

INGENUITY SYSTEMS CITATION GUIDELINES

This document provides a set of guidelines and best practices for citing Ingenuity pathways or Ingenuity content.

GUIDELINES FOR CITING USE OF IPA[®]

This document describes the policies and guidelines for citing IPA in all forms of publication. In general, if any images or results or analyses generated by IPA are published in any form (e.g. print, electronically, etc.), you are required to cite IPA.

CITING IPA

When citing IPA in your publication, choose the most appropriate option from the sample text below.

1. Data were analyzed through the use of IPA (Ingenuity[®] Systems, www.ingenuity.com).

OR

2. The <networks, functional analyses, etc.> were generated through the use of IPA (Ingenuity Systems, www.ingenuity.com)."

In addition, for your convenience, we have provided supplemental text that describes the manner in which analyses (e.g. Networks, Functions, Canonical Pathways, etc.) are generated within IPA. If you have any questions, contact Ingenuity Customer Support at support@ingenuity.com.

ADDITIONAL POLICIES/SUPPLEMENTAL TEXT

Feel free to use the provided text (or modified versions of) as needed for the Materials and Methods section of your manuscript.

1. Network Generation

A data set containing gene (or chemical) identifiers and corresponding expression values was uploaded into in the application. Each identifier was mapped to its corresponding object in the Ingenuity[®] Knowledge Base. A <insert expression value type here> cutoff of <insert expression value cutoff here> was set to identify molecules whose expression was significantly differentially regulated. These molecules, called Network Eligible molecules, were overlaid onto a global

molecular network developed from information contained in the Ingenuity Knowledge Base. Networks of Network Eligible Molecules were then algorithmically generated based on their connectivity.

2. Functional Analysis of an Entire Data Set

The Functional Analysis identified the biological functions and/or diseases that were most significant to the data set. Molecules from the dataset that met the *<insert expression value type here>* cutoff of *<insert expression value cutoff here>* and were associated with biological functions and/or diseases in the Ingenuity Knowledge Base were considered for the analysis. Right-tailed Fisher's exact test was used to calculate a p-value determining the probability that each biological function and/or disease assigned to that data set is due to chance alone.

3. Functional Analysis of a Network

The Functional Analysis of a network identified the biological functions and/or diseases that were most significant to the molecules in the network. The network molecules associated with biological functions and/or diseases in the Ingenuity Knowledge Base were considered for the analysis. Right-tailed Fisher's exact test was used to calculate a p-value determining the probability that each biological function and/or disease assigned to that network is due to chance alone.

4. Canonical Pathway Analysis: Entire Data Set

When publishing part of or an entire Ingenuity canonical pathway(s), cite IPA (see options above) in the reference section of your publication. You may also want to cite some of the references contained within that canonical pathway(s).

Canonical pathways analysis identified the pathways from the IPA library of canonical pathways that were most significant to the data set. Molecules from the data set that met the *<insert expression value type here>* cutoff of *<insert expression value cutoff here>* and were associated with a canonical pathway in the Ingenuity Knowledge Base were considered for the analysis. The significance of the association between the data set and the canonical pathway was measured in 2 ways: 1) A ratio of the number of molecules from the data set that map to the pathway divided by the total number of molecules that map to the canonical pathway is displayed. 2) Fisher's exact test was used to calculate a p-value determining the probability that the association between the genes in the dataset and the canonical pathway is explained by chance alone.

5. Network/My Pathways/ Path Designer Graphical Representation

A network/My Pathways is a graphical representation of the molecular relationships between molecules. Molecules are represented as nodes, and the biological relationship between two

nodes is represented as an edge (line). All edges are supported by at least one reference from the literature, from a textbook, or from canonical information stored in the Ingenuity Knowledge Base. Human, mouse, and rat orthologs of a gene are stored as separate objects in the Ingenuity Knowledge Base, but are represented as a single node in the network. The intensity of the node color indicates the degree of up- (red) or down- (green) regulation. Nodes are displayed using various shapes that represent the functional class of the gene product. Edges are displayed with various labels that describe the nature of the relationship between the nodes (e.g., P for phosphorylation, T for transcription).