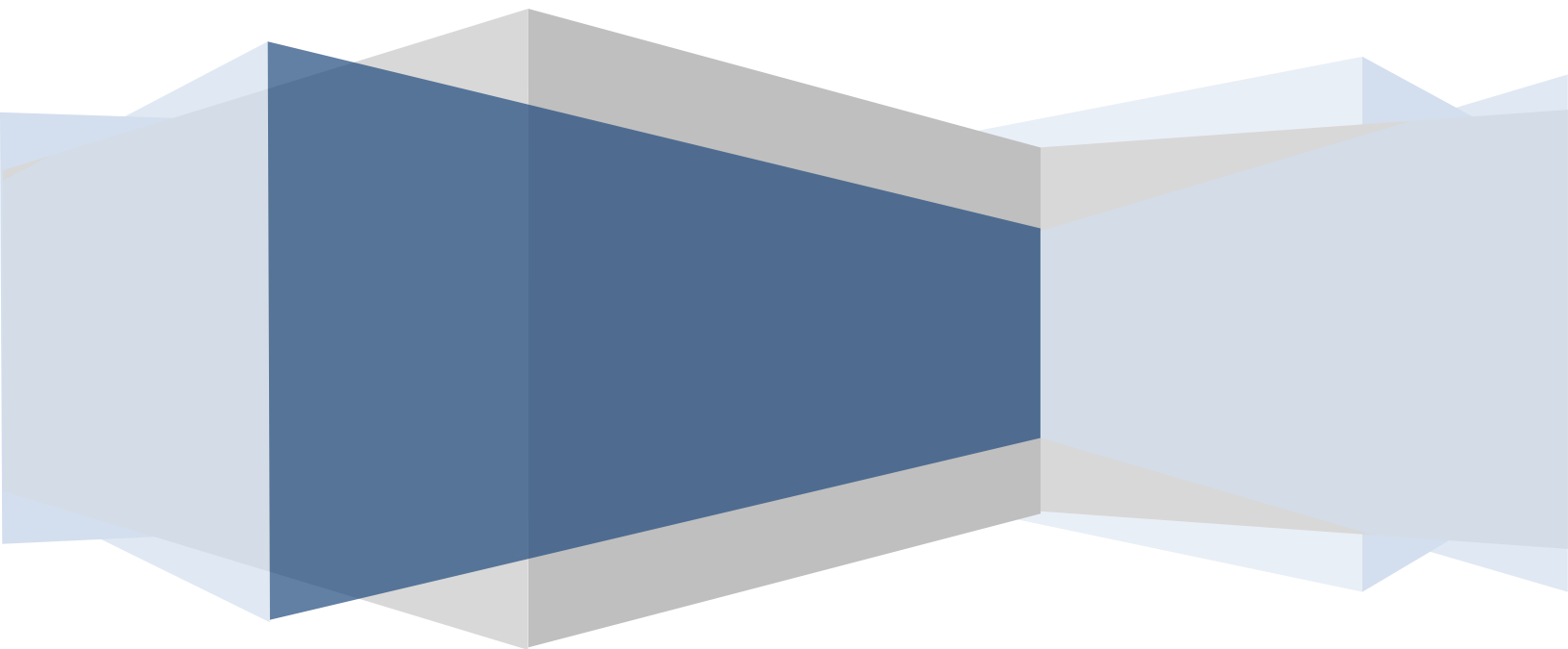




## **IPA Integration Module:**

Increasing the Value of Internal Bioinformatics  
Software and Therapeutic Area Reports with Direct  
Links to Ingenuity Pathways Analysis

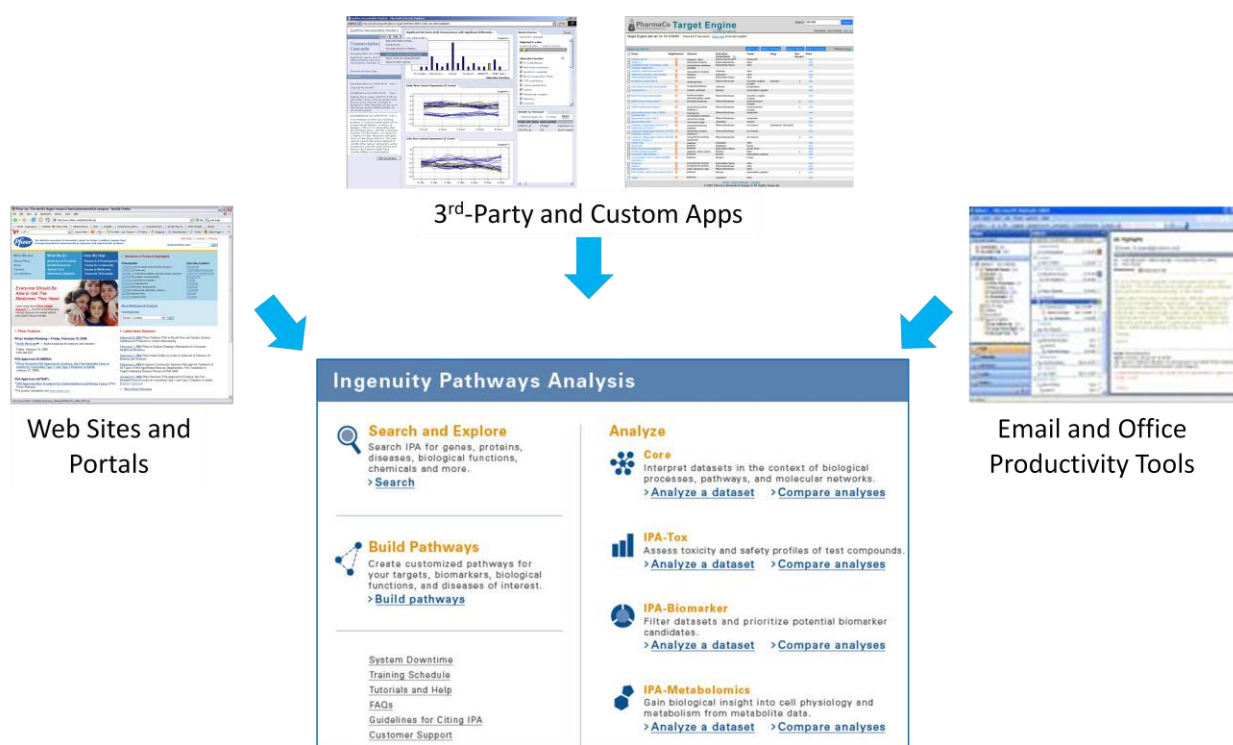


## EXECUTIVE SUMMARY

The Ingenuity Pathways Analysis (IPA) Integration Module enables life science researchers to access the high quality, detail-rich biological and chemical knowledge in IPA directly from their internal websites, applications, and gene catalogues, as well as from internal research reports, e-mails and other shared documents that are part of their daily research workflows. This easy-to-implement module increases the utility of internal web sites, search portals, and research reports by providing direct links to the content and analysis capabilities in IPA, including details on individual genes or lists of genes, their interrelationships, their participation in well-characterized signaling and metabolic pathways, and in cellular and disease processes.

>> For the Integration Module User Guide or to implement the Integration Module, please contact [support@ingenuity.com](mailto:support@ingenuity.com).

>> For a free IPA trial, [click here](#).



## INTRODUCTION

The IPA Integration Module (IPA-IM) provides simple, lightweight URLs to enable direct links from in-house bioinformatics and biological search applications, documents, and reports to the biological and chemical content and analysis capabilities in IPA. By directly linking internal software and documents to IPA, biologists and chemists will be able to quickly traverse from the sites that they routinely use in their research workflows to:

- Rapidly gain biological insight and understanding from their experimental datasets by uploading and analyzing data in IPA that is stored internally in proprietary data warehouses and applications.
- Access a comprehensive overview of scientific findings for a given gene or chemical and obtain detailed information on those molecules including biological functions, molecular interactions and regulatory events, pathways, and pharmacological relevance.
- Review a comprehensive list of the supporting evidence for any relationship between two genes.
- Create and store new pathways from lists of genes.

- Upload datasets and run analyses in a more automated fashion.

Because the IPA-IM is implemented as a suite of URLs, they can be embedded in virtually any application or document without needing any additional software or making any infrastructure changes. This implementation also ensures rapid deployment, enabling researchers without significant software development experience to integrate in-house applications with IPA without extensive training.

## THE PROBLEM

Pharmaceutical companies and academic institutions have responded to the information overload initiated by the genomics era by creating internal web sites, portals, and gene catalogues that serve as a central store for information on targets, chemicals, biomarkers, and experimental data. Therapeutic area research teams have responded to equivalent challenges of communicating their research results with colleagues and collaborators by adopting consistent internal report and presentation formats. While these knowledge management solutions have helped streamline researchers' ability to access information and communicate results, their value and utility would increase dramatically when linked to the comprehensive biological and chemical content and premier analysis tools in IPA that assess the relationships between their molecules of interest.

For example, most in-house search portals, gene catalogues, and indices are successful in generating relevant lists of genes, or highlighting individual genes and chemicals, but life scientists often need to conduct additional and time-consuming searches in order to get detailed information on the genes in the list, to understand what the literature says about a gene or set of genes, and to get a summary of this knowledge in a convenient form with links out to the details and references on specific genes, their relationships, their participation in pathways, diseases, etc.

Similarly, many in-house data warehouses provide researchers with a direct link to relevant experimental datasets, but additional steps are often needed in order to efficiently upload multiple datasets and analyze them in IPA.

The IPA-IM was designed specifically to address these needs, and eliminate the costly additional steps researchers must currently take to gain access to the relevant, timely biological and chemical knowledge and data analysis capabilities of IPA.

## THE SOLUTION

IPA's Integration Module streamlines biological and chemical searches as well as data analysis and interpretation by providing an easy way to execute key IPA features from internal applications and documents. The IPA-IM consists of a suite of easy to implement URLs. These URLs can be embedded in e-mails, documents (MS Office or PDF format for example), web pages, applications, or simply pasted in a web browser address bar. Implementing the URL based IPA-IM is simple, does not require additional hardware or software, and works with both the IPA web start and applet technology.

Some of the common ways that the IPA-IM is being applied in drug discovery and development settings today include enabling researchers to share IPA results with colleagues via e-mail, integrating corporate web sites and search portals with the biological knowledge in IPA, streamlining the data analysis process by linking large data warehouses directly to IPA's data upload process, and creating interactive target reports that link directly out to IPA's Gene Views, Gene Neighborhoods, interactive Canonical Pathways, and Functional Analysis tables.

### Gene and Chemical Identifiers Supported by the IPA-IM:

- Affymetrix
- Affymetrix SNP ID
- Agilent
- Applied Biosystems
- CAS Registry
- CodeLink
- Entrez Gene
- GenBank
- GenPept
- GI Number
- HUGO Gene Symbol
- Illumina
- International Protein Index
- KEGG ID
- PubChem CID
- RefSeq
- UniGene
- UniProt/SwissProt Accession

A complete list of URLs available through the IPA-IM is provided in Appendix A. Here we provide a couple of examples of workflows that are enabled by the IPA-IM.

Example 1: Link directly from an internal, proprietary Gene Index to IPA Gene Views, Gene Neighborhoods

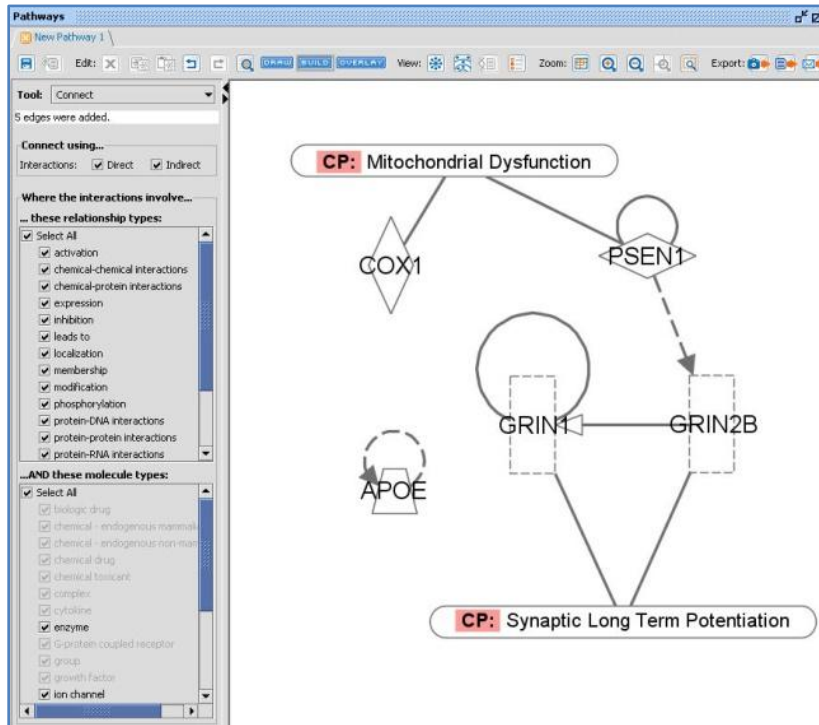
The screenshot shows the PharmaCo Target Engine interface. On the left, a search bar contains 'GDNF'. Below it is a table of search results with columns for Gene, Neighborhood, Disease, Subcellular Compartment, Family, Drug, and New Results. A 'Neighborhood Explorer' window is open on the right, displaying a complex network diagram of genes and their interactions. A 'Molecule Summary' window is also open, showing details for GDNF (Glial cell derived neurotrophic factor), including its protein family, domain, and canonical pathway (Amyotrophic Lateral Sclerosis Signaling).

Example 1: By embedding IPA-IM URLs into a pharmaceutical company’s “Target Engine,” users can traverse directly from a drug target to comprehensive information about that target, including its molecular neighborhood and Gene View.

Example 2: Send a proprietary Gene List from an internal search portal to IPA’s My Pathways and Canonical Pathway Analysis

Gene List - Alzheimer's Disease					
Global Canonical Pathway					
New Pathway					
Network Analysis					
Gene	Neighbor	Canonical Pathways	Cellular Component	Biological Process	Link Out
<input checked="" type="checkbox"/>	GRIN1	Amyotrophic Lateral Sclerosis Signaling; Calcium Signaling; Circadian Rhythm Signaling; Ephrin Receptor Signaling; Glutamate Receptor Signaling; Synaptic Long Term Potentiation	membrane	ion transport	chr9, Entrez, JAX
<input checked="" type="checkbox"/>	COX1	Oxidative Phosphorylation	mitochondrion	electron transport	chr1, Entrez, JAX
<input checked="" type="checkbox"/>	GRIN2B	Amyotrophic Lateral Sclerosis Signaling; Calcium Signaling; Circadian Rhythm Signaling; Ephrin Receptor Signaling; Glutamate Receptor Signaling; Huntington's Disease Signaling; Synaptic Long Term Potentiation	membrane	ion transport	chr12, Entrez, JAX
<input checked="" type="checkbox"/>	PSEN1	Amyloid Processing; Neuregulin Signaling; Notch Signaling	kinetochore; intracellular; membrane fraction; nucleus; integral to nuclear inner membrane; mitochondrion; endoplasmic reticulum; Golgi apparatus; integral to plasma membrane; membrane; axon; dendrite; cytoplasmic vesicle; ciliary rootlet; cell soma	blood vessel development; cell fate specification; neuron migration; membrane protein ectodomain proteolysis; calcium ion homeostasis; apoptosis; anti-apoptosis; ...	chr14, Entrez, JAX
<input checked="" type="checkbox"/>	APOE	LPS/L1-1 Mediated Inhibition of RXR Function	extracellular region; cytoplasm; chylomicron	response to reactive oxygen species; lipid transport; induction of apoptosis; cytoskeleton organization and biogenesis; synaptic transmission, cholinergic; learning and/or memory; circulation; ...	chr19, Entrez, JAX

Example 2a: IPA-IM is used to embed IPA’s search capabilities within a pharmaceutical company’s internal search application, giving researchers instant access to the content and analysis capabilities in IPA.



Example 2b: Send a list of genes selected from your internal, proprietary Gene Index (or portal, hub, etc.) to My Pathways to understand whether or not (and how) those genes are connected.



Example 2c: Send a list of genes selected from your internal, proprietary Gene Index (or portal, hub, etc.) to IPA's Canonical Pathway Analysis to rapidly understand which pathways are most significant to your proprietary gene list.

## THE BENEFITS

The IPA-IM provides benefits to biologist end users of IPA as well as to bioinformaticians who enable therapeutic area researchers through data analysis and development of internal tools.

End user biologists will benefit from greater accessibility to IPA through the tools commonly used in their day-to-day research, including e-mails, corporate portals, and data analysis applications and data warehouses. Integrated tools can be tailored to match users' workflows, and also provide more flexibility in creating custom interfaces for internal tools. Researchers will also benefit from the increased accuracy that comes from automatically passing data between applications (internal data warehouses and IPA), eliminating file format incompatibility issues.

Bioinformaticians and computational biologists will be able to accelerate in-house development of tools, and add value to existing tools by leveraging IPA's comprehensive, highly structured and detail rich biological and chemical content, along with its analysis capabilities and graphical display of biological and chemical relationships. Integrating proprietary in-house tools with the proven, well-adopted capabilities of IPA will lower development costs and increase the ROI on their projects.

## CONCLUSION

Ingenuity Pathways Analysis is a software application that enables researchers to model, analyze, and understand the complex biological and chemical systems at the core of life science research. IPA's Search capabilities provide users with access to the highest quality, detail-rich knowledge available on genes, drugs, chemicals, protein families, cellular and disease processes, and signaling and metabolic pathways. IPA supports analysis of data from all experimental platforms and is used at all stages of the drug discovery and development process, including target identification and validation, biomarker discovery, molecular toxicology, metabolomics, and pharmacogenomics.

By using the IPA-IM to install direct links from internal web sites, search portals, or proprietary research reports to the content and capabilities within IPA, drug discovery and development companies will streamline their researchers' workflows, increase the value and ROI on internal applications, enhance the communication of results, and enable more effective decision making by therapeutic area research teams.

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## APPENDIX A: TABLE OF INTEGRATION MODULE APIS

Name of URL (API)	Description	Output in IPA	Output in HTML	Output in XML
search	Search for biological terms including genes, chemicals, diseases and biological processes	√		
dataupload/ multiupload	Upload single/multi observation dataset	√		
Datanalysis/ multiobsanalysis	Analyze single/multi observation dataset	√		

geneview	Display a Gene View		√	
hasgeneinf	Verify whether a node view or neighborhood exists			√
geneneighbor	Display a Gene's Neighborhood	√		
newpathway	Create a new "My Pathway"	√		
gcpview	Display the Canonical Pathway graph for a single gene or a list of genes	√		
pathwayquery	Display a Canonical Pathway	√		
pathwaylist	Display list of Canonical Pathways & members		√	
relationshipview	Display the molecular relationships between 2 genes		√	
hasrelationshipinfo	Verify whether a relationship exists between 2 genes			√