

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.



Gene expression profiling of lymphoblastoid cell lines from monozygotic twins discordant in severity of autism reveals differential regulation of neurologically relevant genes.

Valerie W Hu, Bryan C Frank, Shannon Heine, Norman H Lee, and John Quackenbush. BMC Genomics. 2006; 7: 118. Published online 2006 May 18.

<http://www.ncbi.nlm.nih.gov/pmc/articles/PMC1525191/?tool=pubmed>

A team of collective researchers at The George Washington University Medical Center, The Institute for Genomic Research, and The Dana-Farber Cancer Institute used IPA to help analyze and interpret gene expression data in their study. IPA's network analyses revealed highly interconnected relationships between genes differentially expressed in monozygotic twins discordant in severity of autism and/or language impairment: the researchers found that many of these genes were part of an extended network centered on TNF and other inflammatory mediators. Furthermore, IPA's global functional analysis revealed that a significant number of the differentially expressed genes were involved in nervous system development and function. These results helped the team to identify gene networks, consisting of genes involved in the development, structure, and/or function of the nervous system, which may play a role in the pathophysiology of autism.