

# Annotating to the Gene Ontology

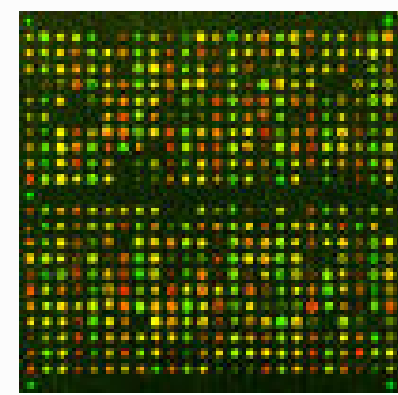
## Does your species show in GO?

Join those already annotating.

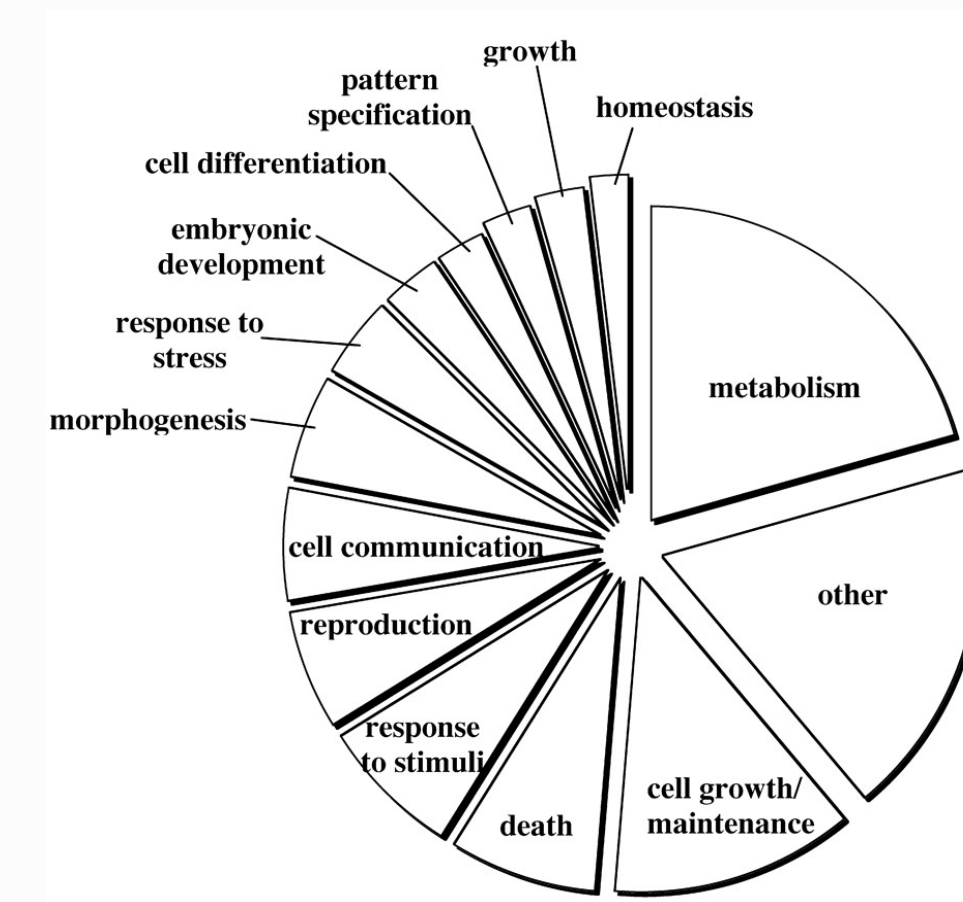


Get results...

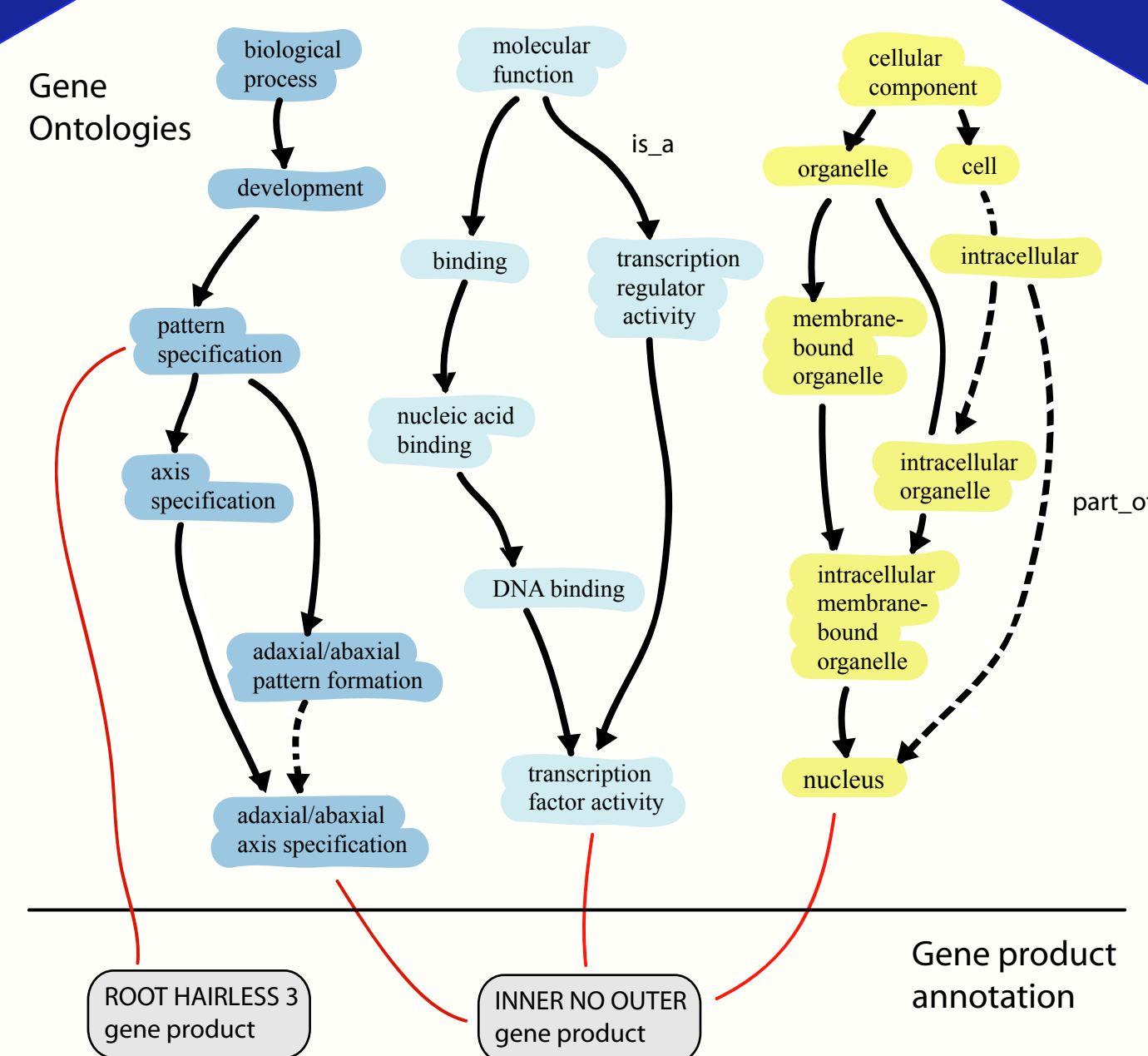
Microarray users



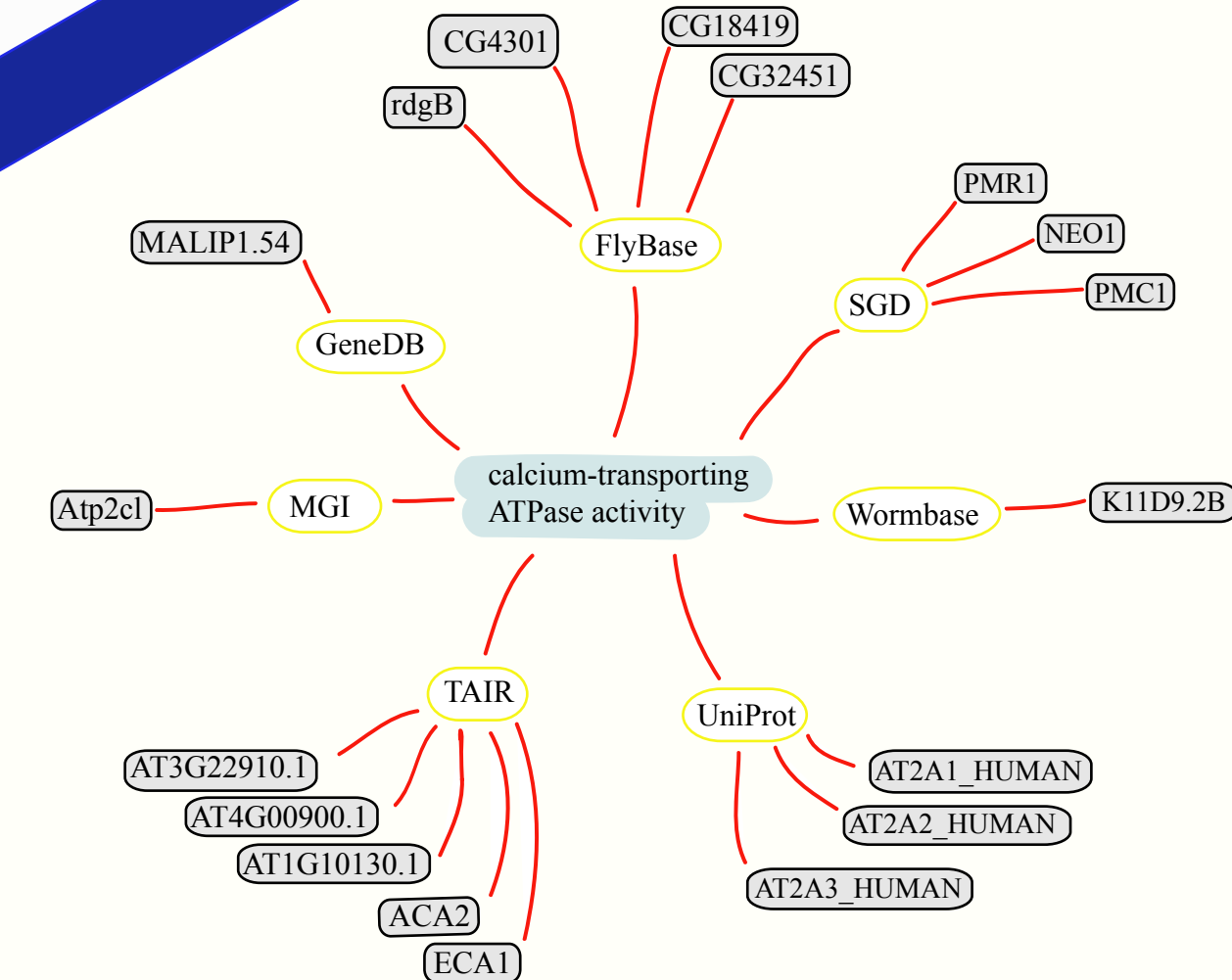
See which processes are affected by treatments, rather than just which gene products.



Whole genome analysis  
(J. D. Munkvold et al., 2004)



Gene products are classified according to the cellular locations and biological process in which they act and the molecular functions that they carry out. (Clark et al., 2005)



Annotation of many species to the GO allows scientists to access information about gene products with the same functions in different organisms. (Clark et al., 2005)

Send your data...

- 1) Read the papers.
- 2) Which gene products?
- 3) Which process, function or location of action?
- 4) What kind of evidence is there?

Compile the information.

In paper PMID:11696550, *aristaless 4* from *Mus musculus* was Inferred by direct assay to have transcription factor activity

Put the information in a spreadsheet and send to the Gene Ontology Consortium at the e-mail address below.

For more information on annotation please see the GO website at:  
[www.geneontology.org/GO.annotation.shtml](http://www.geneontology.org/GO.annotation.shtml)

Send to GO  
email: [go@geneontology.org](mailto:go@geneontology.org)