

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.



Quantitative phosphoproteomic analysis of the STAT3/IL-6/HIF1alpha signaling network: an initial study in GSC11 glioblastoma stem cells.

Nilsson CL, Dillon R, Devakumar A, Shi SD, Greig M, Rogers JC, Krastins B, Rosenblatt M, Kilmer G, Major M, Kaboord BJ, Sarracino D, Rezai T, Prakash A, Lopez M, Ji Y, Priebe W, Lang FF, Colman H, Conrad CA. J Proteome Res. 2010 Jan;9(1):430-43.

<http://pubs.acs.org/doi/abs/10.1021/pr9007927>

“The goal of our study was to provide knowledge about intracellular signaling events in glioma cancer stem cells in response to perturbations by hypoxia, inhibition of STAT3 phosphorylation and IL-6 stimulation. Glioma cancer stem cells (gCSC) are refractory to traditional therapies and new insights are needed to understand their underlying biology. We used IPA to compliment our analysis of multiple comparisons between gCSC treatments. We will continue to employ IPA tools in analysis of global phosphoproteomic data sets. “

*Charles Conrad, M.D.
Professor, Department of Neuro-Oncology
The University of Texas M. D. Anderson Cancer
Center*

This month we are focusing our Science Spotlight on a recent publication in the Journal of Proteome Research which highlights the results of a collaboration between scientists from Pfizer Global Research and Development, MD Anderson Cancer Center, and Thermo Fisher Scientific's Biomarker Research Initiative in Mass Spectrometry (BRIMS) Center. Their study aimed to better understand the signaling events involved in the maintenance of glioma stem cells (GSCs) – which are cells that demonstrate tumor-initiating properties and are hypothesized to contribute to the population of tumor cells resistant to standard cancer therapies. Their approach integrated several innovative technologies to yield a rich data set that captured the phosphoproteome of GSCs treated with the JAK2/STAT3 inhibitor WP1193 in both normoxic and hypoxic conditions. Analysis of phosphoproteomic data in IPA helped validate their approach by identifying effects on expected pathways. Importantly, IPA also provided novel molecular explanations for previously observed effects of WP1193. By confirming the role of key signaling events and feedback loops, and generating novel, testable hypotheses this collaborative effort has provided a more complete understanding of the mechanisms of drug response in glioma stem cells, which may eventually lead to the identification of novel therapeutic interventions.