VIP software
v.1.0

Mini Tutorial
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For comments, questions, suggestions, please contact:
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Feature-to-attribute mapping

Required attributes: X, Y, Size, Color.

Not allowed to use the same proteomic feature twice.

X, Y and Z attributes can be mapped only to Numerical Continuous features.

Size and Color attributes can be assigned to numerical (discrete or continuous) features.

Label attribute can be assigned to text or numerical features.

(1)

(2)

Perform a mapping:

1. From the Mapping tab in Control Panel.

<u>Right click on a text field</u> shows a pop-up menu with the available proteomic features. (Fig.1)

2. From the Features table in the Features Panel.

<u>Right click on the header of a column</u> shows a pop-up menu with the available visualization attributes (Coordinate X, Coordinate Y, Coordinate Z, Size, Color, Label). (Fig.2)
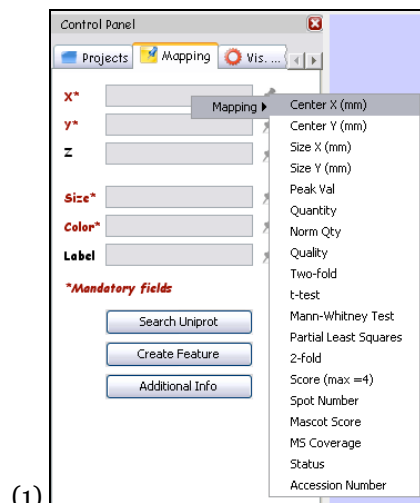
Cancel a mapping:

<u>Press the pin button</u> 📌 next to the respective text field and select a new proteomic feature.
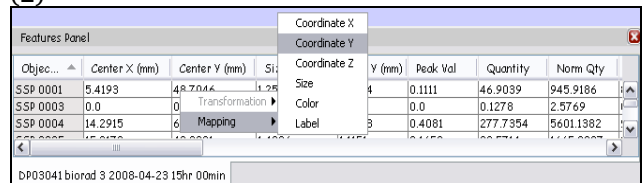
Remember a mapping:

After the mapping process, the text fields (Fig.3) and the corresponding mapped features-columns (Fig.4) are painted with specific colors:
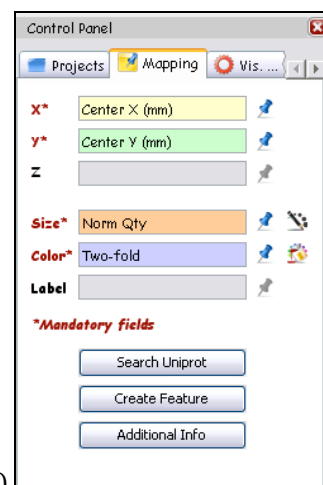
X:	Yellow
Y:	Green
Z:	Cyan
Size:	Orange
Color:	Blue
Label:	Pink

(3)

(4)

Control the Size

Control the radius:

Control Panel → Vis. Configuration tab → Radius Control: <u>Use the spinners</u> to define the minimum and maximum radius of the spheres. <u>Press the</u> 🔵 <u>button</u> for the radius changes to take effect.

Open the Size Map Editor:

1. From the Mapping tab in Control Panel.

Click on the ✎ button next to the size text field.

2. From the Vis. Configuration tab in Control Panel.

Click on the ✎ button in the Radius Control option.

Define the number of the size levels:

> *The values range of the feature that is mapped to the size is shown under the slider.*
>
> *One size point defines 2 size levels (small and large spheres).*
>
> *Two size points define 3 size levels (small, medium and large spheres) and so on.*
>
> *You can add up to 3 size points (create up to 4 size levels).*

Move the slider, use the spinner, or write in the spinner the desired value of the feature.

Press the "Add/Change Size Point" button, to create a size point.

Click on a size point in the Size Points table and press the "Remove Size Point" button, to delete a size point.

Press "Done" to close the window and then press the ✎ button for the size levels assignment to take effect.
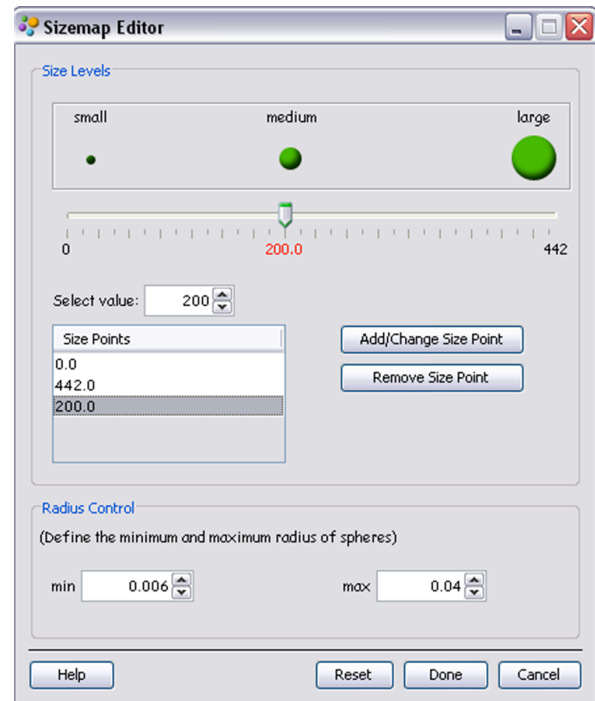
Control the Color

Select an available colormap:

Control Panel → Vis. Configuration tab → Coloring Scheme: Select a colormap from the drop down menu. (Fig.1)

Open the Color Map Editor (Fig.2):

1. From the Mapping tab in Control Panel.

Click on the ✎ button next to the color text field.

2. From the Vis. Configuration tab in Control Panel.

Click on the ✎ button in the Coloring Scheme option.

Use automatic color assignment:

If the feature mapped to Color is numerical and has less than 10 unique and discrete values, VIP automatically creates a colormap with 10 different colors for each and every one of the 10 unique values
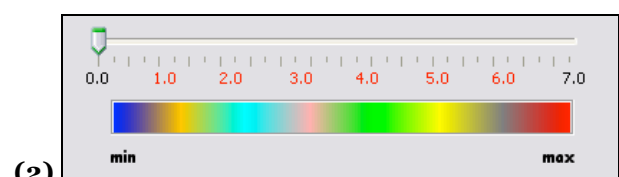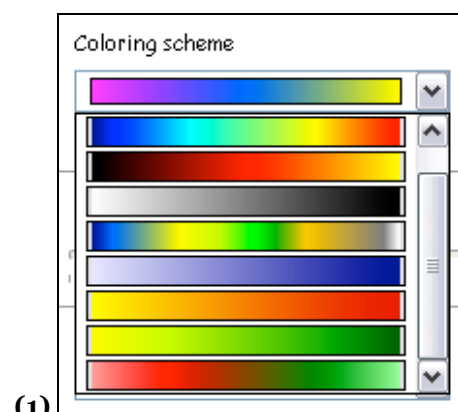
(Fig. 2). To accept the suggested colormap as it is, <u>open the color map editor</u> and <u>press the "Add Colorbar" button</u>. Add a name for the coloring scheme and press the "Add/Rename" button. (Fig. 3)

To indicate the text feature that explains the values of the color-mapped feature in the color bar frame, *before you add the colormap,* <u>press the "Add Description" button</u> in the color map editor and select the desired feature from the drop down menu.

<u>When you are done with the color assignment, press the button</u> for the colors to take effect in the next visualization.

Create a new colormap:

> *The range of the feature values that are mapped to the color is shown over the slider.*

<u>Move the slider,</u> <u>use the spinner,</u> or <u>write in the spinner</u> the desired value of the feature.

<u>Press the "Add/Change Color" button,</u> to create a color point.

<u>Click on a color point in the Color Points table and press the "Remove color Point" button,</u> to delete a color point.
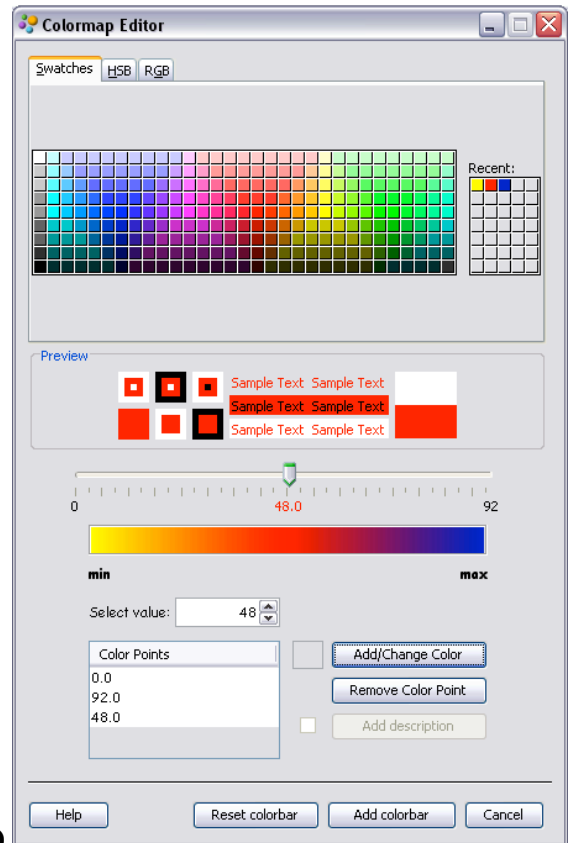
<u>Press "Add Colorbar"</u> to close the color map editor. Add a name for the coloring scheme you created and press the "Add/Rename" button. (Fig. 3)

<u>When you are done with the color assignment, press the button</u> for the colors to take effect in the next visualization.
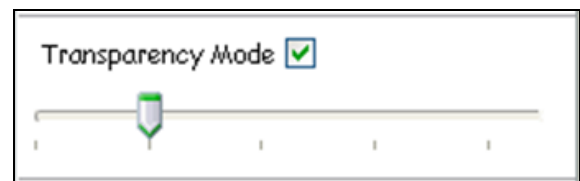
(3)
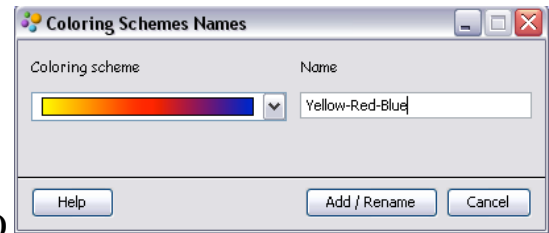
(4)

Spheres Transparency

Enable Transparency:

Control Panel → Vis. Configuration tab → Transparency Mode: <u>Tick the check box</u> to enable transparency. <u>Move the slider</u> to control the transparency level.

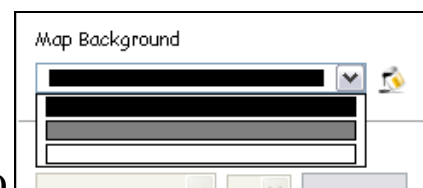<u>Press the button</u> for the transparency mode to take effect.

Visualization Background

Select background:

Control Panel → Vis. Configuration tab → Map Background (Fig.1): Select a color from the drop down menu. The default available colors are black, gray and white.
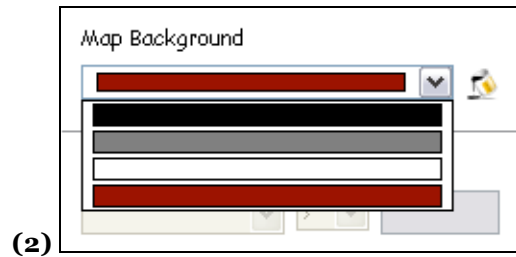
(1)

To select a different color for the background of the visualization click on the 🔦 button next to drop down menu.

Once a new color is selected, it is shown in the drop down menu so that it can be easily used later (Fig.2).

Press the 🔵 button for the new background color to take effect.

(2)

Visual Query (Filtering)

> *A visual query follows the format:*
> *"feature OPERATOR value".*
>
> *For example, the query: "score > 80" will filter the visualization looking for proteins that have been identified by achieving at least a score of 80.*

(1)

Perform a visual query:

Control Panel → Vis. Configuration tab → Elevation (Fig.1): Tick the check box to enable elevation mode. Set the parameters of the query: select feature and operator using the drop down menus, and write the value of the query.

Press the 🔵 button for the visual query to take effect.

The proteins-spheres that meet the given criterion are elevated and detached from the map's level (Fig. 2).

(2)
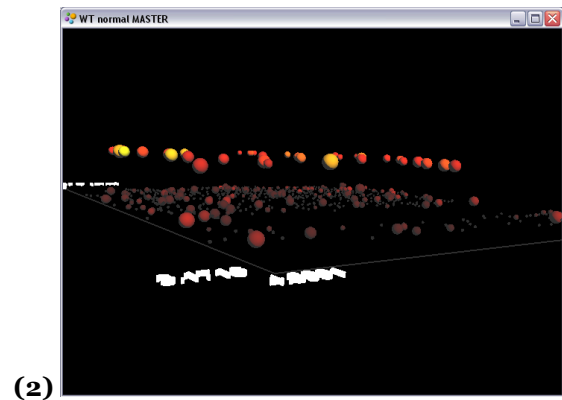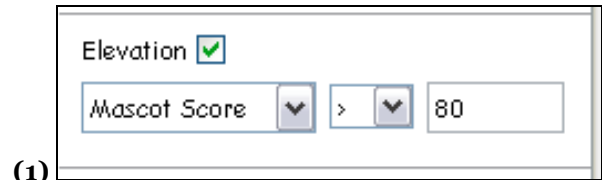
Navigation

Rotate a map:
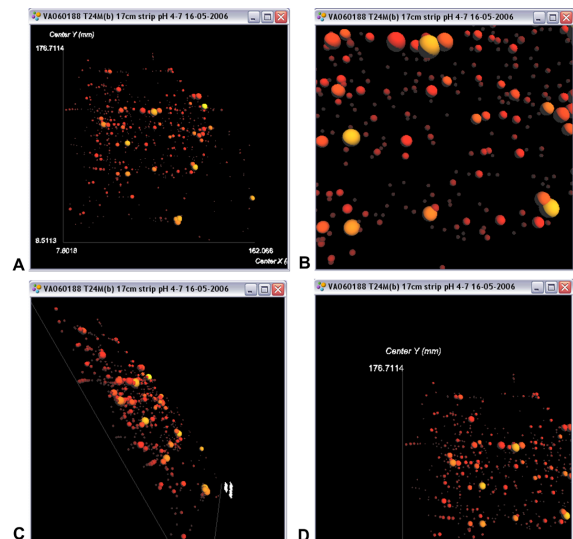Left mouse button / ←,→, Pg up, Pg down.

Move a map:
Right mouse button / Alt+←, Alt+→, Alt+Pg up, Alt+Pg down.

Zoom (in/out of) a map:
Middle mouse button, mouse wheel / ↑, ↓.

Restore a map:
🔍 button from tool bar / +.

Pick mode (Sphere-Table interaction)
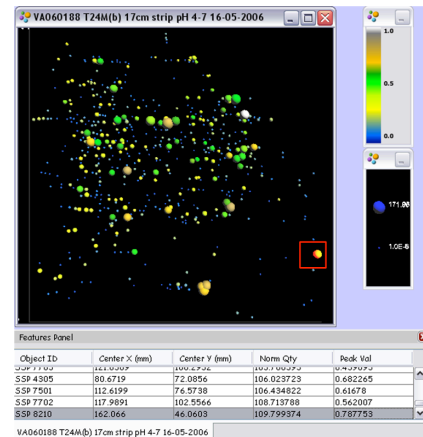
Enable Pick mode:

1. Menu bar → Options → Select Mode → Pick.

or,

2. Toolbar → Drop down menu → Select 👆.

Pick a sphere:

Click on a sphere of the map.

See the sphere light up and the corresponding row in the Features table get highlighted.

This functionality offers interaction between the map and the features workspace and is an easy way to explore all proteomic features that are related to the selected proteomic object.

Pick across maps mode

The Pick across maps mode is a way to perform differential viewing among several maps.

Enable Pick across maps mode:

1. Menu bar → Options → Select Mode → Pick across maps.

2. Toolbar → Drop down menu → Select 🖑.

Pick a sphere:

Click on a sphere of the map.

If the sphere exists under the same Object ID (characterizes uniquely every protein in VIP) in other maps that have been created, you can see the spheres light up in all maps (Fig.1).

This action facilitates the task of comparing different feature values of the same proteomic objects among multiple maps, and thus among multiple 2D gels.
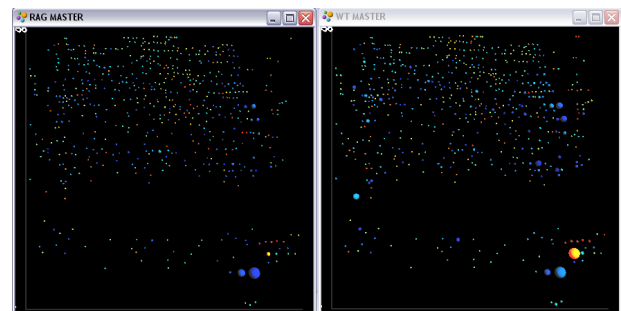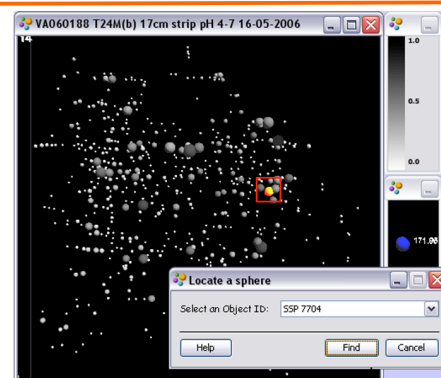

Locate a sphere

Go to Menu bar →Options → Locate sphere.

Use the drop down menu to select the Object ID of the desired sphere.

Press the "Find" button.

See the corresponding sphere light up in the map.

Rapid access to sphere's features

Right click on a sphere displays a pop-up menu that reveals automatically its Object ID as well as the values of user-selected features.

Open the Additional Info frame (Fig.1):

1. Menu bar → Tools → Additional Info.
2. From the Mapping tab in Control Panel.

Click on the "Additional Info" button.

Append features to the pop-up menu:

Use the arrow buttons in the middle of the frame to select any of the available features to appear in the pop-up menu of the spheres.

Press the "OK" button to close the frame.

Right click on a sphere of the map.

See the pop-up menu and the values of the selected features.

This functionality allows retrieving easily and instantly the desired information for every protein, while exploring the map.

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