

6 Ways IPA Helps Accomplish Research Goals Faster

IPA provides both the content and analysis tools required to quickly understand the biological implications of an experiment.

Challenge: Getting Biological Insights from Your Data

Although researchers can establish expression change significance through statistical analysis, the greater challenge is understanding what those results imply about the underlying biology. Purely statistical approaches provide limited value in this regard. To get biological meaning from experimental data, researchers need to be able to efficiently and accurately:

1. Narrow in on what is most biologically important in their data
2. Compare affected processes and pathways across datasets
3. Get a system-wide view of a biological process, including pathways

How IPA Can Help

To provide this kind of insight into the underlying biology, IPA[®] software performs a comprehensive biological [analysis of your data](#) in just minutes and displays the biological implications based upon Ingenuity[®] Knowledge Base information (See Panel A, second page). IPA reduces the time needed to interpret data, results in better insights, and provides biological information that may otherwise be missed. Here are six ways IPA helps researchers quickly gain better biological insights.



IPA and the underlying Ingenuity Knowledge Base provide a comprehensive biological analysis for a better understanding of your data.

Six Ways to Accelerate Research With IPA

1. Search Published Biological Findings

Consider how long it takes to understand the biology of a gene when using PubMed search results. In contrast, [researching a gene](#) with IPA is simple and efficient. IPA provides an organized Gene View summary of important information about that gene that has been published in peer-reviewed literature. The summary includes molecular relationships, functions, disease mechanisms and processes, and canonical pathways in which the gene is involved. Just click on any finding to see the primary citation.

2. Develop a Hypothesis

When building a hypothesis in IPA, a phenotype or disease can be linked with the regulatory molecules or networks that are implicated. The option to [build a pathway](#) to find interesting

IPA users can
click on links for
step by step
instructions

molecular interactions or regulatory factors also exists. After an experiment is complete, the hypothesis can be evaluated by [overlaying molecular data](#) on a pathway.

3. Discover Functions and Pathways

When [uploading expression data](#) into IPA for analysis, a researcher can specify a significance cutoff, study organism, cell line, and other criteria. An IPA Core Analysis will show affected molecular networks, signaling and metabolic pathways, and biological functions. Relationships with molecules not significantly changed in the experiment, plus relationships with molecules reported to interact, are included to provide a deeper understanding of the results.

4. Understand Disease Mechanisms

IPA identifies the diseases related to molecules in a dataset, and the types and functions of [interacting molecules](#) can be graphically displayed to explore underlying disease mechanisms. Other types of molecules (drugs, biomarkers, etc.) can be included to determine their upstream and downstream effects.

5. Identify, Prioritize and Validate Targets

IPA has a large amount of information on [drug targets](#), plus tools to help focus further analysis on those of greatest interest. Candidate targets are validated by upload and comparison with additional datasets, *in silico* published results, and other information provided in the analysis.

6. Collaborate, Communicate, and Publish

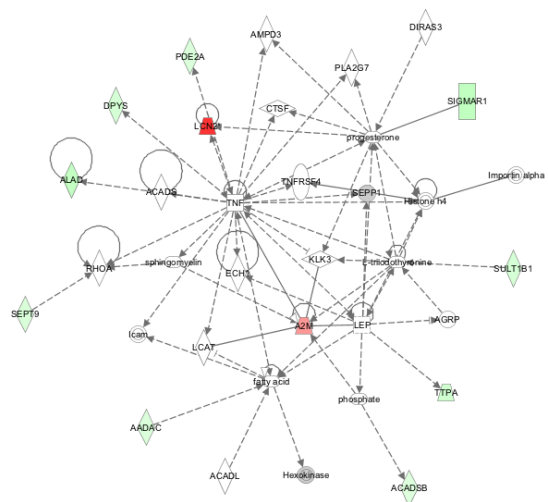
IPA makes it easy to communicate results through [collaboration workspaces](#) and other tools. With Path Designer, pathways can be customized with coloring, legends, and notations for presentation to colleagues. Any pathway, report, or citation can be created, saved, and exported.

From simple biological exploration to targeted data analysis, IPA is the gold standard for comprehensive biological analysis. IPA has been cited by thousands of [peer-reviewed articles](#), which can be accessed with our publication search tool. Take full advantage of a free [IPA trial](#) today, and start seeing how IPA can help accomplish research goals faster!

Panel A. The Ingenuity® Knowledge Base contains ~3.5 million detailed biological and chemical Findings from more than 800 peer-reviewed journals, making it the industry's most comprehensive—and most often cited—collection of Findings. These undergo rigorous quality control before being added to Ingenuity's detailed ontology. Findings include species, cell and tissue type, site and type of mutations, molecular interactions, regulatory events, post-translational modification sites, epigenetic modifications, plus links to primary citations. This allows you to explore, gain insights, and interpret your results in a way otherwise not possible.

"IPA showed us that differentially expressed genes from our microarray experiments between pregnant and non-pregnant mice were connected to a single network with COX-2 in a central role. Ingenuity saved us time and effort and provided us with information that we could not have found with a classic literature search. Ingenuity's software was definitely a step forward in our quest towards a genetic signature for endometrial receptivity."

—Inge Van Vaerenbergh, MS and Claire Bourgain, MD. Ph.D.,
Department of Pathology, University Hospital Brussels,
Belgium



COX-2 network and differentially expressed genes .