

## Ingenuity<sup>®</sup> Science Spotlight:

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



### **Gene expression analyses reveal molecular relationships among 20 regions of the human CNS.**

Richard B. Roth, Peter Hevezi, Jerry Lee, Dorian Willhite, Sandra M. Lechner, Alan C. Foster and Albert Zlotnik. *Neurogenetics* (2006) 7: 67–80.

<http://www.springerlink.com/content/m5165560235j8771/>

Researchers at Neurocrine Biosciences obtained gene expression profiles of 20 central nervous system (CNS) regions in an effort to build a comprehensive molecular profile of the healthy human CNS. The team used IPA's networks, functions and canonical pathways to help define the attributes of different CNS tissues.

For example, in an analysis of a probe set consisting of 1938 gene identifiers that were upregulated specifically in the cerebellum, IPA's network analysis helped the researchers find networks that consisted entirely of genes found in the cerebellum. Functional analysis of these networks revealed functions overrepresented in the cerebellum, including neuronal cell differentiation, neuronal cell development, cell survival, tissue development, and apoptosis. Canonical pathways revealed several cell signaling and metabolic pathways that are important to the function of the cerebellum, including the nitrogen metabolism pathway and the glutamate receptor-signaling pathway. These results helped the research team gain insight into the molecular functions carried out by different sites of the human CNS, to better understand CNS structure-function relationships.