

# WebGIVI: A Website Visualization of Gene and *iTerm*

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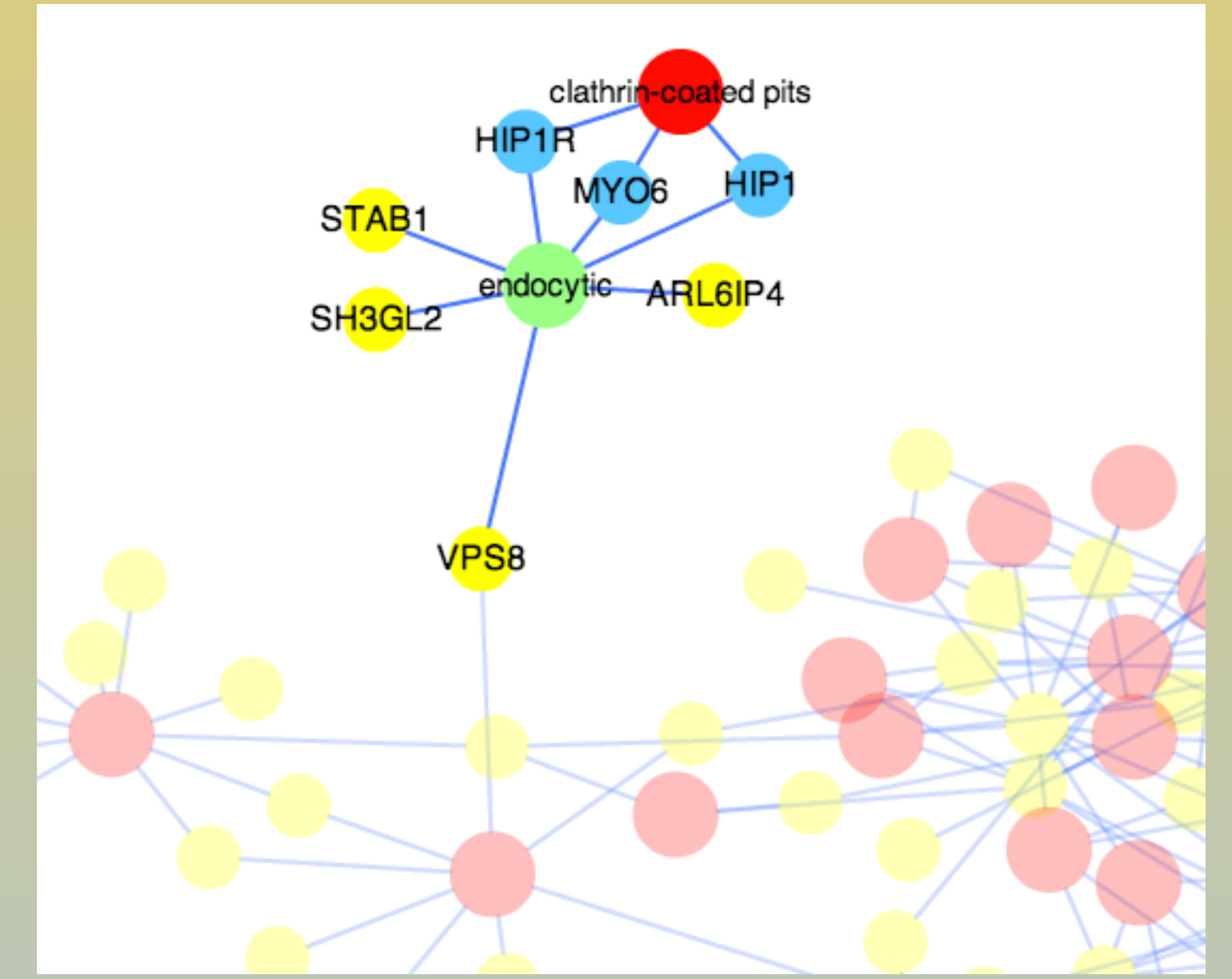
## Introduction:

The challenge of high throughput transcriptome studies is to present the data to researchers in an interpretable format. In many cases, the outputs of such studies are gene lists which are then examined for enriched biological concepts. One approach is to associate genes and informative terms (*iTerm*) that are obtained from the biomedical literature using eGIFT. However, examining large lists of *iTerm* and gene pairs is a challenge. We have developed WebGIVI, a user-friendly web interface

(<http://raven.anr.udel.edu/~sunliang/biolayout/index.php>), which was built via Cytoscape JavaScript graph library and can be used to visualize gene and *iTerm* pairs.

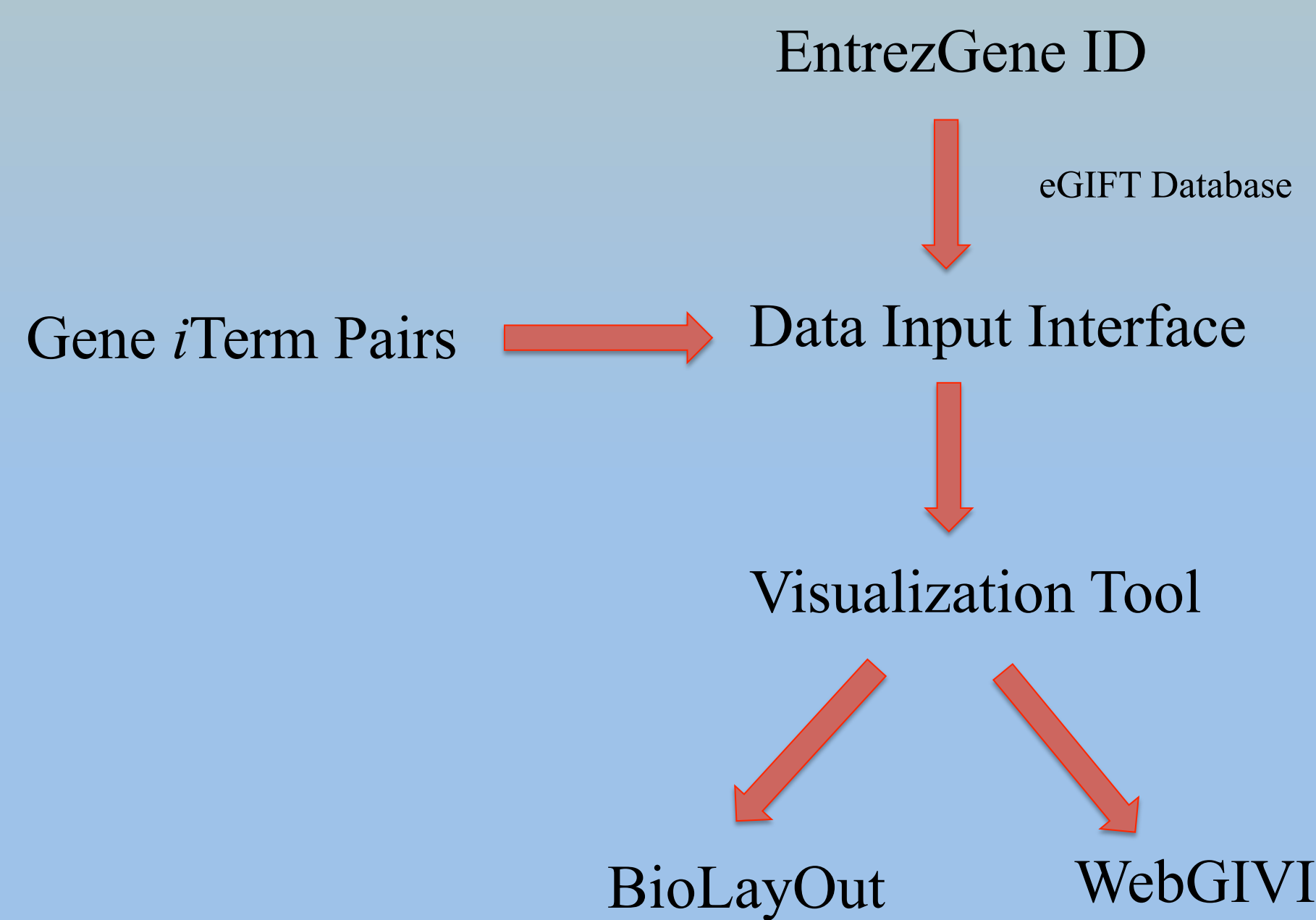
3). **Intersection highlight:** selecting two/multiple *items*, highlights shared genes between these two/multiple genes, and vice versa.

**Figure 4.** Intersection of the gene symbols between two *items*. Gene HIP1R, MYO6 and HIP1 (light blue node) are the shared genes of *items* endocytic and clathrin-coated pits; all other gene and *items* not neighbored are hidden.



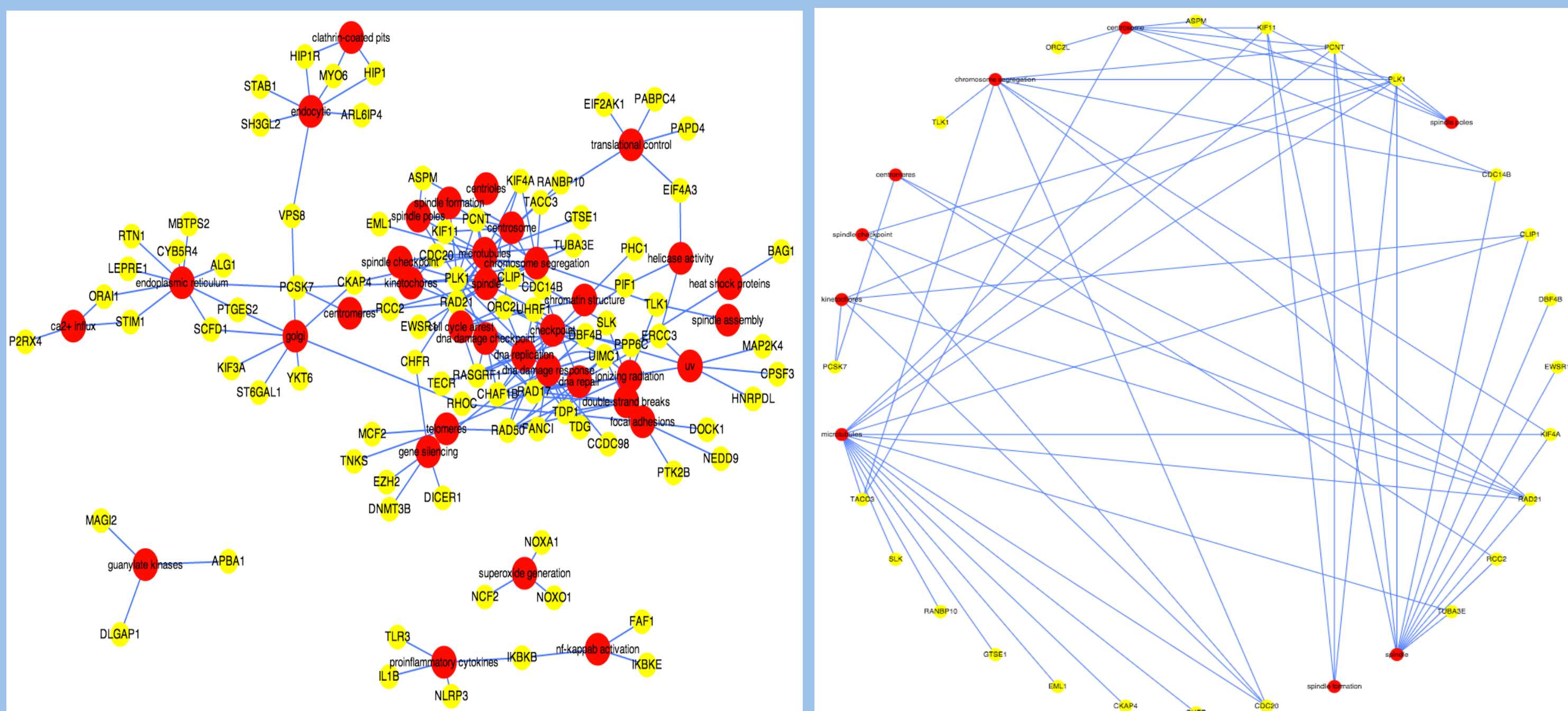
## Materials and Methods:

WebGIVI can accept two input data formats: EntrezGene list and pairwise gene symbol and *iTerm* list.



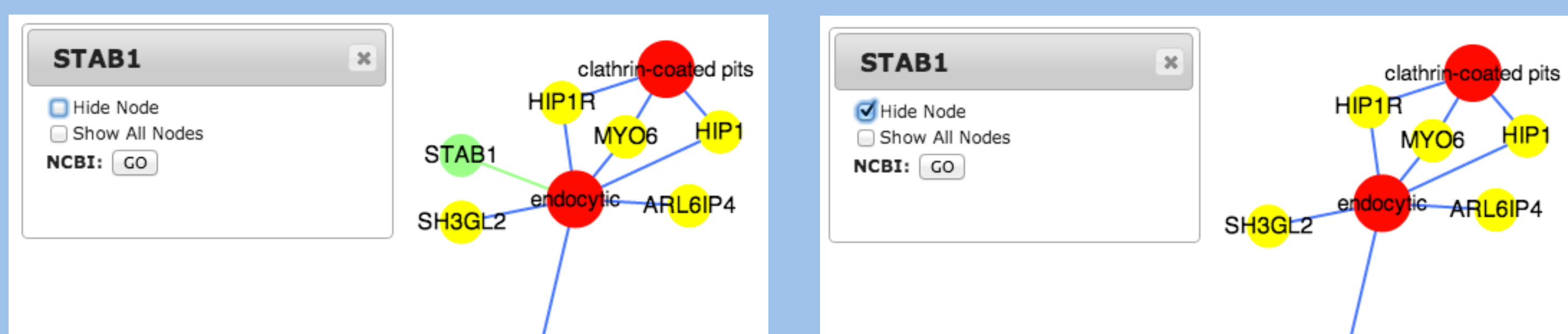
**Figure 1.** Flow Chart of WebGIVI Tool. Gene *iTerm* Pair indicates gene symbol and its associated informative term.

1). **Layout Methods:** genes and *items* can be grouped via force-directed, breadth-first, circle, and random layout algorithm. Force-directed and circle layout network are provided in Figure 2.



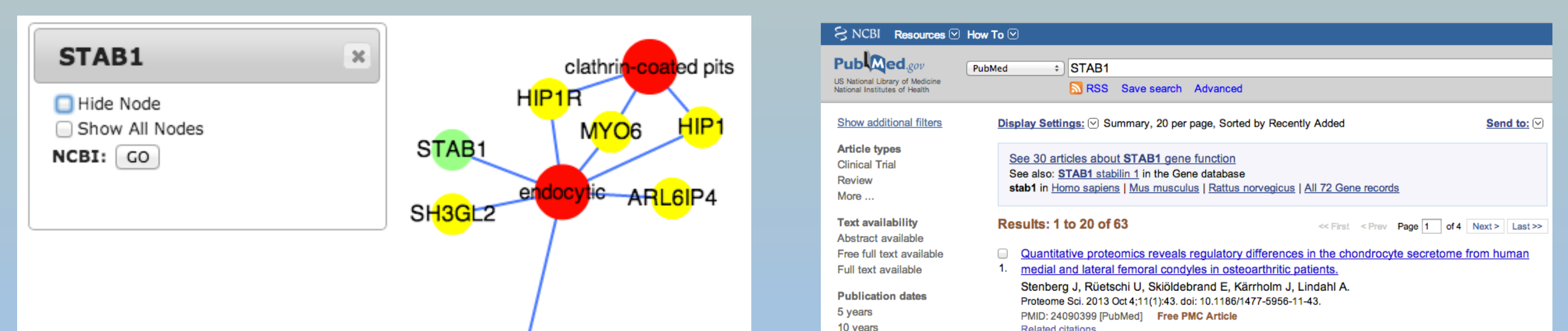
**Figure 2.** Forced-directed layout (left) and circle layout (right). Nodes in red represent *items*; Nodes in yellow represent gene symbols.

2). **Hide/show:** gene/*iTerm* can be hidden or shown according to user's preference.

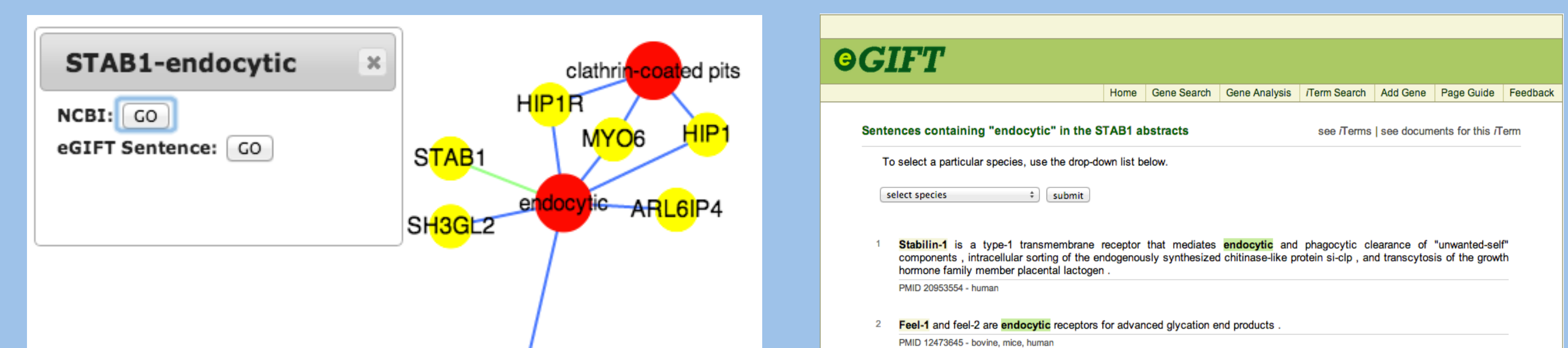


**Figure 3.** Hide/show function: pop-up menu for gene STAB1 via right clicking (left); node STAB1 and edge connected are hidden via checking Hide Node checkbox.

4). **Link Out:** key words of gene, *iTerm* or gene-*iTerm* pair can be linked directly from our graph to NCBI PubMed database and eGIFT database.

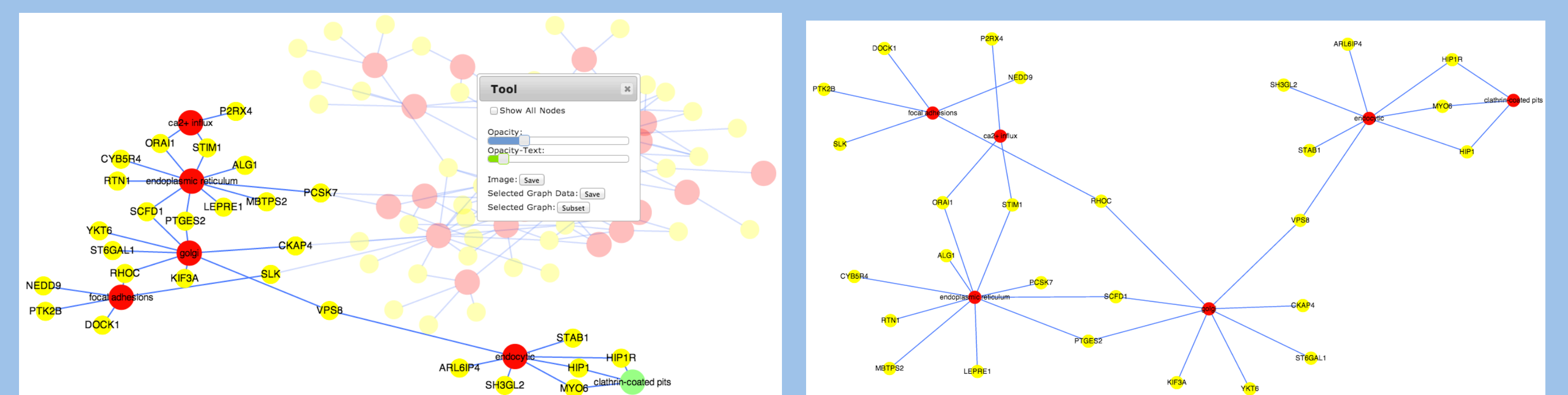


**Figure 5.** Link-out function for gene symbols and *iTerm*. Pop-up menu for gene STAB1 via right clicking node STAB1 (left) and NCBI database for gene STAB1 (right).



**Figure 6.** Link-out function for gene-*iTerm* pair. Pop-up menu for STAB1 and endocytic pair via clicking node STAB1 (left) and eGIFT database for STAB1 and endocytic pair (right).

5). **Graph Subset and Download :** Subset of graph based on selected gene/*items* can be displayed in the same web page. selected gene/*iTerm* can be downloaded as a tab-delimited text. Visualized Graph on the website can also be saved as PNG format.



**Figure 7.** Selected nodes (left) and their subset graph (right). Opacity and Opacity Text of node can be adjust by the slider in the tool window(left).

## Results:

WebGIVI can accept EntrezGene list that will be used to retrieve a gene symbol and *iTerm* list. This list can be resubmitted to visualize the gene-*iTerm* pairs using either WebGIVI or BioLayout. A variety of visualization formats are available in WebGIVI including force directed, tree and circle. Visualized Graph on the website can also be saved as PNG format.

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