

## New Features and Content!

### Support for Additional Species

Upload and analyze datasets from Affymetrix and Agilent canine arrays, and canine identifiers from public gene databases.

### Export Large Annotated Gene Sets

Easily upload, map, annotate and export large gene sets with drug target, protein family, and subcellular localization information.

### Chemicals in Pathways

Search IPA's extensive repository of chemical knowledge to understand the effects of chemicals on biological systems.

### Analysis Summaries

Get to the core of analysis results quickly with focused, summarized reports.

### E-mail Interactive Pathways

Share hypotheses and insights with collaborators by e-mailing interactive networks and pathways.

### Streamlined Data Upload

Upload data quickly without time-consuming data formatting steps. Analyze datasets with mixed gene and protein identifiers.

### Build Gene List Libraries

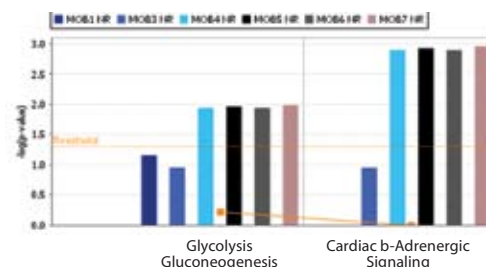
Upload public or proprietary gene lists and signatures into the My List library. IPA Core Analysis and IPA-Tox™ Analysis assess the relevance of those signatures to experimental data.

### Updated Content

Answer key questions and analyze data with the latest update to Ingenuity's detail-rich knowledge base of biological and chemical content, manually curated from the scientific literature.

IPA™ is a software application that provides a complete solution for life scientists who need to:

- Clearly and reliably identify the pathways, molecular mechanisms, and biological processes most relevant to their experimental data or gene lists.
- Find and synthesize biological and chemical knowledge from the scientific literature.
- Communicate results and share insights with project teams and collaborators.



Identify key pathway differences between patient samples.

## Challenge

To realize the full value of 'omics technology, researchers must overcome a substantial data analysis and interpretation bottleneck. IPA addresses that challenge by significantly reducing the time and resources required to progress from data generation to biological insight.

IPA has been designed in direct response to industry initiatives to find more effective molecular biomarkers of disease, PD/PK, and efficacy, and to assess toxicity of compounds earlier in the drug discovery and development process.

## New Features in IPA

### IPA-Biomarker™ Analysis

IPA-Biomarker Analysis identifies the most relevant and promising molecular biomarker candidates from datasets generated at every step of the drug discovery process.

**Biomarker Filters** prioritize biomarker candidates according to key biological criteria:

- Mechanistic connection to disease
- Protein detection in bodily fluids and sentinel tissues
- Transcript detection in tissues
- Human, mouse, and rat ortholog

**Biomarker Comparison Analysis** identifies biomarker candidates that discriminate between or are common to different disease states, drug responses, or patient populations.

Name	Description	-log10(P)	Other(A1)	Human	Plenc Cells	Blood
HBA2	hemoglobin, alpha 2	-1.7295604779485627	x	x	x	x
RPS2 (includes EG-6187)	ribosomal protein S2	-1.7304684277833096	x	x	x	x
HBB (includes EG-30CE)	hemoglobin, beta	-1.8249377466646318	x	x	x	x
HSP91	heat shock 70kDa protein 1	-1.922879776150528	x	x	x	x

Rapidly narrow in on biomarker candidates common to multiple samples.

## Technical Requirements

### Operating System

Windows XP and  
Macintosh 10.3.9, 10.4.6.

### Web Browser

Internet Explorer 6.0  
or higher. Firefox 1.5 or  
higher is recommended.  
For Mac OS, Safari.

### Memory

Minimum of 512MB RAM  
(1GB RAM recommended).

### Java Runtime Environment

Version 1.4.2 or higher.  
Ingenuity Pathways  
Analysis can be accessed  
as a web-hosted or a  
deployed solution.

## IPA-Tox™ Analysis

**IPA-Tox Analysis** uses Toxicity Functional Categories in combination with Toxicity Lists to link experimental data to clinical pathology endpoints, understand pharmacological response, and support mechanism of action and mechanism of toxicity hypothesis generation.

**Toxicity Functional Categories** cover a wide spectrum of well-known drug-related injuries and pathologies in liver, kidney, and heart, that are useful for the drug discovery and development process.

**Toxicity Lists** constitute sets of genes that are known to be perturbed upon compound treatment, and include functional gene groupings based on critical biological processes and key adaptive, defensive, or reparative responses to xenobiotic insult. These lists are manually curated by Ingenuity experts from the molecular toxicology literature.

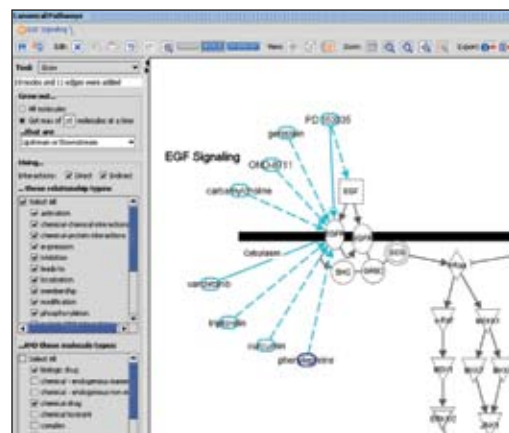


*Generate hypotheses of mechanism of toxicity.*

## Dynamic Signaling and Metabolic Pathways

Users can explore beyond the boundaries of well-characterized signaling and metabolic pathways to incorporate the molecular relationships most relevant to their experimental system.

- Customize pathways using IPA's extensive molecular interaction content.
- Understand chemical effects on genes, find upstream activators, and downstream targets of pathways.
- Drill down to the supporting evidence from the scientific literature.
- Layer in expression, proteomic, copy number data, and more.



*Search for small molecular inhibitors or activators of signaling pathways.*

## Discover the power of Ingenuity Pathways Analysis.

Register for a complimentary and fully functional trial at [www.ingenuity.com/trial](http://www.ingenuity.com/trial).

**INGENUITY**  
S Y S T E M S

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