## Homework 1

Handed out: 9/3/08
Due: 9/08/08
For this homework you will need to do a bit of research online. You'll have to look up IUB/IUPAC codes for DNA ambiguity codes as well as conversion tables between amino-acids and the corresponding codons (genetic code). Please list your bibliographic (online, library, etc.) source for this information.

1. Within the class directory on the glue system you will find a file called HW1_forw.fasta (full path: /afs/glue.umd.edu/class/fall2009/cmsc/423/0101/public/HW1_forw.fasta). Within this file are three DNA sequences in FASTA format. Please create a new FASTA file called HW1_rev.fasta (in your own directory on the glue system) that contains the reverse complement sequence for each of the three sequences. Note, some of the sequences contain ambiguity codes (also called IUB/IUPAC codes). Make sure you reverse complement these codes accordingly.
To submit this section of the assignment you will need to use the 'submit' command as highlighted in the Glue HowTo at: http://www.cbcb.umd.edu/confcour/CMSC423-materials/glue howto.html (also available on the class website)
2. What is the amino-acid sequence encoded in the following DNA sequence (assume gene starts at the first start codon and ends at first stop codon).

TTCGAGGGGCATGTTTGTTGCTATGAATGATAATAAAACAATGCTTTTTATTCCGGGGGCAACCAATTAAGTAATTC
(Trivia: this is a piece of one of the plague's - Yersinia pestis - toxic factors)
3. Match the following amino-acid sequence to the corresponding location in the DNA string shown below.

KLFALTAVALMG
GTATGAAAAAACTAAAATTGTTTGCTCTTACAGCTGTAGCCCTAATGGGTGTTTCAGGTGTA
(Trivia: this is a piece of a bacterial rhodopsin gene - one of the genes involved in photosynthesis. Until 2000 it was believed that only plants were capable of photosynthesis. The discovery of bacterial rhodopsin was done computationally and is one of the advances made possible by genomic analysis).
4. Define the following biological terms (look them up on the Internet and write out a one sentence definition in your own words):

- Frameshift mutation
- Silent mutation

