

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.



“Network modeling approaches, such as IPA, are critical to the understanding of complex diseases, such as cancers, in which causative genes and proteins do not operate in isolation; but rather their interactions account for the disease process.”

Markus Bredel, MD PhD
Director, Northwestern Brain Tumor Institute Research Program
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A Network Model of a Cooperative Genetic Landscape in Brain Tumors.

Markus Bredel; Denise M. Scholtens; Griffith R. Claudia Bredel; James P. Chandler; Jaclyn J. Renfrow; Ajay K. Yadav; Hannes Vogel; Adrienne C. Scheck; Robert Tibshirani; Branimir I. Sikic. JAMA. 2009; 302(3):261-275 (doi:10.1001/jama.2009.997).

<http://jama.ama-assn.org/cgi/content/short/302/3/261?home>

Researchers from several institutions in the area of neuroscience used a systems biology approach to generate a network model of a non random genetic landscape in gliomas. They hypothesized that the genetic and genomic changes that are the hallmark of glioblastoma do not occur at random – but rather that there may be networks of related genetic/genomic changes that promote gliomagenesis, and understanding this network will improve diagnosis and potentially identify novel points of intervention.

To test this hypothesis, they used IPA to integrate and analyze several lines of molecular data including gene dosage, genetic alterations and gene expression – to generate a network model consisting of genes that describes the cooperative nature of these alterations in the promotion of gliomagenesis. They then focused in on the hub genes and hub-interacting genes in the network whose interactions were cooperatively tumorigenic and identified a subset of seven genes that were independently associated with patient survival times. They were able to use this seven-gene set to retrospectively distinguish between high and low-risk patients in terms of patient survival times. They are now looking at using this gene set in prospective clinical studies for patient stratification, and also looking at their potential as therapeutic targets.