

Ingenuity[®] Science Spotlight:

Articles featured in the Ingenuity Science Spotlight represent some of the best and most diverse examples of how IPA[®] has contributed to research across multiple platforms, research areas, and research goals.



Microarray analysis reveals genetic pathways modulated by tipifarnib in acute myeloid leukemia.

Mitch Raponi, Tober T Belly, Judith E. Karp, Jeffrey E. Lancet, David Atkins and Yixin Wang. BMC Cancer 2004, 4:56.

<http://www.ncbi.nlm.nih.gov/pubmed/15329151?dopt=Abstract>

Dysregulated signaling pathways are important contributors to cell proliferation in various types of cancer. The biological activity of numerous proteins in signal transduction pathways requires farnesylation, a posttranslational modification that involves the addition of a farnesyl moiety. Farnesyl transferase inhibitors (FTIs) are a new class of drugs that inhibit tumor growth, presumably by diminishing uncontrolled cell signaling that leads to cancerous cell proliferation.

The FTI tipifarnib is currently in clinical trials for treatment of various cancers and shows promising potential for some blood cancers. To help identify pharmacologic biomarkers of tipifarnib activity and the gene pathways involved in the drug's mechanism of action, scientists conducted differential gene expression analysis in acute myeloid leukemia cells treated with tipifarnib and used IPA to analyze the genes affected by tipifarnib.

Network analysis identified five highly significant networks associated with the cell cycle, proliferation, chemotaxis, and immunity. The networks include genes that are known to be directly or indirectly affected by FTIs. Moreover, Neighborhood Explorer revealed other genes not identified by microarray analysis that may be regulated by tipifarnib. Thus IPA enabled a larger framework for identifying potential tipifarnib gene targets. The genes revealed by the network analysis may be useful for determining candidates for tipifarnib therapy.