

A Core Analysis in IPA® identifies the molecular networks, biological functions, and pathways affected in your expression experiment. The simple steps to running a Core Analysis are outlined below.

Note: For more detailed instructions, open IPA and in the Quick Start window and click on: **Upload & Analyze Example Data > Learn How to Upload Now**

Analysis Steps

1. Format an Excel or tab-delimited text file for analysis
 - Note:** Previously normalized and ratio'ed, containing gene IDs, expression and p-values
 - Single header row
 - Replicates already averaged
2. Login to IPA
 - Select **File > New Core Analysis**
 - Click **Upload**
3. Map columns in your file to IPA columns
 - Specify identifier type and expression value type(s)
 - If you have multiple conditions (for example three compound doses), each of these should be set to one "observation" (observation 1, 2 and 3).
4. Create a new project and save
 - Specify parameters and expression value cutoff (optional)
 - Click on **Recalculate** (optional)
5. Click on **Run Analysis**
 - Wait for "analysis complete" email alert or wait for the 'analysis running' icon in the Project Manager to stop spinning
6. Review results in the Project Manager
 - Open **My projects** and navigate to the 'analysis' folder in the project folder just created
 - Double click on the completed analysis name
7. Review Core Analysis results
 - Review most statistically significant results in Summary
 - See **Quick Card: Basic Core Analysis Interpretation**