1. The structure of four amino acids is given below. Indicate what type of bond the R group of each amino acid will be able to form and the level(s) of structure that this bond could stabilize.

A – ionic bonds  
B – hydrogen bonds  
C – disulfide bonds  
D – hydrophobic interactions

A – tertiary and quaternary  
B – tertiary and quaternary  
C – tertiary and quaternary  
D – tertiary and quaternary

2. In experiments designed by Hershey and Chase to determine what molecule served as the genetic material, $^{35}$S was added to virus replicating within its bacterial host. The new virions were carefully isolated and used to infect fresh bacterial cells in the absence of any radioisotopes. What molecule was labeled with the isotope and where did they find the majority of it? Explain why this is so.

$^{35}$S would label protein molecules and would be found in the protein coats of the virus particles. These coats cannot enter the cells when they become infected so the coats would remain outside the bacterial cells in the supernatant.
3. The diagram below shows a complete strand of DNA hydrogen bonded to two incomplete strands. Indicate the polarity of the two incomplete strands by labeling all of their ends.

\[ 5' \quad \ldots \quad PO_4 \quad 5' \quad 3' \quad \ldots \quad 3' \]

4. One strand of a section of DNA isolated from E. coli reads

\[ 5'\text{-GTAGCCTACCCATAGG-3'} \]

a) Suppose that an mRNA is transcribed from this DNA using the complementary strand as a template. What will the sequence of the mRNA in this region be?

\[ 5'\text{-GUAGCCUACCCAUAGG-3'} \]

b) How many different peptides could potentially be made from this sequence of RNA? Would the same peptides be made if the other strand of the DNA served as the template for transcription?

<table>
<thead>
<tr>
<th>Frame 1</th>
<th>val</th>
<th>ala</th>
<th>tyr</th>
<th>pro</th>
<th>*</th>
<th>* = stop codon</th>
</tr>
</thead>
<tbody>
<tr>
<td>Frame 2</td>
<td></td>
<td>P</td>
<td>T</td>
<td>H</td>
<td>R</td>
<td></td>
</tr>
<tr>
<td>Frame 3</td>
<td>S</td>
<td>L</td>
<td>P</td>
<td>I</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Peptides made from the other strand of DNA would be completely different because it is complementary to the

c) What peptide would be made if translation started exactly at the 5' end of the mRNA in part (a)?

valine-alanine-tyrosine-proline

d) When tRNA\text{Ala} leaves the ribosome, what tRNA will be bound next?

Only after a peptide bond has been formed between alanine and tyrosine will tRNA\text{Ala} leave the ribosome. Thus, the next tRNA that will bind to the ribosome after tRNA\text{Ala} has left is tRNA\text{Pro}. tRNA\text{Tyr} will simply move from the A site to the P site.
5. Which of the following mutational changes would you predict to be the most deleterious to gene function? Explain your answer.

a) Insertion of a single nucleotide near the end of the coding sequence.
b) Removal of a single nucleotide near the beginning of the coding sequence.
c) Deletion of three consecutive nucleotides in the middle of the coding sequence.
d) Substitution of one nucleotide for another in the middle of the coding sequence.

**B - removal of a single nucleotide near the beginning of the coding sequence, will cause the most disruption since it will create a frame shift early in the sequence which could change every amino acid**

6. The figure below represents tRNA that recognizes and binds a particular amino acid (in this instance phenylalanine). What would be the triplet of bases on the mRNA strand that would code for this amino acid? What type(s) of bonds stabilize this cloverleaf structure?

**Triplet codon - UUC**

The bonds that stabilize the cloverleaf are hydrogen bonds between the nucleotide bases.

7. Replication and transcription involve copying of a DNA template into a product. Give three examples of how the **product** of transcription differs from the **product** of replication in eukaryotic cells.

<table>
<thead>
<tr>
<th>Replication</th>
<th>Transcription</th>
</tr>
</thead>
<tbody>
<tr>
<td>product is DNA – contains thymine and deoxyribose</td>
<td>product is RNA – uracil and ribose</td>
</tr>
<tr>
<td>product and template remain together</td>
<td>product is released from template</td>
</tr>
<tr>
<td>all DNA is replicated</td>
<td>only genes are transcribed</td>
</tr>
<tr>
<td>product remains in nucleus</td>
<td>product is transported to cytoplasm</td>
</tr>
<tr>
<td>product is not processed</td>
<td>product is processed</td>
</tr>
</tbody>
</table>
8. You are given 4 strains of *Streptococcus pneumoniae*, one is wild type with a smooth capsule, and three mutant strains (A, B and C) with rough colonies because they lack the capsule. The gene (*cap1*) that codes for the enzyme that synthesizes the capsule material has been identified and cloned and you perform PCR on all four strains using primers that are specific for the *cap1* gene. The results of the gel look like the following:

What conclusions can you reach regarding the types of mutations found in mutants A, B and C?

A – **this mutant appears to contain an insertion since its *cap1* gene since the size of its PCR product is larger than the wild type product**

B – **this mutant appears to contain a deletion since its PCR product is much smaller than the wild type product**

C -- **this mutant may have a point mutation since its PCR product is the size as the wild type product**

You then perform a genetic analysis, as you did in lab, by spotting drops of your PCR products on plates of each of the mutants to see if you can ‘fix’ the mutations through homologous recombination. To your surprise all the mutants are able to ‘fix’ each other. What does this tell you about the relative positions of the mutations within the gene?

It indicates that the different mutations are far enough apart that they can effectively recombine to produce cells with a good copy of the *cap1* gene. If any of them overlapped or were too close together for recombination to occur, then they would not be able to ‘fix’ each other.