

# Annotation Analysis

In addition, to the cytoscape based GO analysis there is a number of web based and R based annotation analysis systems.

One easy to use option with a wide range of gene annotation options is the DAVID resource:

<http://david.abcc.ncifcrf.gov/tools.jsp>

Details on how it works can be found here:

*[Nature Protocols 2009; 4\(1\):44 & Genome Biology 2003; 4\(5\):P3](#)*