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CS123A – Bioinformatics  
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Fall 2014

**Hands-On Exercise #2 – Transcription and Translation**

**Problem #1**

1. D – A Phosphate group
2. B) Thymine is found in DNA but not in RNA. D) There is a 2’ hydroxyl in the RNA monomer but not on the DNA monomer.
3. Four functional groups attached to the alpha carbon. It has the amino group, carboxyl group, side chain, and hydrogen.
4. A – The stop codon is UAA. Note it is not the first UAA but a later UAA.

**Problem #2**

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **5’** | C | **T** | **A** | **A** | **T** | **G** | **G** | **G** | **T** | **C** | **G** | **C** | **3’** | DNA Double Helix |
| **3’** | G | **A** | **T** | **T** | **A** | **C** | C | C | A | **G** | **C** | **G** | **5’** |
| **5’** | C | U | A | **A** | **U** | **G** | G | **G** | **U** | **C** | **G** | **C** | **3’** | mRNA Transcribed |
| **3’** | G | A | U | **U** | **A** | **C** | C | C | A | G | C | G | **5’** | Appropriate tRNA Anticodon |
| **Amino** | Leucine (Leu) | | | Methionine (Met) | | | Glycine (Gly) | | | Arginine (Arg) | | | **Carboxyl** |  |

**Problem #3**

1. The **bottom** strand is the template strand since it is in the 5’ to 3’ orientation.
2. 5’ – GA GCC **AUG** CAU UAU CUA GAU AGU AGG CUC UGA GAA UU – 3’
3. The amino acid sequence is:
   1. **Amino**
   2. Methionine (Met)
   3. Histidine (His)
   4. Tyrosine (Tyr)
   5. Leucine (Leu)
   6. Aspartic Acid (Asp)
   7. Serine (Ser)
   8. Arginine (Arg)
   9. Leucine (Leu)
   10. **Carboxyl**
4. AUG CAU UUA UCU AGA UAG (Stop) which maps to:
   1. **Amino**
   2. Methionine (Met)
   3. Histidine (His)
   4. Leucine (Leu)
   5. Serine (Ser)
   6. Arginine (Arg)
   7. **Carboxyl**

**Problem #4**

A hypothetical protein is any protein that exists but whose functional is not yet known.

1. RNA polymerase moves along the DNA molecule from 3’ to 5’, which in turn builds the RNA from 5’ to 3’. If the RNA molecule is proceeding from left to right along the DNA, and then the bottom strand is the template strand. Note: the top stand is the coding/sense strand.
2. The promoter is upstream of the transcription starting site (TSS). What is more, the promoter does not need to immediately precede the TSS location.
3. The first fifteen nucleotides are:

5’ – CUA AUA UUG UGA GAU – 3’

1. 5’ – AUG UUA UAU CCC GCC – 3’

Amino – Methionine (Met) – Leucine (Leu) – Tyrosine (Tyr) – Proline (Pro) – Alanine (Ala) – Carboxyl

1. No. TAA (UAA in mRNA) starts at position 57. The start codon began at position 22. As such, UAA is not in a single reading frame from this start position (i.e. 57 – 22 = 35 which is not divisible by 3). In the simplest terms, bases 57 to 59 are not an incorrect reading frame for this strand of mRNA.
2. In the mRNA sequence, base #10 is U (T in DNA) and base #11 is A. Inserting the G between bases #11 and #12 makes the promoter region of the mRNA one nucleotide longer but has no effect on the protein since this area of the sequence is before the start codon (AUG) and is itself not a start codon.
3. The current codon for this nucleotide is UAU. If the later “U” (“T” in the DNA sequence) is swapped with a “G”, then the resulting codon is UAG which is the stop codon. This causes premature termination of protein creation after only two amino acids.
4. It has no effect on the protein since the codons for AAC and AAU both map to Asparagine (Asn). These types of mutations are known as ***synonymous*** or ***silent mutations*** since they have no effect on the resulting protein.

**Problem #5**

UAA is a stop codon. If the tRNA is changed to recognize UAA now as Glutamic acid (Glu), then the stop codon in the mRNA would not be properly recognized causing proteins that have stop codon UAA to continue growing in length after their expected termination point.