IPA™ 5.0 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.

**Challenge**

To realize the full value of ‘omics technology, researchers must overcome a substantial data analysis and interpretation bottleneck. IPA 5.0 addresses that challenge by significantly reducing the time and resources required to progress from data generation to biological insight.

IPA 5.0 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 5.0**

**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 Filter** prioritizes 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 orthologs

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

IPA-Tox 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 Functions 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.

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.

Discover the power of Ingenuity Pathways Analysis.

Register for a complimentary and fully functional trial at www.ingenuity.com/trial.