

MINERVA Home

User manual

Admin manual

Examples

# MINERVA platform: User's manual

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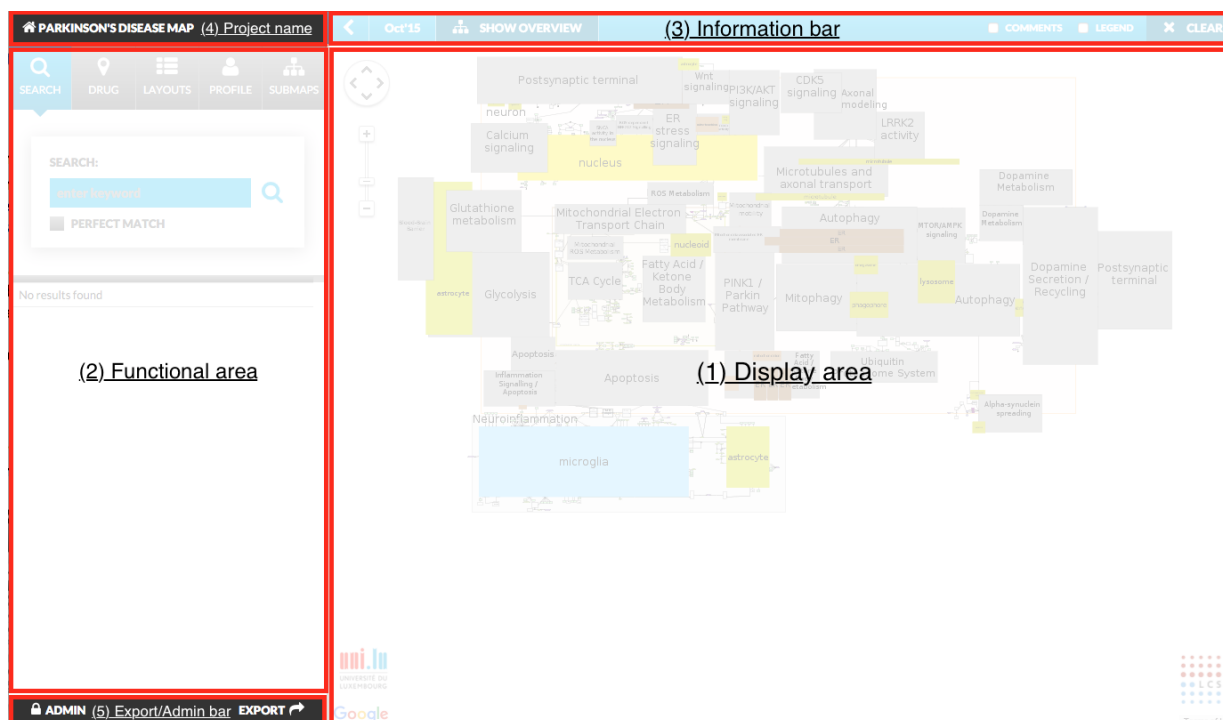
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## User view

User view refers to the visualization and functionalities accessed by users of the content hosted by your MINERVA instance.

## Main view

The main view of the MINERVA platform is summarized in the figure below.



Main components of this view are

- **Display area (1):** where the contents of the projects are visualized
- **Functional area (2):** allowing for advanced interaction with explored content
- **Information bar (3):** containing additional overlay functions
- **Project name (4)**
- **Admin/Export bar (5):** allowing administrator login and advanced export of the contents

## Accessing the project

Your instance of MINERVA platform can host many projects, which are uploaded via the administrator view (see [Admin manual - Add project](#)). They are accessed by a provided, dedicated web address.

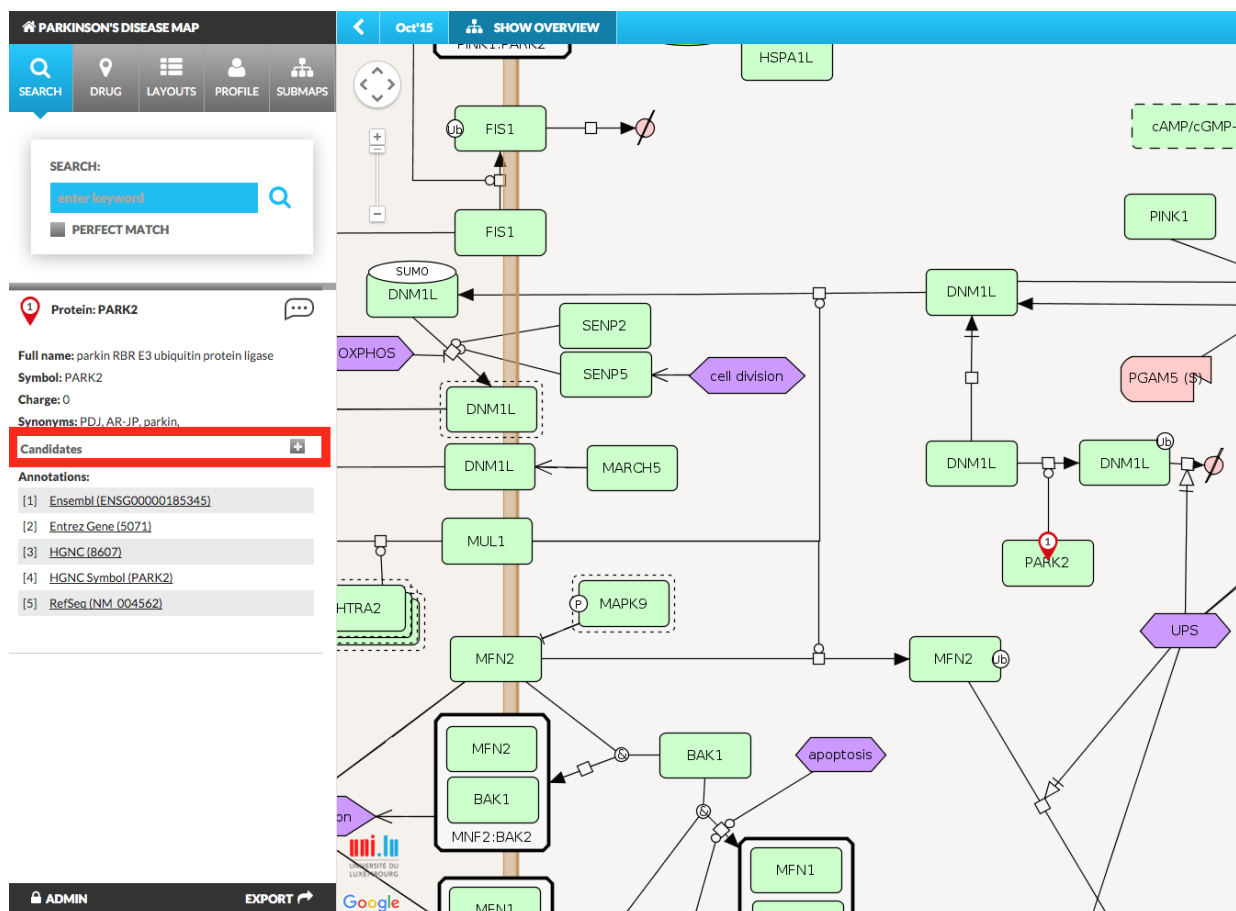
## Exploring the display area

The content is visualized using Google Maps API, and allows similar pan and zoom functionalities. The content is interactive, the user can click on an element or interaction to examine additional details displayed in the left panel (functional area).

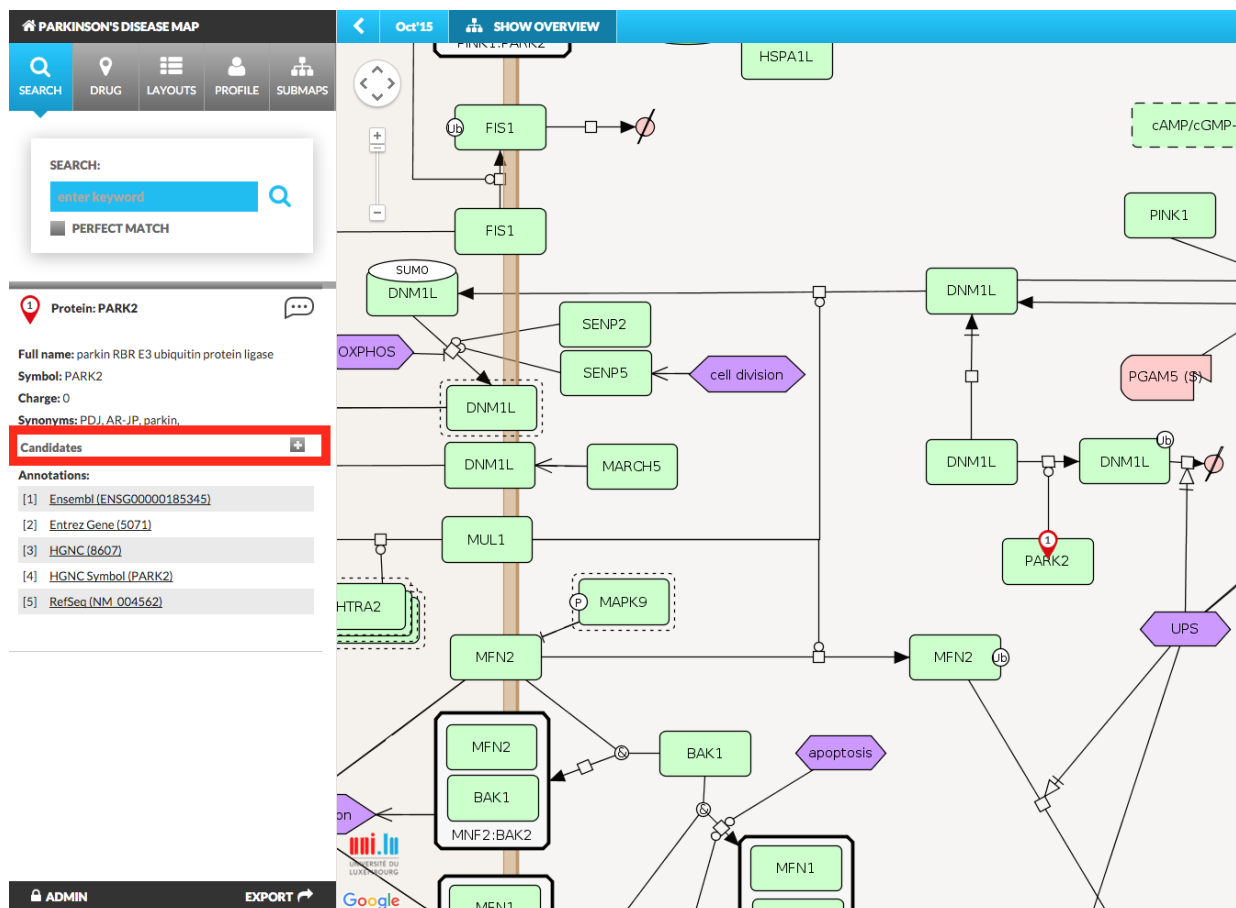
The content is by default displayed in a semantic zoom mode, where compartments and areas in the submitted file cover underlying elements on higher levels of zoom. This view is generated procedurally, directly from the uploaded content. This view is generated automatically from the layout of the CellDesigner file. MINERVA platform calculates coverage of bigger areas by smaller, and assigns them to appropriate zoom levels. For more details see [Section Content curation](#). You can turn off the semantic zoom view by going to the **Layouts** tab in the left panel (functional area), and changing the view to **Network** (see also [Section Layouts](#)).

## Candidate interactions

If provided (see [Admin manual - Add project](#) and [Admin manual - Source file](#)), candidate interactions are displayed in the area that have been identified by exploratory analyses, like text mining in network analysis. Elements, for which candidate interactions are suggested, have **Candidates** bar below their annotation (see below).

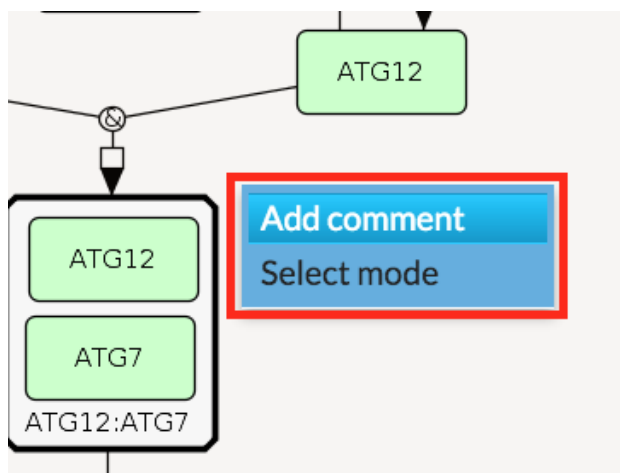


After expanding with the "+" button, a list is revealed with candidate molecules, pathways, or publications pertinent to the selected element (see below). The table of candidates for PARK2 involves a gene suggested by PathExpand analysis (left column) and interactions with genes and pathways suggested by text mining (right column). As text mining allows to link to the source article, the referenced papers were also provided. Some elements are duplicated (ATXN2), as they are suggested by different articles.



## Annotating, selecting and downloading the display area

Right-click in the display area invokes a contextual menu with two options - (see below).



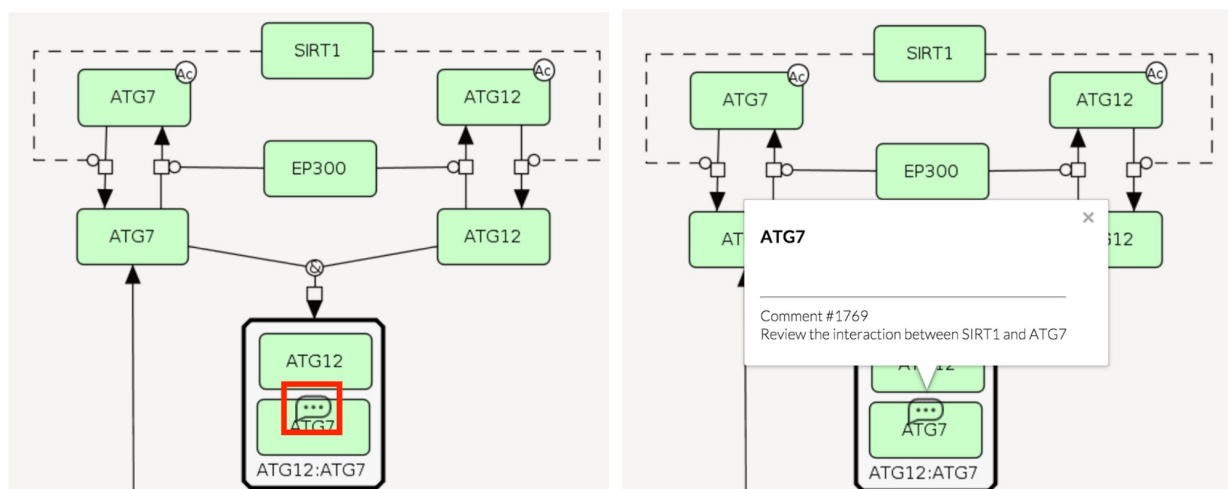
## Add comment

This functionality allows to annotate contents in the display area. Clicking the **Add comment** button invokes a form that can be filled out by the user and sent to the administrators of the project. The field **Pinned** controls, whether the comment will be visible in the map (see below, left).

The image shows two screenshots of the 'COMMENT' form. The left screenshot shows the form with 'Pinned' set to 'Yes' and a comment about SIRT1 and ATG7. The right screenshot shows the form with 'Pinned' set to 'No' and a dropdown menu for 'Type'.

**Type** field is a drop-down menu, listing elements nearby to the click location. This allows to choose and attach the comment to a particular element or interaction (see above, right).

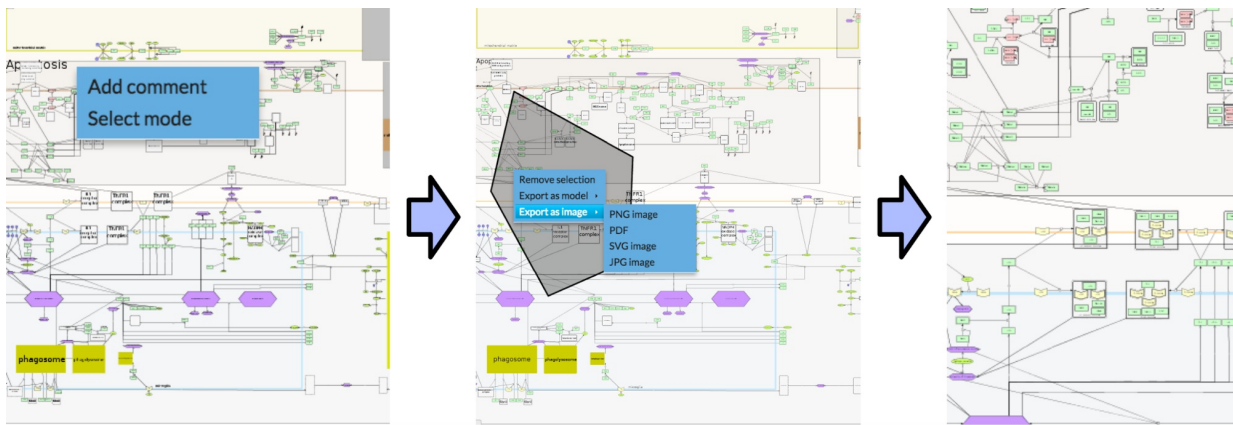
After sending, and if the field **Pinned** was set to **Yes**, the comment becomes visible in the display area, as shown below, to the left (after checking the **Comments** checkbox, see [Comments](#)).



Clicking on the comment bubble displays annotated element and the text of the comment (see above, right). Name and email are not disclosed, they will be accessible only to project and platform administrators (see [Admin manual - Comments](#)).

## Select mode

Clicking the **Select mode** enables the functionality supported by Google Maps API, allowing to select an arbitrary shape in the display area. The shape then can be downloaded in various formats, either as a model (.xml file) or as an image (see below).



- **Export as model** produces a file acceptable by either CellDesigner, or pure SBGN editors, containing the editable fragment of the selected display area. Importantly, in the case of CellDesigner export, all additional annotations provided by MINERVA platform are downloaded as well.
- **Export as image** produces a rectangular image containing the selection. Export to vector graphics is supported, allowing to modify and enhance the downloaded image.

## Content curation

MINERVA framework handles SBGN-compliant format, produced either by CellDesigner (<http://www.celldesigner.org>) or SBGN editors, like SBGN-ED (<https://immersive-analytics.infotech.monash.edu/vanted/addons/sbgn-ed>). MINERVA relies on such externally curated content.

Moreover, a number of additional functionalities of MINERVA operates on metadata that can be provided in the SBGN-compliant file itself. These are the following:

- **Processing of existing annotations:** annotations to elements or interactions embedded within CellDesigner file (MIRIAM > Add relation) are automatically parsed and processed. They can be used to extensively annotate elements (see [Admin manual - Configure automatic annotation](#)) and they can be verified by MINERVA platform against a set of predefined content-governing rules (see [Admin manual - Configure automatic verification](#)).
- **Procedural generation of semantic zoom** : information on complexes and overlaying compartments is extracted from SBGN-compliant files to generate **Pathways and compartments** view, where on the high level of zoom bigger compartments overlay smaller ones, and on the middle levels of zoom contents of complexes are masked. Moreover, in CellDesigner, TextArea elements can be used to draw named rectangles covering functionally important areas. These will be incorporated into the generation of the semantic zoom as well. For this, you will need to create an additional area by
  - clicking **Edit > Add layer**
  - enabling **Layer** toolbox by checking **View > Change toolbar visible > Layer**
  - drawing **TextArea** objects using a corresponding button
- **Cross-platform SBGN translation:** CellDesigner files can be uploaded to be displayed in pure SBGN notation (see [Admin manual - Fields of the Add project window](#)), and SBGN-displayed content can be downloaded as a pure SBGN file.

For explanation and examples on content curation and annotation, see [Examples - CellDesigner file upload and annotation](#).

## Functional area

Functional area (the panel to the left from the display area) displays additional information about selected elements and interactions, allows to query the content, generate custom layouts and browse submaps.

## Search

**Search** tab allows to search for particular elements or interactions in the displayed map. Also, under this tab, the panel displays detailed information on selected elements or interactions (see below).



The panel is used in the following way:

- **Search field:** Type your search query here, separating multiple elements with comma ','. Search will look for similar names and synonyms of elements in the map. To search for an identifier of an interaction, you need to add **reaction:** prefix to the searched identifier. The **search** bubbles indicate hits in the display area. They have different colors for multiple search items and are clickable, showing information as in the left panel.
- **Perfect match** tick box: If this box is ticked, terms with an exact match to the query will be returned. In the case of large networks or broad queries the search results may be capped to ensure the performance of the system. The limit of displaying search results can be configured via the Admin view (see [Admin manual - Configuration](#)).

Direct link to the elements in the display area is possible, as the search query can be provided within the web address of the displayed project. An address constructed as follows:

```
your.webserver.address/?search='search query'
```

is a link executing the search for a given **search query** in the default project of your MINERVA instance. For example, an address

```
your.webserver.address/?search=reaction:xyz123
```

will directly point to an interaction with id **xyz123**. Referring to a given project on your MINERVA instance requires additionally to pass the project identifier in the address, as shown below. Identifiers of projects are accessible using the Admin view.

```
your.webserver.address/?id='project id'&search='search query'
```

## Drug

**Drug** tab in the functional panel allows to search for known drug targets and display them in the map. Targets will be marked by bubbles in the display area. Please, note that they have different shape than the **search** result bubbles.

- **Find targets** field: type your search query here, separating multiple drug names with comma ,. DrugBank and ChEMBL will be queried for known targets to be displayed in the map.
- Drug description, synonyms and all known targets will be displayed in the left panel.

## Layouts

**Layouts** tab allows to display or generate custom coloring of elements and interactions in the map. It is composed of two sections - general layouts and custom layouts (see below).

- **View** column contains buttons (**magnifying glass** icon) allowing to switch to a corresponding layout. Mouseover over the button displays a short description of the dataset, if provided on upload
- **Data** column contains buttons, where applicable, allowing to download the dataset used to generate the layout.



- **List** of uploaded layouts containing
  - **View** column with buttons enabling switching between custom layouts
  - **Data** column with buttons allowing the user to download the dataset used to generate the layout. The users have access only to their respective datasets.
  - **Edit** column with buttons allowing the user to provide description to the uploaded datasets
- **Adding** section with **Name** field to annotate and **+Choose** button to upload your custom dataset.

## Upload custom data - format

For examples of basic and advanced data upload, see [Examples - Custom data upload by registered users](#). Description of the format follows below.

**Basic format** The basic format of file containing the uploaded data is two-column, tab-separated text file, with the columns **Name** and **Value**.

- **Name** column contains the names of elements to be colored
- **Value** column contains the values normalized to [-1,1] range.

Basic format will look for names of the elements provided in the **Name** column among the names of elements in a given network and for the matching ones will assign them colors: red for negative values, green for positive values, with the saturation proportional to the value.

**Advanced format** The advanced format allows for by identifier matching, custom color assignment and coloring of interactions. Advanced format foresees two parts of the uploaded dataset - header and body.

Header lines have to start with '#'. It can contain the following elements:

- **Version** # `VERSION=xyz` - a version of this custom layout
- **Name** # `NAME=xyz` - a name that will be automatically assigned upon upload
- **Description** # `DESCRIPTION=xyz` - a description that will be automatically assigned upon upload

Body is a table with a following set of columns:

- **Name, Value** - same as in basic layout
- **Compartment** - name of a compartment in which coloring should take place
- **Chebi** - ChEBI identifiers of elements to be colored
- **Entrez gene** - Entrez identifiers of elements to be colored
- **Gene ontology** - Gene Ontology identifiers of elements to be colored
- **Ensembl** - Ensembl identifiers of elements to be colored
- **Hgnc symbol** - HGNC symbols of elements to be colored
- **Uniprot** - Unprot identifiers of elements to be colored
- **ReactionIdentifier** - ID of interaction to be colored (interactions coloring only)
- **LineWidth** - linewidth of the colored interaction (interactions coloring only)
- **Color** - color of the colored element.

The dataset for upload may be integrated and sparse, i.e. a document may contain all columns at once, and, where irrelevant, their content may be left blank. In other words, you can color interactions and elements in the same dataset, leaving blank fields in **ReactionIdentifier** and **LineWidth** for elements, and leaving blank fields in **Name** for interactions.

## Upload custom data - procedure



After choosing the dataset to upload, pressing **Generate** button will invoke a comment, initiate generation and reduce the amount of available custom layouts (see below, left). The progress status will automatically update (see below, right) and when the progress reaches 100%, your custom layout is ready to be displayed.

You will be notified by email when your layout is ready. The email will also contain the list of elements in your dataset not found in the map.









Important reminder:

- The number of available layouts is configured in the Admin view (see [Admin manual - User manager](#))
- The number of available layouts is common for all projects hosted on your MINERVA instance. If a user is registered in a number of projects and uploads custom datasets in all of them, the global number of available custom layouts will be reduced with each uploaded layout.











 **Info** File processed successfully.  
Generating layout. 

#### GENERAL LAYOUTS:

Name ↕	View	Data
Pathways and compartments		
Normal		
Ageing brain		
PD substantia nigra		

#### GENERAL LAYOUTS:

Name ↕	View	Data
Pathways and compartments		
Normal		
Ageing brain		
PD substantia nigra		

#### CUSTOM LAYOUTS:

Name ↕	View	Data	Edit
SHSY-5Y transcriptome (status: Generating - 0.00%)			



#### ADDING

NAME:

SHSY-5Y transcriptome


FILE:

+ Choose

AVAILABLE LAYOUTS: 9

GENERATE

#### CUSTOM LAYOUTS:

Name ↕	View	Data	Edit
SHSY-5Y transcriptome (status: Generating - 71.01%)			



#### ADDING

NAME:

SHSY-5Y transcriptome

FILE:

+ Choose

AVAILABLE LAYOUTS: 9

GENERATE

## Login/Profile

The **Login** tab is visible for an anonymous user, upon immediate access to a project hosted on your MINERVA instance. It allows a registered user to type in their login and password, or to request for an account from the administrators of this MINERVA instance. Platform administrators can register new users (see [Section 3.4 User manager](#)) and configure **Request an account** functionality (see [Admin manual - Configuration](#)).

After login, the tab name changes to **Profile**, displaying information on the registered, logged in user. After the successful login the user gains the possibility to upload custom layouts (see [Section Layouts](#)).

## Submaps

The **Submaps** tab summarizes all the submap networks uploaded together and linked to the main network of this project hosted by your MINERVA instance. See [Admin manual - Source file](#) to learn how to upload the submaps together with the main file.

The **Submaps** tab displays the tab with the **Name** column, and the column with the buttons displaying corresponding submaps. The submaps show as a pop-up window on top of the main map, and are synchronized with respect to search queries and displaying layouts. This means that search results and search target bubbles will be visible in the main map and the displayed submaps. Similarly, coloring for layouts are mirrored in the submaps (see figures below).

**PARKINSON'S DISEASE MAP** Oct'15 SHOW OVERVIEW COMMENTS

SEARCH DRUG LAYOUTS PROFILE SUBMAPS

SEARCH:  PERFECT MATCH

**Protein: SLC6A3**

Full name: solute carrier family 6 (neurotransmitter transporter), member 3  
 Symbol: SLC6A3  
 Former symbols: DAT1,  
 Charge: 0  
 Synonyms: DAT,  
 Annotations:

- [1] Ensembl (ENSG00000142319)
- [2] Entrez Gene (6531)
- [3] HGNC (11049)
- [4] HGNC Symbol (SLC6A3)
- [5] RefSeq (NM\_001044)

ADMIN EXPORT

Google

chain

SLC6A3

Na+

Diagram showing the SLC6A3 protein structure and its interaction with PARK2 and other proteins. The diagram includes a list of proteins: ACSL4, ATAD1, ATP5A1, ATP5B, ATP5F1, C15D1, CPT1A, FASN, GHTM, HSD1A, HSD1B, HSD1L, MDXFA4, MDXFA5, MDXFA6, NME2, and others. The diagram also shows a submodel of PARK2 substrates, including proteins like ACSL4, ATAD1, ATP5A1, ATP5B, ATP5F1, C15D1, CPT1A, FASN, GHTM, HSD1A, HSD1B, HSD1L, MDXFA4, MDXFA5, MDXFA6, NME2, and others.

**PARKINSON'S DISEASE MAP** Oct'15 SHOW OVERVIEW COMMENTS LEGEND CLEAR

SEARCH DRUG LAYOUTS PROFILE SUBMAPS

GENERAL LAYOUTS:

Name	View	Data
Pathways and compartments	<input checked="" type="checkbox"/>	<input type="checkbox"/>
Normal	<input checked="" type="checkbox"/>	<input type="checkbox"/>
Ageing brain	<input checked="" type="checkbox"/>	<input type="checkbox"/>
PD substantia nigra	<input checked="" type="checkbox"/>	<input type="checkbox"/>

CUSTOM LAYOUTS:

Name	View	Data	Edit
SHSY-5Y transcriptome (status: OK)	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>

ADDING

NAME:

FILE:

AVAILABLE LAYOUTS: 9

Diagram showing the SLC6A3 protein structure and its interaction with PARK2 and other proteins. The diagram includes a list of proteins: ACSL4, ATAD1, ATP5A1, ATP5B, ATP5F1, C15D1, CPT1A, FASN, GHTM, HSD1A, HSD1B, HSD1L, MDXFA4, MDXFA5, MDXFA6, NME2, and others. The diagram also shows a submodel of PARK2 substrates, including proteins like ACSL4, ATAD1, ATP5A1, ATP5B, ATP5F1, C15D1, CPT1A, FASN, GHTM, HSD1A, HSD1B, HSD1L, MDXFA4, MDXFA5, MDXFA6, NME2, and others.

## Information bar

Information bar is the topmost part of the user view, containing the **Show overview** button, **Comment** and **Legend** checkboxes and **Clear** button. The **Clear** button clears all search results currently shown in the display area. The remaining functionalities are detailed below.

## Show overview

This button invokes a static image associated with the displayed content. It may be a graphics facilitating the understanding of the underlying network, or any other visual cue that the content curator decided to present. The initial image displayed with the **Show overview** button can be linked to:

- another static image to be displayed next
- a defined area in the displayed content
- a set of elements or interactions.

Detailed information on how to configure **Show overview** images display is provided in [Admin manual - Source file](#).

## Comments

If this checkbox is checked, the comments provided by users with **Pinned** option set to **Yes** will become visible in the display area (see also [Section Add comment](#)).

## Legend

If this checkbox is checked, the legend describing element and interaction types will be displayed.

# Export

The export page contains three tabs, allowing to download the hosted content in different formats.

- Elements export tab allows to narrow down and download the list of elements in the hosted networks. Available filters include:
  - **Type** - filters the exported elements by the SBGN-compliant type
  - **Columns** - filters the contents of exported file by selecting, which columns should be included (see below).
    - **Name** - name of the element
    - **Compartment** - compartment containing the element
    - **Component** - CellDesigner specific, TextArea covering the element, see also Section 4.1.4. Content curation
    - **Type** - SBGN type of the element
    - **Id** - identifier in the system
    - **Parent complex** - complex element containing this element
  - **Submodel** - name of the subnetwork containing this element
  - **Annotations** - filters the annotations of elements in the downloaded file; by default all annotation types are considered
  - **Included/excluded compartments** - filters the elements by compartments they are in; by default all compartments are considered as "included", none as "excluded".
- Network export tab allows to narrow down and download the interactions in the hosted networks. Importantly, the exported network file is not a fixed-column table. As interactions are in fact hyperedges, each line may contain different number of reactants, products and identifiers. Available filters include:
  - **Nodes** - filters the nodes of exported interactions by the SBGN-compliant type
  - **Annotations** - filters the annotations of elements and interactions in the downloaded file; by default all annotation types are considered
  - **Included/excluded compartments** - filters the elements by compartments they are in; by default all compartments are considered as "included", none as "excluded".

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