

A Core Analysis in IPA® is a comprehensive biological analysis that includes biological functions, networks, diseases, and canonical pathways affected in your dataset. The simple steps below will help you get started interpreting the results. For more detailed instructions, open IPA and go to **Help > Help Manual > Training** and look for the recorded Training Webinars at the bottom of the page.

1. Open your completed Core Analysis for the microarray data of interest in the Project Manager.
2. Click on the **Summary** tab to review the top networks, biological functions, pathways, and molecules significantly affected in your experiment.

Functional Analysis

1. Click on the **Functions** tab to review a chart of the functions that are the most affected in your experiment, ranked from most to least likely to be affected.
2. Click on a bar of interest to display details about a function in the Table and Tree views.
3. In Tree view, select a high-level function and any low-level functions of interest.
4. Under the low-level function, click on a hyperlinked **function name** to access its details (or "Findings"), such as experiment type and supporting literature citation.
5. Review the p-value (Calculated by right-tailed Fisher's Exact Test) indicating the likelihood that the molecules in your dataset are associated with a function due to chance alone.
Note: Lower p-value means higher significance.
6. Click **Customize Chart** to alter the bar chart to display only function categories and high-level functions of interest.

Pathway Analysis

1. Click on the **Canonical Pathways** tab to review a bar chart of the well-characterized pathways that are affected the most in your experiment.
2. Mouse over pathway of interest to see which up or down-regulated molecules in your dataset are in the specified pathway.
3. Click on the pathway bar in the chart to display the affected molecules in your dataset.
4. Click on **Open Pathway** to visually overlay the expression values in the dataset onto the selected canonical pathway.
5. Select **View Report** to read details about the corresponding canonical pathway.
6. View the interactions and relationships of molecules affected in your experiment with the molecules in the pathway.
7. Click on **Customize Chart** to display only the pathways of interest.

Network Analysis

1. Click on the **Networks** tab to see the molecular interactions.
Note: Highly connected networks are likely to represent significant biological function.
2. Select a network corresponding to a set of biological functions of interest.
3. Click on **View Networks** to display a network of affected molecules and associated expression values in the dataset.
4. Click on the molecules and relationships for details that can help make the mechanistic connections needed to generate hypotheses from the experimental data.