

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.



Labor-Associated Gene Expression in the Human Uterine Fundus, Lower Segment, and Cervix.

Radek Bukowski, Gary D. V Hankins, George R Saade, Garland D Anderson, and Steven Thornton. PLoS Med. 2006 Jun;3(6):e169. Epub 2006 Jun 13.

<http://www.ncbi.nlm.nih.gov/pmc/articles/PMC1475650/>

Scientists from the University of Texas Medical Branch at Galveston and the University of Warwick used global gene expression and IPA to understand the molecular mechanisms that underlie the physiological process of labor. Their analysis of labor-associated gene expression profiles may eventually lead to more rational approaches to treating the problems that occur in labor.

To test their hypothesis that labor results from the coordinated expression of large numbers of genes organized into co-regulated networks, the research team analyzed expression of over 12,000 genes in biopsies taken from the uterine fundus, lower segment, and cervix of women before or after the onset of labor. They identified several clusters of co-expressed genes from each region, and subsequently performed a functional analysis using IPA. IPA enabled the team to determine that many genes within the same cluster shared similar functions or had functions relevant to the process of labor, strengthening their hypothesis that labor-associated genes were co-regulated. Identification of these functionally related, co-regulated genes provides insight into the molecular mechanism of how labor occurs, and may facilitate the design of more effective treatments for problems encountered in childbirth such as preterm labor and failure to progress.