Questions for the Library construction labs- due Wed March 7

1. What differences do you see in the number of the colonies of the different ligation transformations(L1-L4)? What could account for this difference?
2. Based on the results of the plasmid prep, what is the average size of the insert seen? What percent of the colonies have inserts? Based on this data, and the fact that genome is 4.3 million base pairs, how many colonies would you have to screen to cover the entire genome?
3. The strain of *E. coli* that allows high light production from the lux gene does not allow alpha complementation of the beta glactosidase gene. What change would be needed in this *E. coli* to allow alpha complementation? How would alpha complementation help in assessing how well the creation of a genomic library worked?
4. What are some ways we could increase the chances of successfully cloning the lux operon?