- 1. Go to <a href="http://www.yeastgenome.org/">http://www.yeastgenome.org/</a> and find 3 candidate genes of known f(x) and one of undefined f(x) that you predict to be altered by DMSO treatment. Make a hypothesis as to whether or not you anticipate this gene to go Up or Down in the DMSO treated yeast and why.
- 2. What GO biological processes and molecular mechanisms are associated with your candidate genes?
- 3. Where, subcellularly does the protein reside in the cell?
- 4. What other proteins are known or inferred to interact with yours? How was this interaction determined? Is this a genetic or physical interaction?
- 5. Find the expression of at least one of your known genes in another public ally deposited microarray data set?
  - a) Name of data set and how you found it?
  - b) What is the largest Fold change observed for this gene in the public study?
- 6. Now that you are microarray technology experts can you give me two reasons the observed transcript level difference may not be confirmed through a second technology like RTQPCR?