Knowledge-based Learning Outcomes

Upon completion of *Transcription and Translation Explored*, students should be able to:

1. Define gene expression, transcription, and translation, and explain why they are essential for all cells.
2. Describe the cellular locations where transcription and translation occur, and what molecule is produced by each process.
3. Explain how DNA and RNA encode information for building polypeptides in the sequences of nucleotides.
4. Define DNA, RNA, tRNA, mRNA, amino acid, polypeptide, and protein, and describe the role of each in gene expression.
5. Distinguish between:
   - DNA and RNA
   - coding and template DNA strands
   - pre-mRNA and mRNA
   - amino acids, polypeptides, and proteins
6. Define a gene and explain which parts of a gene are transcribed and translated and which are not.
7. Summarize the key changes to RNA during RNA processing and what effect these changes have on RNA and resulting polypeptide.
8. Describe the key molecules and events involved in the initiation, elongation, and termination of transcription.
9. Describe the key molecules and events involved in the initiation, elongation, and termination of translation.
10. Identify key regulatory sequences/locations and their function in transcription and translation (promoter, terminator, start codon, etc.).
11. Explain how three DNA/RNA bases are used to specify each amino acid in the polypeptide, and explain why 2-base codons would be insufficient.
12. Explain the relationship between codons and anticodons, as well as the functional importance of their interaction for translation.
13. Recount the roles and cellular locations of RNA polymerase and ribosomes.
14. List the different types of mutation (point, frameshift, sense, missense, etc.) and explain their effect (or lack of effect) on amino acid sequence.
15. Explain qualitative differences in gene expression between prokaryotic and eukaryotic cells.

Skills-based Learning Outcomes

Upon completion of *Transcription and Translation Explored*, students should be able to:

1. Use a codon table to determine the amino acid sequence specified by the open reading frame of an mRNA molecule.
2. Guide prokaryotic and eukaryotic cells through the processes of transcription, RNA processing, and translation, noting the differences between them.
3. Predict qualitative effects of drugs or perturbations that alter transcription, RNA processing, or translation.
4. Given a DNA sequence with promoter and terminator, indicate which strand is transcribed and determine the RNA sequence produced.
5. Predict possible effects of point and insertion/deletion mutations on amino acid sequence and overall function of protein.
6. Predict what would happen if a eukaryotic gene were transplanted into a prokaryotic cell.
7. Generate a DNA or RNA sequence that produces a given amino acid sequence, and then use this process to identify mutations that could cause observed differences between two amino acid sequences.
8. Predict the qualitative effect of skipping intron splicing or performing alternative splicing on a molecule of pre-mRNA in a eukaryotic cell.