

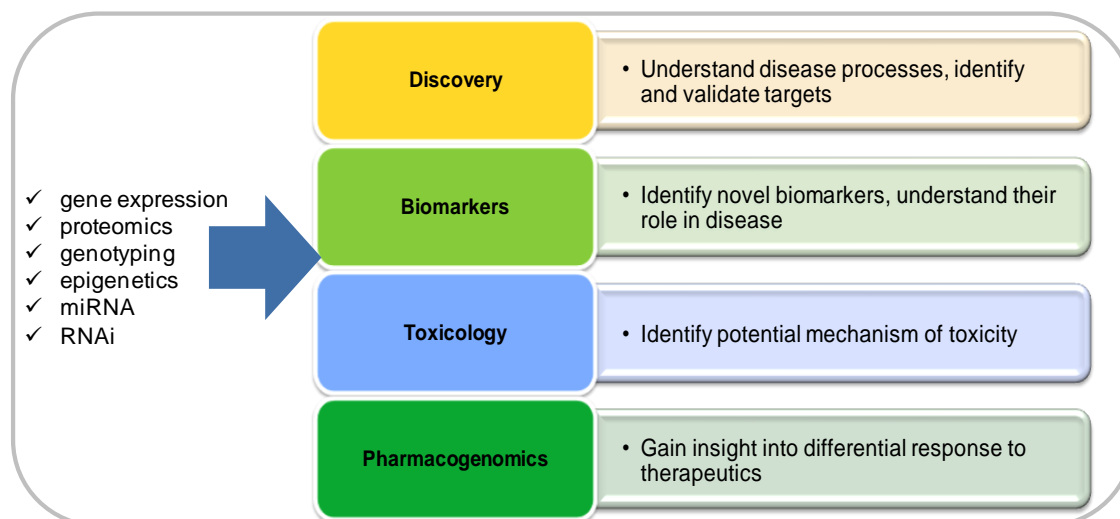
IPA IN PRACTICE

Overview

IPA is a software application that enables life science researchers to better understand the biological and chemical systems at the core of life science research. With IPA, researchers can analyze 'omics data, search for targeted biological and chemical information, and build their own biological models.

The powerful capabilities of IPA are a direct result of Ingenuity's uniquely structured knowledge base of biological findings and relationships. These findings are manually structured and curated from the full text of articles published in hundreds of peer-reviewed journals, including Nature, Science, Journal of Virology, Cancer Research, Journal of Immunology, Cell, [and many others](#).

IPA can be used across multiple platforms and in many different areas of drug discovery:



IPA is used to advance research in key therapy areas:

- Classification and prediction of clinical Alzheimer's diagnosis based on plasma signaling proteins. **Nat Med.** 2007 Oct 14 (*CNS disorders*)
- ATM and ATR substrate analysis reveals extensive protein networks responsive to DNA damage. **Science.** 2007 May 25 (*Oncology*)
- Identification of Differentially Activated Cell-Signaling Networks Associated with Pichinde Virus Pathogenesis by Using Systems Kinomics. **J Virol.** 2007 Feb;8 (*Infectious disease*)
- **Genomic analysis of increased host immune and cell death responses induced by 1918 influenza virus.** *Nature.* 2006 Oct 5; 443(7111):578-81. (*Immune & Inflammatory disease*)

To access a complete list of our publications, searchable by area of research, please visit the Ingenuity website at <http://www.ingenuity.com/library/search-pub.html>

"IPA was very helpful in the analysis of our data leading to a publication in Nature Medicine. Thanks for creating such a fantastic discovery tool!" - Markus Britschgi, Ph.D. Stanford University

"IPA is a fast and powerful tool in the analysis of results of functional screens. It has been a great help to us in building networks of the hits that were identified in our siRNA screen. Based on these analyses, we were able to direct our follow-up experiments leading to meaningful results and valuable insights." - Roderick Beijersbergen, Ph.D, Division of Molecular Carcinogenesis, The Netherlands Cancer Institute