Problem Set 04

1. How does the Shine Delgarno sequence work to initiate translation in bacteria and archaea? What molecule has the anti-Shine Delgarno sequence? Explain in a few sentences and draw a diagram. How does this differ from translational initiation in eukaryotes?

2. A new operon is discovered with 5 genes. How many promoters with a -10 and -35 region for sigma factor binding does it have? How many Shine Delgarno sequences? Explain your answer.

3. How many ribosomes are in an E. coli cell that is doubling every 100 minutes compared to every 24 minutes? How does this scale with ribosomes per dry mass? What cellular constraints would cause cells to do this? *Hint: Look at Cell Bio by the Numbers readings for this week!*

4. List 3 ***different*** benefits that gene regulation can confer to organisms.

5. You've discovered a new species of bacteria just got the results back from sequencing its genome. Its genome was smaller than its relatives and your genome annotation predicts that this species is missing many transcription factors that are commonly found in its relatives. Develop a hypothesis about this species's ecological niche based on this information. Explain your rationale and give some examples that support your theory.

6. An *E. coli* mutant is discovered that cannot express the genes in the *lac* operon under the "right" conditions. Explain how the *lac* operon *should* work. Then, describe a plausible mutation in the regulators of the *lac* operon that could cause a mutant phenotype where the *lac* operon doesn't respond appropriately. Include what gene is mutated, describe the effect on that protein's function, and explain what mutant phenotype would be observed where the *lac* operon behaves differently than the wild type.

7. Diagram gene regulatory circuits for a negative feedback loop vs. a positive feedback loop. Explain the functional importance of this gene regulatory network structure compared to a comparable network without feedback.

8. Describe 3 **conceptual** steps which must occur in the process of cell differentiation.

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9. From the sequencing of the human genome, we believe that there are approximately 21,000 protein-coding genes in the genome, of which 1500–3000 are transcription factors. If every gene has a tissue-specific and signal-dependent transcription pattern, how can such a small number of transcriptional regulatory proteins generate a much larger set of transcriptional patterns?

10. Is cell differentiation a feature unique to multicellular eukaryotes? Discuss the molecular mechanisms behind how nitrogen fixation in the filamentous cyanobacteria *Anabeana* and the parallels to eukaryotic developmental processes.