by the user  |
|---|
| acterisation of source substance m dipboard No.1 (image provided by user)  Source Sou |
| files/M<br>profile<br>iles use<br>Using<br>ormati<br>or skin<br>Protei  |

Т

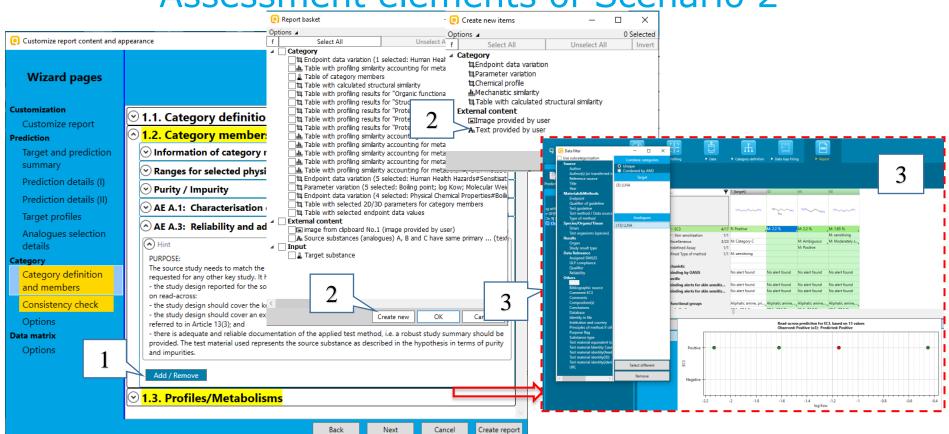
| Prediction<br>Target and prediction<br>summary<br>Prediction details (I)<br>Prediction details (II)<br>Target profiles<br>Analogues selection<br>details<br>Category   | Category definition<br>Category men<br>formation of cate<br>anges for selected physicoc<br>urity / Impurity<br>E A.1: Characterisation of s                                 | Table with profiling results for<br>Table with profiling similarity ac<br>Table with profiling similarity ac<br>Table with profiling similarity ac<br>Table with profiling results for<br>Table with profiling similarity ac<br>Table with profiling results for<br>Table wit  | counting for metabolism ("Autoxidat<br>counting for metabolism ("Skin meta<br>counting for metabolism ("Skin meta<br>ted: Human Health Hazards#Sensiti<br>counting for metabolism ("Autoxidat<br>ismilarity<br>Organic functional groups" | tization acc<br>ation simulat<br>Labolism sim<br>tization by (<br>ation simulat<br>Labolism sim<br>Liabolism sim<br>Liabolism sim<br>Lisation)<br>ation simulat | 4 | AE A.1:<br>Table   | ovided by the user<br>Characterisation of<br>of category member<br>S Name<br>-18-8 Iminol<br>propyl<br>9-55-7 DMAP/     | s<br>ois-3-<br>amine<br>A  | ANCE<br>SMILES<br>NCCCNCCCN<br>CN(C)CCCN   | Structure         HighIII1IIII1_IIIIII |
|--|---|--|---|---|---|--|---|--|--|--|
| Target and prediction<br>summary       Image: Constraint of the second secon | formation of cate<br>anges for selected physicoc<br>urity / Impurity<br>E A.1: Characterisation of s  | The Endpoint data variation (1 sele     The Table with profiling exitative, as     Table with profiling exitative, as     Table with profiling results for     Table with profiling results     Table with profiling resul  | cted: Human Health Hazards#Sensitä<br>counting for metabolism ("Autoxidat<br>Ismilarity<br>'Organic functional groups"<br>'Structure similarity'<br>tedd: Human Health Hazards#Sensitä<br>I: Boling point; Igo Kow; Molecular W           | itisation)<br>ation simulat<br>itisation#[s]  | 4 | 1 56<br>2 10   | -18-8 Iminol<br>propyl<br>9-55-7 DMAP/  | amine<br>A   | CN(C)CCCN  |  |
| summary<br>Prediction details (I)<br>Prediction details (II)<br>Target profiles<br>Analogues selection<br>details<br>Category  | anges for selected physicoc<br>urity / Impurity<br>E A.1: Characterisation of s   | Table of category members<br>Table with calculated structure<br>Table with profiling results for<br>Table with profiling results for<br>Ta Table with profiling results for<br>Table with profili | similarity<br>Organic functional groups"<br>'Structure similarity"<br>cted: Human Health Hazards#Sensiti<br>I: Boiling point; log Kow; Molecular W  | itisation#[s]   |   |  | 9-55-7 DMAP/  | A.   |  | H <sub>3</sub> C NH2   |
| Prediction details (II)<br>Target profiles<br>Analogues selection<br>details<br>ategory  | E A.1: Characterisation of s  | 日本 Endpoint data variation (5 sele<br>日本 Parameter variation (5 selected<br>日本 Endpoint data variation (4 sele   | cted: Human Health Hazards#Sensiti<br>I: Boiling point; log Kow; Molecular W  |   |   | 3 10   | 245.2   |  | NCCN   |  |
| Target profiles<br>Analogues selection<br>details<br>ategory   |   | Endpoint data variation (4 sele  |   | Weight; Va  |   |  | 7-15-3 Ethyle   | nediamine  | neen   | H2N NH2  |
|  | POSE:<br>substance which is used as the source<br>:ssed whether:  | Table with selected endpoint of External content     External content     Garage from cipboard No.3 (rm     A Source substances (analogues)     Grouping     Tablet performance     Jinput     A struct publication  |   |   |   |  | 1-40-0 DETA<br>from clipboard No.1<br>et A Source A   |  | NCCNCCN<br>ed by user)<br>Source C   | H2N~~Nr  |
| Category defin<br>and members 1 - the<br>Consistency check Nam<br>Options Add  | e chemical identity of the analogue is s<br>ss; and<br>e impurity profile is clear.<br>ne, CAS and/or EC number, chemical st<br>Id / Remove<br>E A.3: Reliability and adequ | tructure should be provided.   | JI JI   | Cancel  |   | Source<br>The ta<br>identif<br>Primar<br>bindin<br>Positiv | e substances (analog<br>rget and source subs<br>ied: Aldehyde and Bi<br>y group is defined ba<br>g alerts for skin sens | ues) A, B and C<br>tances are activ<br>s aldehyde;<br>ased on the aler<br>itization profiler | C have same primary a<br>ivated as a result of sk<br>at with highest perform<br>r accounting for SS me | (text provided by user)<br>aliphatic amine as the target substa<br>in metabolism. Two alerting group:<br>mance: Bis aldehyde according to P<br>etabolism;<br>s A, B and C (references for the dat  |

Two AE (AE A.1 and A.3) related to Scenario 2 are included in the Category definition and members section.

• **AE A.1 Characterization of source substance.** The user should open the *Report basket* by clicking the *Add/Remove* button (1) and manually select the item *Table with category members (2)*.Click OK button (3). If impurities/additives of the used analogues are available, they will appear under the **AE A.1** in *Purity / Impurity*. The current analogues have no additives/impurities.

Example of how the AE A.1. will look in the generated report is shown on the right(4).

• AE A.3 Reliability and adequacy of the source study should be filled in manually (5) (see on the next slide)



**AE A.3:** Click the **Add/Remove** button (1) and create new item with textual content (2) (see slide 55). In the text field paste the following example text: "*The all three source substance are tested according to the Local lymph node assay (LLNA) The study is used to predict the skin sensitization effect concerning LLNA study for the target substance"* Additionally a snapshot of the filter by test conditions window (3) could be added to confirm the consistency regarding the assay (create new image item).

|   |  | AE A.3: Reliability and adequacy of the source study<br>image from clipboard No.2 (image provided by user)  |
|---|--|---|
| Customization   | ✓ Information of category members  |   |
| Customize report<br>Prediction  | Ranges for selected physicochemical properties and calculated parameters   |   |
| Target and prediction summary   | <ul> <li>⊘ Purity / Impurity</li> </ul>  |   |
| Prediction details (I)  |  | Comparison and a second an |
| Prediction details (II)   | AE A.3: Reliability and adequacy of the source study   | Kanny         Jaka Age 100 K         Kanny K         Kanny K         Kanny K         Kanny K           Mark         Mark Mark Mark Mark Mark Mark Mark Mark   |
| Target profiles<br>Analogues selection<br>details<br>Category<br>Category definition<br>and members<br>Consistency check<br>Options<br>Data matrix<br>Options | Hint     PURPOSE:     The source study needs to match the default REACH requirements in terms of reliability and adequacy as     requested for any other key study. It has to be assessed whether:         - the study design reported for the source study is adequate and reliable for the purpose of the prediction based         on read-across:         - the study design should cover the key parameters in the corresponding test method referred to in Article 13(3);         - the study design should cover an exposure duration comparable to or longer than the corresponding method         referred to in Article 13(3); and         - there is adequate and reliable documentation of the applied test method, i.e. a robust study summary should be         provided. The test material used represents the source substance as described in the hypothesis in terms of purity         and impurities.         Add / Remove | The all three source substance are tested according (text provided by user)<br>The all three source substance are tested according to the Local lymph node assay (LLNA)<br>The study is used to predict the skin sensitization effect concerning LLNA study for the target substance<br><b>1.3. Profiles/Metabolisms</b><br>Profiles used for grouping/subcategorization:<br>- Using of "Skin metabolisms imulator" Combined parent and products requirements: Schiff base<br>formation >> Schiff base formation with carbonyl compounds >> Bis aldehydes (Protein binding aler   |
|   | Image from clipboard No.2 (image provided by user)     Edit     Preview     A     The all three source substance are tested according (text provide     Edit     Preview   | for skin sensitization by OASIS) (primary grouping) - Protein binding alerts for skin sensitization by OASIS with Skin metabolism simulator (subcategorization)   |
|   |  | - Structure similarity (subcategorization)  |

| Customize report content and a  | ppearance – 🗆 X   |  |
|---|---|--|
| Wizard pages  |   | AE 2.1: Compounds the test organism is exposed to  |
| Customization<br>Customize report<br>Prediction   | <ul> <li>⊙ 1.1. Category definition</li> <li>○ 1.2. Category members</li> </ul>   | Target substance (A) and the source substances are all (text provided by user)<br>Target substance (A) and the source substances are all aliphatic amines. • None of them has protein<br>binding alert identified in the parent structure • None of them undergo autoxidation transformation and<br>respectively do not activate as a result of abiotic<br>oxidation • All of the substances (target and sources) undergo skin metabolism transformations resulting in |
| Target and prediction summary   | <ul> <li>○ 1.3. Profiles/Metabolisms</li> <li>○ List of profiles/metabolisms</li> </ul>   | activation. In other words, the substances are activated enzymatically in the skin by producing aldehyde<br>and bis aldehyde metabolites • A schematic illustration of the skin metabolism is provided here:   |
| Prediction details (I)<br>Prediction details (II)<br>Target profiles<br>Analogues selection | <ul> <li>AE 2.1: Compounds the test organism is exposed to</li> <li>→ Hint</li> <li>PURPOSE:</li> <li>In this scenario, it is claimed that different compounds have the same effects for the property under consideration.</li> <li>Such different compounds may be the source and target substances themselves and/or their (bio)transformation</li> </ul> | image from clipboard No.6 (image provided by user)   |
| details<br>Category<br>Category definition<br>and members                                   | products. It has to be assessed whether:<br>- the compounds to which the test organism is exposed (after administration of the source and the target<br>substances) have been established in the documentation; and<br>- the provided evidence supports the explanation.  | QSAR Toolbox 4.4 QSAR TOOLBOX TPRF v4.4  |
| Consistency check<br>Options  | Add / Remove           A         Target substance (A) and the source substances are all (text provide Edit Preview 2)   | Chemicals category 3 / 13  |
| Data matrix<br>Options  | Image from clipboard No.6 (image provided by user)  | $H \xrightarrow{H} H \xrightarrow{Oxidative} O \xrightarrow{deamination} C \xrightarrow{C} C \xrightarrow{-C} + NH_3$  |
|   | Back Next Cancel Create report  |  |

An example text and illustration related to **AE 2.1: Compounds the test organism is exposed to** is shown above.

# Report

## Assessment elements of Scenario 2

| <ul> <li>Customize report content and a</li> </ul> | ippearance – 🗆 X  |
|--|---|
| Wizard pages                                       |   |
| Customization<br>Customize report                  | <ul> <li>② 2.1. Physicochemical similarity</li> <li>○ 2.2. Structural similarity</li> </ul> |
| Prediction<br>Target and prediction                | Structural similarity   |
| summary  | © Comments on structural similarity   |
| Prediction details (I)                             | ⊘ AE A.2: Link of structural similarity and differences with the proposed prediction        |
| Prediction details (II)                            | O 2.3. Mechanistic similarity   |
| Target profiles<br>Analogues selection             | Sechanistic similarity  |
| details  | ⊙ Comments on mechanistic similarity  |
| Category   | ⊘ AE 2.2: Common underlying mechanism, qualitative aspects                                  |
| Category definition<br>and members                 | ⊙ 2.4. Additional endpoints   |
| Consistency check                                  | © <u>2.5. Other AEs</u>   |
| Options  | ● AE 2.3: Common underlying mechanism, quantitative aspects                                 |
| Data matrix  | • AE 2.4: Exposure to other compounds than to those linked to the prediction                |
| Options  | ○ AE 2.5: Occurrence of other effects than covered by the hypothesis and justification      |
|  | ○ AE A.4: Bias that influences the prediction   |
|  |   |
| AEs included to the Consistency check              | section are six.  |
|  | Back Next Cancel Create report  |

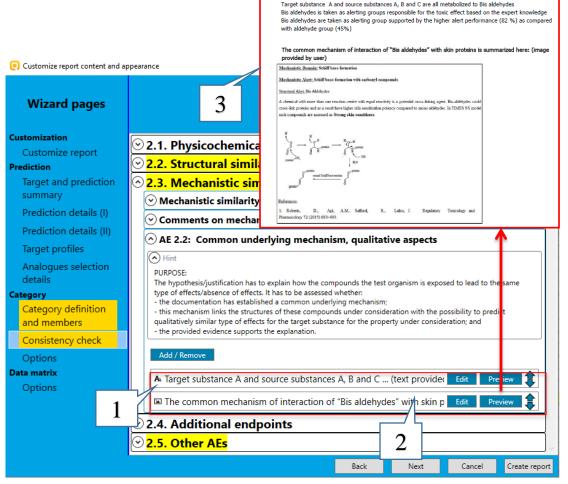
| Customize report content and app     Wizard pages | pearance — D X   | Table with calculated structural similarity<br>Options<br>Mode: Hologram, CombineAllFeatures<br>Measure: Dice<br>Molecular features: AtomCenteredFragments<br>Atom characteristics: AtomType, CountHAttached, Hybridization |
|---|--|---|
| Customization                                     | Structural similarity  | Calculated structure similarity   |
| Customize report                                  | Structure similarity profilers   | 1 11 18 19  |
| Prediction  | Options 🖌 2 Selected   | CAS 56-18-8 CAS 109-55-7 CAS 107-15-3 CAS 111-40-0  |
| Target and prediction                             | f Select All Unselect All Invert   | 1 100% 37.5% 61.5% 87.5%  |
| summary   | Image: Chemical elements   | CAS 56-18-8   |
| Prediction details (I)                            | Groups of elements   | 11 37.5 % 100% 36.4 % 28.6 %  |
| Prediction details (II)                           | □ Lipinski Rule Oasis<br>✓ Organic functional groups                               | 18 61.5 % 36.4 % 100% 72.7 %  |
| Target profiles                                   | Organic functional groups (nested) Organic functional groups (US EPA)              | CAS 107-15-3  |
| Analogues selection                               | Organic functional groups, Norbert Haider (checkmol)                               | 19 87.5 % 28.6 % 72.7 % 100%<br>CAS 111-40-0  |
| details   | ✓ Structure similarity  □ Unclassified   |   |
| Category  | Add / Remove   | Table with profiling results for "Organic functional groups"  |
| Category definition                               |  | 1 CAS# 56-18-8 2 CAS# 109-55-7 3 CAS# 107-15-3  |
| and memb  | Table with calculated structural similarity  | H2N NH NH2 H3C NH2 H2N  |
| Consistenc 1                                      | Table with profiling results for "Organic functional groups"                       | CH3 NH2 NH2 NH2   |
| Options 📕   | · · · · · · · · · · · · · · · · · · ·  | Amine, primary Amine, primary   |
| Data matrix                                       | Table with profiling results for "Structure similarity"                            | Amine, secondary Amine, tertiary Aliphatic amine, primary   |
| Options   | ⊙ Comments on structural similarity  | Aliphatic amine, primary Aliphatic amine, primary<br>Aliphatic amine, secondary Aliphatic amine, tertiary   |
|   |  | Alphade animy secondary Alphade anime, cerdary  |
|   |  | 4 CAS# 111-40-0   |
|   | Hint   | H <sub>2</sub> N NH <sub>2</sub>  |
| 2   | Add / Remove   | Amine, primary  |
|   |  | Amine, secondary  |
|   | A Structural similarity between Target substance A and (text provid Edit Preview 1 | Aliphatic amine, primary<br>Aliphatic amine, secondary  |

#### **AE A.2**. Link of structural similarity and differences with the proposed prediction is related to the structural similarity of the final category.

All items in the report basket related to the structural consistency of the category (1) are added automatically. The following example text can be added for AE A.2. (2) by analyzing the structural similarity items:

- Structural similarity between Target substance A and 3 source substances A, B and C according to Str.similarity profiler is in the range of [29-88%]
- They all have primary aliphatic amine based on the OFG profiler, while the target substance A and source substance B have additional secondary aliphatic amine and the source substance A has additional tertiary amine functional group.

| Customize report content and ap             | oppearance – – >   |   |
|---|--|---|
| Wizard pages                                |  |   |
| Customization<br>Customize report           | ⊙ 2.3. Mechanistic similarity  | All items in the report backet related to the |
| Prediction                                  | © Mechanistic similarity   | All items in the report basket related to the |
| Target and prediction                       | Mechanistic similarity   | mechanistic consistency of the category (1)   |
| summary                                     | Options  3 Selected  | are added automatically.                      |
| Prediction details (I)                      | f Select All Unselect All Invert   | ,   |
| Prediction details (II)<br>Target profiles  | <ul> <li>Suitable</li> <li>Protein binding alerts for skin sensitization according to GHS</li> <li>Protein binding alerts for skin sensitization by OASIS</li> <li>Protein binding by OASIS</li> </ul> |   |
| Analogues selection<br>details              | ▷ □ Plausible ▷ □ Unclassified   |   |
| Category                                    | Simulators Options  2 Selected   |   |
| Category definition                         | f Select All Unselect All Invert   |   |
| and members<br>Consistency check<br>Options | <ul> <li>✓ Suitable</li> <li>✓ Autoxidation simulator</li> <li>✓ Skin metabolism simulator</li> <li>P Plausible</li> <li>▶ Unclassified</li> </ul>   |   |
| Data matrix                                 | Add / Remove   |   |
| Options                                     | Lable with profiling similarity accounting for metabolism ("Skin me Edit Preview   |   |
| 1   | Table with profiling results for "Protein binding alerts for skin sensi Edit Preview   |   |
| 1   | Alert performance         Preview         \$   |   |
|   | © Comments on mechanistic similarity   |   |
|   |  |   |
|   | Back Next Cancel Create repo   | rt  |



AE 2.2: Common underlying mechanism, gualitative aspects

Target substance A and source substances A, B and C ... (text provided by user)

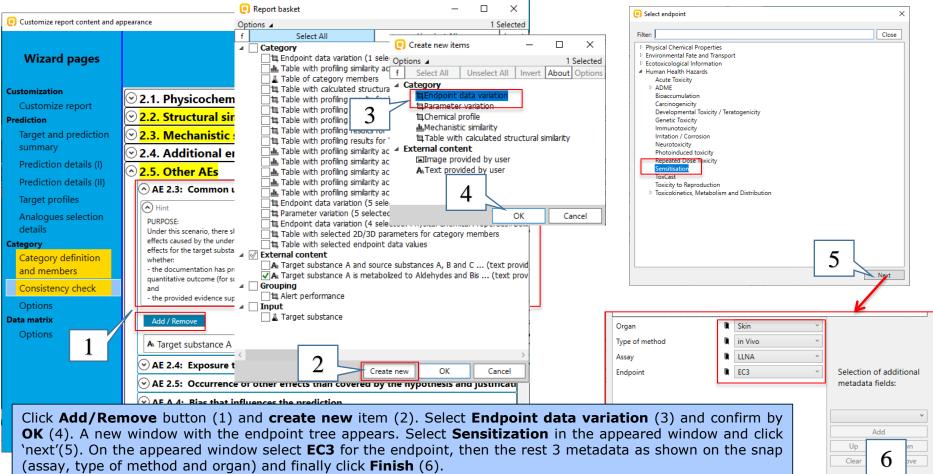
**AE 2.2. Common underlying mechanism, qualitative aspects** is related to the mechanistic similarity of the final category.

The following example text summarizing the results of the provided mechanistic similarity items can be added (1):

- Target substance A and source substances A, B and C all produce metabolite that is recognized as "Bisaldehyde" according to the "Protein binding alerts for skin sensitization by OASIS" profiler
- As a result of skin metabolism, along with the Bisaldehyde metabolite there are also generated simple aldehydes.
- By applying evaluation of alert performance the results showed that the "Bis aldehyde" has higher positive performance (82%) as compared with the simple aldehyde group (45%).

Additionally, metabolic maps (for each of the analogues), produced by external software or found in the literature, could be included to AE in order to support the mechanistic similarity of the category. In the current case mechanism of interaction of "Bis aldehyde" with skin proteins is added as external report item (2). How the AE looks like in the report is given too (3)

| Customize report content and a   | ppearance – 🗆 X   | AE 2.3. Common underlying mechanism,  |
|--|---|---|
| Wizard pages<br>Customization<br>Customize report<br>Prediction<br>Target and prediction<br>summary  | <ul> <li>⊙ 2.1. Physicochemical similarity</li> <li>⊙ 2.2. Structural similarity</li> <li>⊙ 2.3. Mechanistic similarity</li> </ul>  | <ul> <li>quantitative aspects is also related to the mechanistic similarity of the final category. The following information could be included here:</li> <li>1) textual or illustrated explanation why the common underlying mechanism leads to the same quantitative outcome (for source and target) with regard to the prediction of the property under consideration; and</li> </ul>  |
| Prediction details (I)<br>Prediction details (II)<br>Target profiles<br>Analogues selection<br>details<br>Category<br>Category definition<br>and members<br>Consistency check<br>Options<br>Data matrix<br>Options | <ul> <li>◆ 2.4. Additional endpoints</li> <li>◆ 2.5. Other AEs</li> <li>◆ AE 2.3: Common underlying mechanism, quantitative aspects</li> <li>◆ Hint         PURPOSE:         Under this scenario, there should be no biologically significant quantitative differences for the same type of         effects caused by the underlying mechanism or the differences should be used in a conservative prediction (i.e.         effects for the target substance are not likely to be under-predicted, worst case approach). It has to be assessed         whether:         - the documentation has provided an explanation why a common underlying mechanism leads to the same         quantitative outcome (for source and target) with regard to the prediction of the property under consideration;         and         - the provided evidence supports the explanation.         Add / Remove         Add / Remove         </li> </ul> | <ul> <li>Example text:</li> <li>Target substance A is metabolized to Aldehydes and Bis aldehydes</li> <li>It is expected that Bis-aldehydes as the alert with higher alert performance is responsible for the toxic effect</li> <li>Source substances A, B and C are metabolized to aldehydes and bis-aldehydes, too</li> <li>The available experimental EC3 values for the source substances corresponds to the positive effect.</li> <li>Similar toxic effects observed in sources substances supports the prediction for the target</li> <li>Toxic effects of all source substances and target are supported by the identified additional SS data</li> </ul> |
|  | A Target substance A is metabolized to Aldehydes and Bis (text pro       Edit       Preview         A Target substance A is metabolized to Aldehydes and Bis (text pro       Edit       Preview         A E 2.4: Exposure to other compounds than to those linked to the prediction       A E 2.5: Occurrence of other effects than covered by the hypothesis and justificati         A E A.4: Bias that influences the prediction       A E A.4: Bias that influences the prediction   | <ul> <li>2) evidences supporting the explanation.</li> <li>Include all available SS EC3 data for the target chemical and the source substances in all Toolbox database. See how to do this on the next two slides.</li> </ul>   |



This new item will provide information not only for the EC3 values used in read-across analysis, but for all available EC3 data for the chemicals from the category.

Back

Finish

| Wizard pages   |   |        |  |  |  |                    |
|--|---|--------|--|--|--|--------------------|
| ustomization   | 🕑 2.1. Physicochemical similarity   | ^      |  |  |  |                    |
| Customize report<br>rediction  |   |        |  |  |  |                    |
| Target and prediction  |   |        |  |  |  |                    |
| summary  | ⊙ 2.4. Additional endpoints   |        |  |  |  |                    |
| Prediction details (I)   |   | ור     | 2.5. Other AEs   |  |  |                    |
| Prediction details (II)  | AE 2.3: Common underlying mechanism, quantitative aspects   |        |  | <mark>derlying mechanism, quanti</mark><br>an Health Hazards data variati  |  |                    |
| Target profiles  | Hint  | וור    | Position   | Variation  | unit (family)  | Number of chemical |
| Analogues selection details  | PURPOSE:<br>Under this scenario, there should be no biologically significant quantitative differences for the same type of  |        | Sensitisation#Skin#in<br>Vivo#LLNA#EC3   | 0.882 ÷ 5.8  | %(Skin sensitization EC3(ratio))   | 4                  |
| tegory<br>Category definition<br>and members<br>Consistency check<br>Options | effects caused by the underlying mechanism or the differences should be used in a conservative prediction (i.e. effects for the target substance are not likely to be under-predicted, worst case approach). It has to be assessed whether:<br>- the documentation has provided an explanation why a common underlying mechanism leads to the same quantitative outcome (for source and target) with regard to the prediction of the property under considera and - the provided evidence supports the explanation. |        | Target substance A<br>It is expected that I<br>toxic effect<br>Source substances<br>The available exper<br>Similar toxic effects | is metabolized to Aldehydes a<br>Sis-aldehydes as the alert with<br>A, B and C are metabolized to<br>imental EC3 values for the sou<br>observed in sources substance | and Bis (text provided by user)<br>ind Bis aldehydes<br>higher alert performance is could by<br>aldehydes and bis-aldehydes, too<br>urce substances corresponds to a po-<br>es supports the prediction for the<br>tare supported by the identified addit | sitive effect.     |
| ta matrix  | Add / Remove  |        | AE 2.4: Exposure to<br>Not provided by use   |  | hose linked to the prediction  |                    |
| Options  | Endpoint data variation (1 selected: Human Health Hazards#Sensit Edit Preview   |        | AE 2.5: Occurrence<br>Not provided by use  |  | ed by the hypothesis and justifica   | ion                |
| 1  | A Target substance A is metabolized to Aldehydes and Bis (text prc Edit Preview   |        |  |  |  |                    |
|  | ○ AE 2.4: Exposure to other compounds than to those linked to the prediction  |        | QSAR Toolbox 4.4<br>Database version: 4.4  | QSAR TOO   | DLBOX  | TPRF               |
|  | $\odot$ AE 2.5: Occurrence of other effects than covered by the hypothesis and justific   | ati    |  |  |  |                    |
|  |   | $\sim$ |  |  |  |                    |
|  |   |        |  |  |  |                    |

| Customize report content and a  | ppearance – $\Box$ X   | Example text for AE 2.4. Exposure to other compounds than to those linked to the prediction:  |
|---|--|---|
| Wizard pages<br>Customization<br>Customize report<br>Prediction<br>Target and prediction<br>summary   | <ul> <li>⊘ 2.1. Physicochemical similarity</li> <li>⊙ 2.2. Structural similarity</li> <li>⊙ 2.3. Mechanistic similarity</li> </ul>   | <ul> <li>No impurities are available for the Source substances.</li> <li>The target substance A and the source substances A,B and C are enzymatically transformed to the reactive species "bisaldehyde" and simple "aldehyde".</li> <li>Aldehydes are not expected to cause skin sensitization effect by the expert knowledge;</li> <li>No other reactive metabolites are produced based on the enzymatic transformations.</li> </ul>   |
| Prediction details (I)<br>Prediction details (II)<br>Target profiles<br>Analogues selection<br>details<br>Category<br>Category definition<br>and members<br>Consistency check<br>Options<br>Data matrix | <ul> <li>◆ 2.4. Additional endpoints</li> <li>◆ 2.5. Other AEs</li> <li>◆ AE 2.3: Common underlying mechanism, quantitative aspects</li> <li>◆ AE 2.4: Exposure to other compounds than to those linked to the prediction</li> <li>◆ Hint</li> <li>Add / Remove</li> <li>◆ AE 2.5: Occurrence of other effects than covered by the hypothesis and justification</li> <li>◆ Hint</li> <li>Add / Remove</li> <li>◆ AE A4: Bias that influences the prediction</li> </ul> | <ul> <li>Example text for AE 2.5. Occurrence of other effects than covered by the hypothesis and justification:</li> <li>Target substance A and source substances B, C and D metabolize to "Bis aldehyde".</li> <li>"Bis aldehyde" is responsible for the skin sensitization effect of the source substances.</li> <li>No PBA for chromosomal aberration are identified in the target and source substances, nor in the structures of their metabolites.</li> <li>In general, the "aldehyde" moiety is well known alerting group for protein binding. In this respect, all toxicity effects which are based on covalent interaction with protein molecules could be considered as relevant.</li> </ul>  |
| section is p  | Add / Remove   | <ul> <li>Example text for AE A.4. Bias that influences the prediction:</li> <li>Target chemical is activated as result of skin metabolism by producing reactive metabolites – Bisaldehyde and simple aldehyde.</li> <li>The source chemicals have been selected based on the same reactivity pattern discovered for the target chemical, i.e. all source chemicals are activated as a result of skin metabolism producing same reactive metabolites – Bis aldehyde and simple aldehyde.</li> <li>The mechanism of interaction with skin proteins is Schiff base formation.</li> <li>Illustration of the enzymatic transformation is provided to AE 2.1.</li> <li>Illustration of the mechanism of interaction of Bis aldehyde to skin proteins is aldehyde to skin proteins is provided to activity.</li> </ul> |

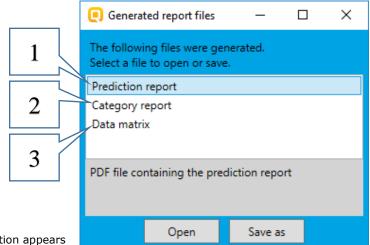
## **Report** Generation

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

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

# **RAAF AEs are included in the second** file.

All generated files should be provided when submitting a prediction.



\*Before appearing of the window with the report files additional window with information appears including how many chemicals used in the prediction belongs to the restricted databases. You can close it.

P

## **Report** Generated report files

| liction r  | -   |   |  |  |   | 0540 7  |   |  |
|--|---|---|--|--|---|---|---|--|
| QSAR   | Toolbox prediction for singl  |   |  |  |   | QSAR To   | olbox report for c  | ategory  |
|  | (in accordance with RAAF scena  | rio 2)  | The selected F   | RAAF scenari   | 0   |   |   |  |
| L  | (   |   | is specified in  | the first page   | e 🔶   | (in accord  | dance with RAAF sce   | nario 2)   |
| Date: 24 Mar 2020<br>Author(s):<br>Contact details:  |   |   |  |  |   |   |   |  |
|  | Target information  |   |  | <u>1, Cat</u>  | tegory definiti   | on  |   |  |
| Structural Information   | Numerical identifiers   | Chemical names  |  | 1.1.   | Category defir  | nition  |   |  |
|  |   |   |  | Cat  | egory name  |   |   | manually editable fie  |
| SMILES:  | CAS#: 56-18-8   | 1,3-Propanediamine,   |  |  | Not provided by   | the user  |   |  |
| NCCONCCON  | Other: EC Number:2002612  | N-(3-aminopropyl)-<br>1,3-Propanediamine,   |  |  | vered (target) e  |   |   | <b>0</b> 44  |
| Structure  | to .  | N1-(3-aminopropyl)-<br>1,3-propanediamine,  |  |  | - Human Health  | Hazards/Sensitisati   | on: EC3, LLNA, in Vivo, S   |  |
|  |   | n-(3-aminopropyl)-  |  |  | egory hypothes<br>Not provided by   |   |   | manually editable fe   |
|  |   |   |  |  | Category men  |   |   |  |
| A  | B C D E   | F G H   | I J K  | L M N  |   | egory members   |   |  |
|  |   |   |  |  |   |   |   |  |
| Data m   | Target chemical   | Neighbour #1  | Neighbour #2   | Neighbour #3   |   |   |   |  |
| Data m   | atrix rep   | Ort Neighbour #1  | Neighbour #2   | Neighbour #3   | le of categor   | y members   | CMTI EC   | Chruchure  |
| Data m   | atrix rep   | ort Neighbour #1  | Neighbour #2   | Neighbour #3   | le of categor<br>CAS  | v members<br>Name   | SMILES  | Structure  |
|  |   | H3C Neighbour #1  | Neighbour #2   | Neighbour #3   | le of categor   | Name<br>Iminobis-3-   | SMILES  | Structure  |
|  |   |   | H <sub>2</sub> N NH <sub>2</sub>   | Neighbour #3   | CAS<br>56-18-8  | v members<br>Name   | NCCONCCON   | Structure  |
|  |   | Harris Meighbour #1   | H2N NH2  | Neighbour #3   | le of categor<br>CAS  | Vame<br>Iminobis-3-<br>propylamine  |   | H2N~NHNH2  |
| Structure<br>CAS number  | H2N   | H3C NH2<br>CH3  | H2N NH2  | 111-40-0   | le of categor<br>CAS<br>56-18-8<br>109-55-7   | v members<br>Name<br>Iminobis-3-<br>propylamine<br>DMAPA  | NCCONCCON<br>CN(C)CCCN  | Structure           11/214-0111           11/21-0111           11  |
| Structure  | H2N~~NH1~~NH2   | H3C NOH2  | H <sub>2</sub> NNH <sub>2</sub>  | H21~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~  | CAS<br>56-18-8  | Vame<br>Iminobis-3-<br>propylamine  | NCCONCCON<br>CN(C)CCCN  | H2N~NHNH2  |
| Structure<br>CAS number<br>Chemical name   | H2N   | H3C NH2<br>CH3  | H2N NH2  | 111-40-0   | le of categor<br>CAS<br>56-18-8<br>109-55-7<br>107-15-3   | y members<br>Name<br>Iminobis-3-<br>propylamine<br>DMAPA<br>Ethylenediamin  | NCCONCCON<br>CN(C)CCON<br>te NCCN   | H34~ H4~ H4  |
| Structure<br>CAS number<br>Chemical name<br>Other identifier   | 56-18-8<br>Iminobis-3-propylamine<br>NCCCNCCCN  | HgC Vietz<br>CH3<br>109-55-7<br>DMAPA   | H2N NH2<br>107-15-3<br>Ethylenediamine   | H <sub>2</sub> N, , , , , , , , , , , , , , , , , , ,  | le of categor<br>CAS<br>56-18-8<br>109-55-7   | v members<br>Name<br>Iminobis-3-<br>propylamine<br>DMAPA  | NCCONCCON<br>CN(C)CCCN  | H34~ H4~ H4  |
| Structure CAS number Chemical name Other identifier SMILES Parameters Boiling point  | 56-18-8<br>Iminobis-3-propylamine<br>NCCCNCCCN  | HgCNHg<br>L109-55-7<br>DMAPA<br>CN(C)CCCN   | H2N NH2<br>107-15-3<br>Bthylenediamine<br>NCCN   | H <sub>2</sub> N <sub>2</sub> , <sub>10</sub> , - NH2<br>111-40-0<br>NCCNCCN<br>NCCNCCN  | le of categor<br>CAS<br>56-18-8<br>109-55-7<br>107-15-3   | y members<br>Name<br>Iminobis-3-<br>propylamine<br>DMAPA<br>Ethylenediamin  | NCCONCCON<br>CN(C)CCON<br>te NCCN   | H34~ H4~ H4  |
| Structure CAS number Chenical name Other identifier SMIES Parameters Boiling point log kow   | 56-18-8<br>Imnobis-3-propylamine<br>NCCCCCCN<br>unit<br>'C 228<br>-1.15   | HgCNARG<br>109-55-7<br>DMAPA<br>CNICICCCN<br>134<br>-0.45   | H2N  | HgNv_ypy_ltr2<br>111-40-0<br>NCCRCCN<br>NCCRCCN<br>189<br>-2.13  | le of categor<br>CAS<br>56-18-8<br>109-55-7<br>107-15-3<br>111-40-0   | y members<br>Name<br>Iminobis-3-<br>propylamine<br>DMAPA<br>Ethylenediamin<br>DETA  |   | H3 <sup>K</sup> V <sup>H</sup> V <sup>H</sup> V <sup>H</sup><br>H3 <sup>C</sup> V <sup>H</sup> V <sup>H</sup><br>H3 <sup>C</sup> V <sup>H</sup><br>H3 <sup>C</sup> NH2<br>H2 <sup>H</sup> NH2<br>H2 <sup>M</sup> V <sup>H</sup>  |
| Structure CAS number Chenical name Other identifier SMIES Parameters Boiling point log Kov Molecular Weight Molacular Weight   | 56-18-8           Iminobis-3-propylamine           NCCCNCCN           unit           'C           228           -1.15           Da           131           mHg           0.013  | HgCNHg<br>NHg<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG   | H <sub>2</sub> N   | HgNy 107 HH2<br>111-40-0<br>NCCNCCN<br>NCCNCCN<br>189<br>-2.13<br>103<br>0.274   | le of categor<br>CAS<br>56-18-8<br>109-55-7<br>107-15-3<br>111-40-0<br>s for selecte  | y members Name Inninoble-3- propylamine DMAPA Ethylenediamin DETA d physicochemica  | INCONCON<br>CN(C)CCON<br>INCON<br>NCONCON<br>Al properties and calcu  | H3 <sup>K</sup> V <sup>H</sup> V <sup>H</sup> V <sup>H</sup><br>H3 <sup>C</sup> V <sup>H</sup> V <sup>H</sup><br>H3 <sup>C</sup> V <sup>H</sup><br>H3 <sup>C</sup> NH2<br>H2 <sup>H</sup> NH2<br>H2 <sup>M</sup> V <sup>H</sup>  |
| Structure CAS number Chenical name Other identifier SMLES Parameters Bolling point log Kow Molecular Weight Vapor Pressure (Antoine method) Water Solubility   | 56-18-8<br>Iminobis-3-propylamine<br>NCCCNCCCN<br>unit<br>"C 228<br>Da 131  | HgCNHg<br>109-55-7<br>DMAPA<br>см(с)сссм<br>134<br>-0.45<br>102   | H2N  | H <sub>2</sub> N <sub>2</sub> , <sub>101</sub> , <sup>101</sup><br>111-40-0<br>NCCNCCN<br>NCCNCCN<br>189<br>-2.13<br>103   | le of categor<br>CAS<br>56-18-8<br>109-55-7<br>107-15-3<br>111-40-0<br>s for selecte  | y members<br>Name<br>Iminobis-3-<br>propylamine<br>DMAPA<br>Ethylenediamin<br>DETA  | INCONCON<br>CN(C)CCON<br>INCON<br>NCONCON<br>Al properties and calcul   | H3 <sup>K</sup> V <sup>H</sup> V <sup>H</sup> V <sup>H</sup><br>H3 <sup>C</sup> V <sup>H</sup> V <sup>H</sup><br>H3 <sup>C</sup> V <sup>H</sup><br>H3 <sup>C</sup> NH2<br>H2 <sup>H</sup> NH2<br>H2 <sup>M</sup> V <sup>H</sup>  |
| Structure CAS number Chenical name Other identifier SMIES Parameters Boiling point log Kov Molecular Weight Molacular Weight   | 56-18-8           Imnobis-3-propylamine           NCCENCCN           unit           'C           228           -1.15           Da           131           mHg           0.0913  | HgCNHg<br>NHg<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG<br>NHG   | H <sub>2</sub> N   | HgNy 107 HH2<br>111-40-0<br>NCCNCCN<br>NCCNCCN<br>189<br>-2.13<br>103<br>0.274   | le of categor<br>CAS<br>56-18-8<br>109-55-7<br>107-15-3<br>111-40-0<br>s for selecte  | y members Name Iminobis-3- propylamine DMAPA Ethylenediamin DETA d physicochemica p parameters data   | INCONCON<br>CN(C)CCON<br>INCON<br>NCONCON<br>Al properties and calcul   | H3 <sup>K</sup> V <sup>H</sup> V <sup>H</sup> V <sup>H</sup><br>H3 <sup>C</sup> V <sup>H</sup> V <sup>H</sup><br>H3 <sup>C</sup> V <sup>H</sup><br>H3 <sup>C</sup> NH2<br>H2 <sup>H</sup> NH2<br>H2 <sup>M</sup> V <sup>H</sup>  |
| Structure CAS number Chenical name Other identifier SMILES Parameters Boiling point Ig Kow Moiscular Weight Vapor Pressure (Antoine method) Water Solubility   | 56-18-8           Iminobis-3-propylamine           NCCENCCN           unit           'C           228           -1.15           Da           131           meHz           0.0313           mg/L           16-06   | HgC<br>109-55-7<br>DMAPA<br>CNICJCCCN<br>134<br>-0.45<br>102<br>9.41<br>16+06   | H2N  | HgNy 100 - 111-400<br>NCCNCCN<br>189<br>-2.13<br>103<br>0.274<br>1E406   | le of categor<br>CAS<br>56-18-8<br>109-55-7<br>107-15-3<br>111-40-0<br>s for selecte<br>Table with 20   | y members Name Iminoble-3- propylamine DMAPA Ethylenediamin DETA d physicochemica atamme  | INCONCON<br>CN(C)CCON<br>INCON<br>NCONCON<br>Al properties and calcul<br>variation  | H3 <sup>K</sup> V <sup>H</sup> V <sup>H</sup> V <sup>H</sup><br>H3 <sup>C</sup> V <sup>H</sup> V <sup>H</sup><br>H3 <sup>C</sup> V <sup>H</sup> V <sup>H</sup><br>H3 <sup>C</sup> V <sup>H</sup><br>H3 |
| Structure CAS number Chenical name Other identifier SMLES Parameters Boiling point log Kow Molecular Weight Vapor Pressure (Antoine method) Water Solubility Profilers Profilers   | 56-18-8           Iminobis 3-propylamine           NCCCNCCN           unit           "C           228           Da           135           Da           14           0.0513           mg/L           15-66           stion           Parent and 5 metabolite(s);  | HgC<br>109-55-7<br>DMAPA<br>CN(C)CCN<br>134<br>-0.45<br>102<br>9.41<br>126-06<br>Parent and 12 metabolite(s);   | H2N  | H <sub>2</sub> N <sub>2</sub> , h <sub>1</sub> , h <sub>1</sub> , h <sub>1</sub><br>111-40-0<br>NCCNCCN<br>NCCNCCN<br>129<br>-2.13<br>-2.13<br>-0.274<br>16+06<br>Parent and 5 metabolits(s);  | le of categor<br>CAS<br>56-18-8<br>109-55-7<br>107-15-3<br>111-40-0<br>s for selecte<br>Table with 21<br>Parameter ni   | y members Name Inmobile-3- propylamine DMAPA Ethylenediamin DETA d physicochemica parameters data ime 103   | INCONCON<br>CN(C)CCON<br>INCON<br>NCON<br>NCONCON<br>Internation<br>Variation<br>Variation  | H3K         H3K         H4K           H3C         H3C         H3K           H3K         H2K         H4K           H2K         H1K         H4K  |
| Structure CAS number Chemical name Other identifier SMILS Parameters Boiling point log Kow Molecular Weight Vapor Pressure (Antoine method) Water Solubility Profiles sued for grouping/subcategoriza  | 56-18-8           Iminobis-3-propylamine           NCCONCCN           unit           °C           228           Da           131           me/L           15-66           rtion           Parent and 5 metabolite(s);           Has all of the required categories: Schl           base formation >Schlf base formation   | HgC   | H2N  | HgN, 111-40-0<br>NCCNCCN<br>NCCNCCN<br>189<br>-2.13<br>103<br>0.274<br>18+06<br>Parent and 5 metabolite(s);<br>Has all of the required astagories. Schiff<br>base formation Schiff base formation  | le of categor<br>CAS<br>56-18-8<br>109-55-7<br>107-15-3<br>111-40-0<br>s for selecte<br>Table with 21<br>Parameter ni<br>it   | y members Name Iminobis-3- propylamine DMAPA Ethylenediamin DETA d physicochemica o parameters data ime 103 -2.1                                      | NCCONCCCN<br>CN(C)CCCN<br>ne NCCN<br>NCCNCCN<br>al properties and calcu<br>variation<br>Variation<br>+ 228<br>(3 + -0.45  | H3 <sup>K</sup> H3 <sup>K</sup> H4 <sup>K</sup> H3 <sup>K</sup> H3 <sup>K</sup> H4 <sup>K</sup> H3 <sup>K</sup> H2 <sup>K</sup> H4 <sup>K</sup> H3 <sup>K</sup> H1 <sup>K</sup> H1 <sup>K</sup> <td< td=""></td<>  |
| Structure CAS number Chenical name Other identifier SMIES Parameters Boiling point log Kow Molecular Weight Vapor Pressure (Antoine method) Water Solubility Profiles Profiles used for grouping/subcategoriza Using of "Skin metabolism simulator" CC   | 56-18-8           Imnobis-3-propylamine           NCCCXCCN           unit           'C           228           -1.15           Da           131           mm/g           16-06           trion           all of the required categories: Schilbase formation >> Schilf base formation >> Schil   | HgC         109-55-7           DMAPA         ON(C)CCCN           134         -0.45           102         9.41           1E+06   | H2N  | HgN         HgN         HgN           111-40-0         NCCNCCN           NCCNCCN         NCCNCCN           189         -2.13           103         0.274           18-06         IE+06   | te of categor<br>CAS<br>56-18-8<br>109-55-7<br>107-15-3<br>111-40-0<br>s for selecte<br>Table with 21<br>Parameter nu<br>it<br>Veight   | y members Name Iminobis-3- propylamine DMAPA Ethylenediamin DETA d physicochemics o parameters data mme 103 -2.1 60.1                                 | NCCONCCON<br>CN(C)CCON<br>ine NCON<br>NCCNCON<br>al properties and calcul<br>variation<br>Variation<br>Variation<br>1 + 228<br>13 + -0.45<br>1 + 131  | H3 <sup>K</sup> H3 <sup>K</sup> NH           H3 <sup>C</sup> NH         NH2           H2 <sup>N</sup> NH2         NH2           H2 <sup>N</sup> NH2         NH2           Intervention         NH2         NH2  |
| Structure CAS number Chemical name Other identifier SMILS Parameters Boiling point log Kow Molecular Weight Vapor Pressure (Antoine method) Water Solubility Profiles sued for grouping/subcategoriza  | 56-18-8           Imnobis-3-propylamine           NCCCXCCN           unit           'C           228           -1.15           Da           131           mm/g           16-06           trion           all of the required categories: Schilbase formation >> Schilf base formation >> Schil   | HgC   | H2N-VIH2<br>107-15-3<br>Ethylerediamine<br>NCCN<br>105<br>162<br>601<br>19<br>16-06<br>16-06<br>19<br>16-06<br>19<br>16-06<br>16-06<br>19<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06<br>16-06 | H <sub>0</sub> N <sub>0</sub> , H <sub>0</sub><br>111-40-0<br>NCCNCCN<br>NCCNCCN<br>129<br>-2.13<br>103<br>0.274<br>14+06<br>Parent and 5 metabolite(s);<br>Has all of the required astagories. Schiff<br>base formation schiff base formation<br>with carbony(compounds >> bis<br>with carbony(compounds >> bis   | le of categor<br>CAS<br>56-18-8<br>109-55-7<br>107-15-3<br>111-40-0<br>s for selecte<br>Table with 21<br>Parameter ni<br>it<br>Veight<br>sure (Antoine                            | y members Name Iminoble-3- propylamine DMAPA Ethylenediamin DETA d physicochemica 103 -2.1 0 cmethod) 0.05  | NCCONCCON           CN(C)CCCN           CN(C)CCCN           In NCCN           NCCNCCN           In Properties and calcul variation           Variation           + 228           13 + -0.45           + 131           913 + 19                                  | H3 <sup>K</sup> NH           H3 <sup>C</sup> NH2           H3 <sup>C</sup> NH2           H2 <sup>N</sup>   |
| Structure CAS number CAS number Chemical name Other identifier SMIES Parameters Boiling point log kow Molecular Weight Molecular Weight Molecular Weight Water Solubility Profilers Profilers Profilers Profilers Dentify Skin metabolism simulator* CC Shiff base formation with formation >> Schiff base formation with centoryl compodex >> Bis allehydes (f  | 56-18-8           Iminobis-3-propylamine           NCCRVCCN           unit           °C         228           0         -1.13           0.013         151.3           mm/t         0.021.6           1         154.5           mm/t         0.021.6           trion         Frede           1         154.6           mark         0.021.6           trion         Frede           1         154.6           1         154.6           1         154.6           1         154.6           1         154.6           1         154.6           1         154.6           1         154.6           1         154.6           1         154.6           1         154.6           1         154.6           1         164.7           1         164.7           1         164.7           1         164.7           1         164.7           1         164.7           1         164.7           1         164.7  | HgC   | H2N-VII-2<br>107-15-3<br>Ethylenediamine<br>NCCN<br>103<br>162<br>163<br>164<br>163<br>164<br>164<br>164<br>164<br>164<br>164<br>164<br>164  | HgHu- Har- HPS<br>111-40-0<br>NCCNCCN<br>NCCNCCN<br>NCCNCCN<br>129<br>- 2.13<br>103<br>- 103<br>- 104<br>- | te of categor<br>CAS<br>56-18-8<br>109-55-7<br>107-15-3<br>111-40-0<br>s for selecte<br>Table with 21<br>Parameter nu<br>it<br>Veight   | y members Name Iminobis-3- propylamine DMAPA Ethylenediamin DETA d physicochemics o parameters data mme 103 -2.1 60.7                                 | NCCONCCON           CN(C)CCCN           CN(C)CCCN           In NCCN           NCCNCCN           In Properties and calcul variation           Variation           + 228           13 + -0.45           + 131           913 + 19                                  | H3 <sup>K</sup> H3 <sup>K</sup> NH           H3 <sup>C</sup> NH         NH2           H2 <sup>N</sup> NH2         NH2           H2 <sup>N</sup> NH2         NH2           Intervention         NH2         NH2  |
| Structure CAS number CAS number Chemical name Other identifier SMILES Parameters Boiling point log Kow Molecular Weight Vapor Pressure (Antoine method) Water Solubility Profiles Profiles Profiles Profiles used for grouping/subcategoriza Using of "Skin metabolism simulato" CG parent and products requirements. Schif formation >> Schiff bass Straation by CG primary grouping)   | S6-18-8     Iminobis-3-propylamine     NCCRUCCN unit     C 228     -1.15     Da     1.15     Da     Schift base formation > 35  | HsG<br>109-55-7<br>DMAPA<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>C | H2N-<br>107-15-3<br>Ethylenediamine<br>NCCN<br>103<br>1-62<br>601<br>109<br>109<br>109<br>109<br>109<br>109<br>109<br>1  | Holing of the second se   | le of categor<br>CAS<br>56-18-8<br>109-55-7<br>107-15-3<br>111-40-0<br>s for selecte<br>Table with 21<br>Parameter nu<br>it<br>Veight<br>sure (Antoine<br>bility                  | members Name Iminoits-3- propylamine DMAPA Ethylenediamin DETA d physicochemica parameters data me 103 -2.1 60. method) 0.05                          | NCCONCCON           CN(C)CCCN           CN(C)CCCN           In NCCN           NCCNCCN           In Properties and calcul variation           Variation           + 228           13 + -0.45           + 131           913 + 19                                  | H3 <sup>K</sup> NH           H3 <sup>C</sup> NH2           H3 <sup>C</sup> NH2           H2 <sup>N</sup>   |
| Structure CAS number Chenical name Other identifier SMILES Parameters Boiling point [og Kow   Molecular Weight Vapor Pressure (Antoine method) Water Solubility Profiles Profiles used for grouping/subcategorizat Using of "Skin metabolism simulator" Cc parent and products requirements: Schill formation >> Schill base formation with carbonyl cemponds >> Bis aldehydes (Is binding learts skin sensitization by C (primary grouping)                         | Solution     Solution  | Hyperformation with carbony companys with arbony compounds so that formation with carbony companys so that base formation with carbony compounds so that base fo  | H2N  | Halfson and the second  | le of categor<br>CAS<br>56-18-8<br>109-55-7<br>107-15-3<br>111-40-0<br>s for selecte<br>Table with 21<br>Parameter nu<br>it<br>Veight<br>sure (Antoine<br>bility                  | members Name Iminoits-3- propylamine DMAPA Ethylenediamin DETA d physicochemica parameters data me 103 -2.1 60. method) 0.05                          | NCCONCCCN           CN(C)CCCN           CN(C)CCCN           ne         NCCN           NCCNCON           al properties and calcul           variation           Variation           + 228           13 + -0.45           1 + 131           913 + 19           06 | H3 <sup>K</sup> NH           H3 <sup>C</sup> NH2           H3 <sup>C</sup> NH2           H2 <sup>N</sup>   |
| Structure CAS number CAS number Chemical name Other identifier SMILES Parameters Boiling point log Kow Molecular Weight Vapor Pressure (Antoine method) Water Solubility Profiles Profiles Profiles Profiles used for grouping/subcategoriza Using of "Skin metabolism simulato" CG parent and products requirements. Schif formation >> Schiff bass Straation by CG primary grouping)   | Solution     Solution  | HsG<br>109-55-7<br>DMAPA<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CCN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>CN(C)CN<br>C | H2N-<br>107-15-3<br>Ethylenediamine<br>NCCN<br>103<br>1-62<br>601<br>109<br>109<br>109<br>109<br>109<br>109<br>109<br>1  | Holing of the second se   | le of categor<br>CAS<br>56-18-8<br>109-55-7<br>107-15-3<br>111-40-0<br>5 for selecte<br>Table with 21<br>Parameter ni<br>it<br>Veight<br>sure (Antoine<br>billty<br>Table with PI | y members Name Iminobis-3- propylamine DMAPA Ethylenediamin DETA d physicochemica 0 parameters data ime 103 -2.1 method) 0.00 1E4 hysical Chemical Pn | NCCONCCON<br>CN(C)CCON<br>ine NCON<br>NCONCON<br>all properties and calcul<br>variation<br>Variation<br>Variation<br>+ 228<br>13 + 0.45<br>14 + 131<br>213 + 19<br>-06<br>operties data variation   | H3 <sup>K</sup> H3 <sup>K</sup> NH         NH           H3 <sup>C</sup> NH         NH         NH         NH           H2 <sup>H</sup> NH   |
| Structure  CAS number Chemical name Other identifier SMIES  Parameters Boiling point log kow Molecular Weight Molecular Weight Molecular Weight Water Solubility Profiles Profiles Profiles Profiles used for grouping/ubcategorized Using of "Skin metabolism simulats" CC parent and products requirements. Schif formation >> Schifbase formation with formation >> Schifbase formation by C primary grouping) Protein binding alerts for skin sensitization by C | S6-18-8     Iminobis-3-propylamine     NCCNCCN unit     C     228     115     Da     1.15     Da     S0     Da     S0     Da     S0     S0 | Hack-constructions and the construction of the  | H2N  | Holi-Conception<br>111-40-0<br>NCCKCCN<br>NCCKCCN<br>NCCKCCN<br>129<br>- 2.13<br>- 103<br>- 103   | le of categor<br>CAS<br>56-18-8<br>109-55-7<br>107-15-3<br>111-40-0<br>s for selecte<br>Table with 21<br>Parameter nu<br>it<br>Veight<br>sure (Antoine<br>bility                  | y members Name Iminobis-3- propylamine DMAPA Ethylenediamin DETA d physicochemica 0 parameters data ime 103 -2.1 method) 0.00 1E4 hysical Chemical Pn | NCCONCCCN           CN(C)CCCN           CN(C)CCCN           ne         NCCN           NCCNCON           al properties and calcul           variation           Variation           + 228           13 + -0.45           1 + 131           913 + 19           06 | H3 <sup>K</sup> H3 <sup>K</sup> NH         NH           H3 <sup>C</sup> NH         NH         NH         NH           H2 <sup>H</sup> NH   |

The OECD (Q)SAR Toolbox for Grouping Chemicals into Categories

## Congratulation

- You have now been introduced to the RAAF scenario;
- You have now been introduced to the *Report basket*.
- You have now been introduced to the AEs related to Scenario 2.
- Note, proficiency comes with practice!