

Getting Started in IPA[®]

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Click to sign up for a free two-week trial of IPA

What is IPA and how can it help you?

IPA is web-based software that provides you with the ability to understand biology at multiple levels by integrating data from a variety of experimental platforms and providing insight into the molecular and chemical interactions, cellular phenotypes, and disease processes of your system. IPA provides the right biological context to facilitate informed decision-making, advance research project design, and generate new testable hypotheses.

You can use IPA with or without data. For example, you can uncover novel insights by analyzing data derived from expression and SNP microarrays, proteomics experiments, and small-scale experiments that generate gene lists. With IPA, you can also search for targeted and relevant information on genes, proteins, chemicals, and drugs, and use that information to your own biological models or get up to speed in a relevant area of research.

IPA is distinct from other tools because it is an all-in-one solution that leverages the Ingenuity[®] Knowledge Base, the largest data base of its kind, which houses the biological and chemical relationships extracted from scientific literature. The information is uniquely structured so scientists can ask complex biological questions to gain rapid and reliable insight into their experimental data or create relevant biological models to move forward in their research. IPA's unique value has been proven by the many hundreds of publication citing it and its broad adoption across major pharmaceutical companies and leading research institutions. To see publications that feature IPA, [click here](#), or go to our website at www.ingenuity.com.

How do I get access?

Free trial:

Researchers with a valid institutional email address can sign up for a free trial simply by going to www.ingenuity.com and clicking on the 'Free Trial' button in the top right corner of the page, or you can [click here](#). After you sign up for a trial, you will receive an email with your username and password. You can log into IPA at <https://analysis.ingenuity.com/pa/>.

License:

If your institution already has a license, you can sign up for access to IPA by clicking going to www.ingenuity.com and clicking on "Add me to my institution's license" at the top of the page. You will receive an email with your user name and password. You can log into IPA at <https://analysis.ingenuity.com/pa/>. To purchase a license for yourself or your institution, please contact sales@ingenuity.com.

Entry Points into IPA

There are three general ways of getting started with IPA:

Without data:

- Start with search terms related to a therapeutic area, disease or function for additional research, study or experimental designs
- Start with a small number of genes or chemicals (1-300), including drugs, such as a list of drugs for repurposing, understanding the context of a drug target, or candidate genes from SNP genotyping analysis

If you are interested in learning more about a small set of genes, chemicals/drugs, or disease, you can use IPA as a visual literature search tool to help you understand and stay current in biological interactions and relationships relevant to your projects. These analyses generally start with a small list of genes, proteins or chemicals (1-300), or one or more search terms of a cellular function or disease.


With data:

- Start with a large dataset, typically thousands of data points, such as expression and SNP microarrays, proteomics experiments, and small-scale experiments that generate gene lists.

If you have a large dataset to analyze, involving several hundred to tens of thousands of molecules, you will want to run an analysis appropriate to your interests, such as a Core Analysis, IPA-Tox[®] analysis, IPA-Metabolomics[®] analysis, or IPA-Biomarker[®] analysis (see Analysis Types and Features). These analyses begin with upload of your data, setting analysis criteria, running the analysis, and interpreting the results. The results provide information on how your dataset overlaps molecules associated with various diseases and cellular functions, and that are part of canonical pathways. These results often give a good indication of what cellular processes your data set is related to and will often lead to further investigation of these relationships by building custom networks/pathways. In addition, you can view molecular networks that show how the significant molecules in your dataset are known to interact with one another and other closely interacting molecules.

To learn more about running a basic analysis, please see [Core Analysis and Comparison Analysis Workflow](#) in IPA Help.

Logging in to IPA

1. Access IPA at <https://analysis.ingenuity.com/pa/>
2. The first time you log in, you will be prompted to create a shortcut to IPA on your desktop. Clicking “Yes” will allow you to access IPA directly from your desktop.
3. When prompted, enter your login and password information. This was sent to you via email when your account was first activated. If you don't have your login or password, please contact Customer Support at 650.381.5111, or support@ingenuity.com.
4. If this is your first time logging into IPA, we suggest changing your password to something that is easier for you to remember and more secure. To change your password, go to File, Preferences, Change Password and fill out the entire form. Ingenuity's password policy requires all passwords to be at least 8 characters in length and contain both letters and numbers. Passwords are also case-sensitive.
5. When you need to access IPA again, just click on the desktop icon to access your IPA account. It will look like this: 

Technical Troubleshooting

1. If you are having problems, first please check to see if your computer meets the technical requirements listed here: http://www.ingenuity.com/login_troubleshooting.html.
 - If you are unsure of your operating system version, go to Control Panel, System to check which one is installed on your computer.
 - If you are unsure of your Internet Explorer web browser version, go to the Help menu at the top of the web browser and choose About Internet Explorer. Update the browser if necessary. You can update your browser at <http://www.microsoft.com/windows/ie/downloads/default.asp>.
2. IMPORTANT: Java Runtime Environment (JRE) is the program required to run Java applications and applets on your computer. We recommend the use of JRE version 1.5.0_10 or newer for PC, and the most current version recommended for your Mac OS. To download, please go to http://www.ingenuity.com/login_troubleshooting.html.
 - If you are unsure of your JRE version, open your control panel, click on the Java icon, and go to the section "About". Please note that IPA will be phasing out JRE 1.4.2. Additionally JRE versions 1.5.0_07, 1.5.0_08, and 1.5.0_09 are incompatible with Java WebStart. We recommend all users upgrade to JRE version 1.5.0_10 or newer.
3. Pop-Up blockers: Internet browser pop-up blockers may prevent the launching of IPA. To avoid this issue, inactivate any pop-up blockers for the site <https://analysis.ingenuity.com/pa/> before signing into the application.

Common FAQs for Getting Started

Q. What file formats can I use to upload my data into IPA?

- A. IPA now accepts any Excel file for data upload. Please see [Uploading your Data with the IPA Column Picker](#) in IPA Help for more details.

Q. Can datasets containing multiple identifier types be mapped?

- A. Yes. For more details, please see [Uploading your Data with the IPA Column Picker](#) in IPA Help.

Q. How large can my dataset be?

- A. There is a 65,000 row and 18MB file size limit on dataset files uploaded into the application.

Q. What identifiers are supported in IPA?

- A.
- | | | | |
|----------------------|--------------------|-------------------------------|---------------------------------------|
| • Affymetrix | • dbSNP | • Illumina | • PubChem CID |
| • Affymetrix SNP | • Entrez Gene | • International Protein Index | • RefSeq |
| • Agilent | • GenBank | • KEGG ID | • UniGene |
| • Applied Biosystems | • GenPept | • Metabolomics | • UniProt/Swiss Prot Accession |
| • CAS Registry | • GI Number | • miRBase (mature) | • MicroRNAs w/Entrez Gene Identifiers |
| • CID | • HMDB | • Proteomics | |
| • CodeLink | • HUGO Gene Symbol | | |

Q. What species identifiers are accepted for analysis by IPA?

- A. IPA accepts the upload and analysis of human, mouse, rat, and canine identifiers. IPA also accepts chemical identifiers.

In addition to human, mouse, and rat, for the following species, we accept Entrez Gene, GenBank, Refseq, GenPept identifiers as well as some array-specific data. The identifiers for these species are mapped according to their HomoloGene to the ortholog information in the Ingenuity Knowledge Base. The supporting content for these specific species is not yet linked to their mappings (i.e. the content will be specific to human, mouse, and rat). Species marked with a * indicate that we only support Affymetrix identifiers of this species.

Arabidopsis thaliana
Bos taurus (bovine)

Caenorhabditis
elegans*

Gallus gallus
(chicken)

Pan troglodytes
(chimpanzee)

Danio rerio
(zebrafish)
Canis lupus
familiaris (canine)

Drosophila
melanogaster*
Macaca mulatta
(Rhesus Monkey)*

Saccharomyces
cerevisiae
Schizosaccharo-
myces pombe

Q. How do I upload data?

A. For more detailed instructions, please see [Uploading Your Data](#) in IPA Help.

1. Go to File, Upload dataset
2. Browse to select the file from your computer and click Open
3. Select a File Format. For questions on file format or to get a template to format your data, please see [Formatting Your Data](#) in IPA Help.
4. Select an identifier type. You can select more than one identifier type if needed.
5. Select an array platform. For more information, please see [Array Platform Used in Experiment](#) in IPA Help.
6. Specify the contents of the columns in your dataset and review how IPA labels each column. IPA will automatically identify IDs, expression values, etc., but you can override this if needed. For more information on expression values types, please see [Data Upload Definitions](#) in IPA Help.
7. Edit observation names (column headers) if needed.
8. Click the Save or the Save and Create Analysis button.

Q. Can I create a customized pathway for my targets, biomarkers, processes, or diseases of interest and see how it relates to other biological functions?

A. Yes. You can create pathways from lists, search results, functional analysis results, or networks. You can also create pathways from scratch. Additionally, you can overlay canonical pathways, toxicity lists, biological functions, and other biological groupings onto your pathway to understand how the molecules or genes in your pathway relate to your overlaid function. For more information, please see [Creating My Pathways](#) in IPA Help.

Q. How do I find all the genes or chemicals associated with a specific function or disease? (Ex: How do I find molecules associated with liver damage?)

A. Use a Function and Disease search. In the search bar, select "Gene/Chemicals associated with Functions/Diseases" and type your term into the search bar. Use quotation marks to search for an exact match ("lung cancer") and use an asterisk for wildcard matches (lung*). The result is a list of genes and chemicals associated with that term. To learn about more advanced searching, using combinations of criteria please see [Advanced Search](#) in IPA Help.

Q. What kinds of questions can Functional Analysis help me answer?

- A. To see how to answer the below questions, please see [Questions that Functional Analysis Can Answer](#) in IPA Help.
- Did my experiment work as expected? Are the genes that are coming up as significantly changed actually related to the biology I am studying?
 - How do I compare functions at different stages or experimental conditions?
 - Is my treatment causing adverse events in my system such as hepatotoxicity?
 - What is the biology of these new genes-of-interest?
 - I would like to rank which genes are most important to my experiment based on their functions instead of on their expression values.
 - Are there any new genes I did not know about that affect the biology of my system?
 - I would like to highlight the biology associated with a group of functions, merged networks, or pathways.
 - Which genes are involved in a particular disease? Are there any mutant genes or proteins involved in this disease?

Analyses Types and Features

IPA Analysis Type
(Links to IPA Help)

What it Does

Core Analysis	Allows you to interpret large and small datasets in the context of biological processes, pathways and molecular networks.
Core Comparison Analysis	Allows you to analyze changes in biological states across experimental conditions. Analyze datasets representing multiple treatments and understand which biological processes and/or diseases are relevant to each condition.
IPA-Metabolomics® Analysis	Provides you with a way of analyzing metabolite data to learn more about cell physiology and metabolism.
IPA-Metabolomics Comparison Analysis	Allows you to analyze changes in biological states across experimental conditions. Analyze metabolite datasets representing multiple treatments and understand which biological processes and/or diseases are relevant to each condition.
IPA-Tox® Analysis	Allows you to assess toxicity and safety of compounds-of-interest early in the development process. Toxicity analysis rapidly displays the relevant toxicity phenotypes and clinical pathology endpoints associated with a dataset.
IPA-Tox Comparison Analysis	Allows you to analyze changes in relevant toxicity phenotypes and clinical pathology endpoints across observations and understand which toxicity functions and/or pathways are relevant to each timepoint or dose.
IPA-Biomarker® Analysis	Allows you to identify and prioritize the most relevant and promising molecular biomarker candidates from datasets from nearly any step of the drug discovery process or disease research. Prioritize molecular biomarker candidates based on contextual information such as mechanistic connection to diseases or detection in bodily fluids. Identify biomarker candidates that discriminate between or are common to a disease state and/or drug response.
IPA-Biomarker Comparison Analysis	Identifies biomarker candidates that discriminate between or are common to a disease state and/or drug response. Prioritizes molecular biomarker candidates based on contextual information such as mechanistic connection to diseases, detection in bodily fluids. Identifies biomarker candidates that discriminate between multiple samples.

IPA Feature (Links to IPA Help)	The Question it Addresses
Networks	What regulatory relationships exist between the genes/ proteins in my dataset?
Functions	Which biological and disease processes are most relevant to my genes of interest?
Canonical Pathways	Which well-characterized cell signaling and metabolic pathways are most relevant in my data?
Search	How do I query the Ingenuity Knowledge Base about specific genes, processes, diseases, drugs, families, or subcellular locations? (view white paper)
My Pathways and My Lists	How can I build a library of biological models that I can also use in analyzing expression data?
Contextual Data Analysis	How can I narrow in on molecules or relationships with a specific set of biological or chemical criteria?
Path Designer	How can I modify my pathways for publications and presentations? (view white paper)

Compare	Which molecules are unique or in common between more than one IPA entity?
Emailing Interactive Pathways, Analysis Summaries, Shared Projects	How can I communicate and share my results with my colleagues and collaborators?
Path Designer, Interactive Pathways	How can I publish my results from IPA?
IPA Integration Module	Can I seamlessly transition between my internal application or database into IPA? (view white paper)

Training and Help Resources

Online Training

Ingenuity has free, online trainings every Thursday to cover basic and advanced workflows in IPA. These are usually held at 7 am or 10 am Pacific time. Regularly featured topics are listed below.

- Getting Started in IPA
- Using IPA as a Search & Exploratory Tool
- IPA Data Analysis using Functions and Pathways
- IPA Data Analysis using Network Analysis
- Molecular Toxicology Analysis
- Biomarker Filter and Comparison Analysis

To view upcoming Thursday Trainings and register, please visit our website at www.ingenuity.com.

To view pre-recorded training videos in IPA Help, please [click here](#).

Scientific Seminars

Ingenuity also offers a scientific seminar series that is designed to answer specific research questions. A recent example focused on Prostate Cancer, and examined how to use IPA to find markers of prostate cancer, determine pathways affected in various types of cancers, and identify signature genes affected by prostate cancer.

To view upcoming Scientific Seminars and register, please visit our website at www.ingenuity.com.

To view pre-recorded Scientific Seminars in IPA Help, please [click here](#).

IPA Help

The help section in IPA is a comprehensive, keyword-searchable resource designed to help you quickly find the information you need on IPA. Just click on "Tutorials and Help" at the bottom of the IPA Welcome Screen. Among other things, IPA Help includes:

- [Workflows](#)
 - [Training Videos](#)
 - [Tutorials](#)
 - [Legend](#)
 - [Feature Descriptions](#)
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Online Library

The online library of materials on our website includes various posters, training videos, datasheets, case studies, and whitepapers which demonstrate the ways IPA can help your research. Some examples of these are listed below.

- [Search IPA Publications](#) - Search publications generated using IPA, searchable by area of research, research goal, experimental platform, or keywords.
- [Search and Explore whitepaper](#) - Use search to rapidly generate testable hypotheses and streamline experimental planning
- [Path Designer whitepaper](#) - Create publication-quality graphics that are interactive with the Ingenuity Knowledge Base to clearly communicate experimental insights and system models.
- [Integration Module whitepaper](#) - Quickly integrate IPA's content and analysis capabilities into internal tools and workflows.

See more information in our online library at www.ingenuity.com/library/index.html

Contact Us

Ingenuity Customer Support: Ingenuity Systems offers its comprehensive product support to both fully licensed users and to users of free trials. PhD-level scientists are available to answer your scientific and technical questions; please contact us at:

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