Chapter 17.

1. What organism did Beadle and Tatum use in their research? What made it so amenable to their research aims? Why did some of their mutants grow with some substances while others didn't? What did this tell them about the relationship between genes and enzymes?

☒ Beadle and Tatum used bread molds **(Neurospora crassa)** exposed to X-rays which created mutants that were unable to survive on minimal media. They identified three classes of arginine-deficient mutants each lacking a different enzyme necessary for synthesizing arginine. The mutants will grow on substances that had a supplement they weren't defective in. They came up with the *one gene-one enzyme* hypothesis which states that the function of a gene is to dictate the production of a specific enzyme. It was later restated as the one gene-one polypeptide hypothesis because not all proteins are enzymes.

2. What is the central dogma of molecular biology? What exceptions to it have we studied in class?

☒ The **central dogma** of molecular biology is the flow of genetic information from DNA to RNA to protein. An exception to the central dogma is when RNA molecules act as templates for DNA synthesis (RNA to DNA to RNA; retrovirus).

3. What is a codon? Why do we need triplet codons in our cells? What codon starts translation, and which amino acid does it encode?
What is a stop codon?

☒ A **codon** is an mRNA nucleotide triplet, also the DNA nucleotide triplets along the nontemplate strand. We need triplet codons to be able to code for all 20 amino acids. AUG codes for methionine, which starts translation. A stop codon is a stop signal that marks the end of translation.

4. You should be able to spot an open reading frame within a nucleic acid and be able to translate it into protein given the genetic code.

☒ Know how to translate nucleic acid sequences into protein using a reading frame. Find genetic codes, starting with AUG and end with stop codons (UAA, UAG, UGA).

5. The jellyfish green fluorescent protein can make a transgenic mouse glow in the dark.What does that say about the genetic code?

☒ The fact that the jellyfish green fluorescent protein can make a transgenic mouse glow says that the genetic code must have evolved very early in the history of life because the same DNA instructions can be used by both a jellyfish and a mouse.

6. What are the stages of eukaryotic transcription? What is the enzyme that carries it out? In which direction does this enzyme function? How does the enzyme know which nucleotide to put where? From where does the energy for polymerization come? What differences are there between prokaryotic and eukaryotic transcription?

☒ the stages of eukaryotic transcription is initiation, elongation, and termination. the stages in depth are (1) *initiation;* after RNA poly binds to the promoter, the DNA strands unwind, and the polymerase initiates RNA synthesis at the start point. (2) *elongation;* the polymerase moves downstream, unwinding the DNA and elongating the RNA transcript. in the wake of the transcription, the DNA strands re-form a double helix. (3) *termination;* the RNA transcript is released, and the polymerase detaches from the DNA. **RNA polymerase** is an enzyme that pries the two strands of DNA apart and joins together RNA nucleotides complementary to the DNA template strand. RNA polymerases can only assemble a polynucleotide in its 5'3' direction. it doesn't need a primer to start.

7. What is a promoter? What is the relationship between promoters and transcription factors? Where does RNA synthesis begin? Where does it end?

☒ A **promoter** is the DNA sequence where RNA polymerase attaches and initiates transcription. Only after transcription factors (collection of proteins) are attached to the promoter does RNA polymerase II bind to it. RNA synthesis starts at the **start point** (the nucleotide where RNA synthesis actually begins). it ends at the **terminator** (sequence that signals the end of transcription).

8. What is the RNA called when it is first made? What modifications are done to it to make it into an mRNA? What are the functions of these modifications?

☒ RNA is called pre-mRNA transcript when it's first made. **RNA processing** is when both ends of the primary transcript are altered, certain interior sections of the RNA molecule are cut out and the remaining parts are spliced together. the modifications produce and mRNA molecule ready for translation.

9. What is the relationship between an open reading frame, a 5'UTR and a

3'UTR? How does the cell know where and when to place a poly A tail? How is it made?

CDS = coding dna sequence = only sequence that is translated into protein
ORF = open reading frame= entire gene sequence 5'-utr + transcript (all exons + introns) + 3'-utr

Some genes have exons that contain open reading frame (ORF), which codes for specific portion of complete protein. Some exons have both UTR and coding sequences but other exons have only coding sequences. The **poly A tail** (50-250 adenine nucleotides) is placed at the 3' end of DNA sequences. UTRs (Untranslated regions) are the parts of the mRNA that will not be translated into protein, but have other functions such as ribosome binding. The notation 5' and 3' refer to the direction of the DNA template in the chromosome and is used to distinguish between the two untranslated regions.

10. What is the difference between an intron and an exon? Which is left in the mRNA? Which is cut out?

☒ An **intron** is a noncoding segment of nucleic acid that lies between coding regions and an **exon** is a coding segment of nucleic acid that are spliced together and are usually translated into amino acid sequences. the introns are cut out of the mRNA and the exons are left in.

11. How are mRNA's spliced? What is a spliceosome? What is the difference between an snRNA, a SNRNP and a spliceosome? What does the intron look like after it has been spliced out?

☒ Particles called small nuclear ribonucleoproteins (snRNPs) recognize the splice sites at the end of each intron. **spliceosomes** are large assemblies of several different snRNPs joined with additional proteins. it reacts with certain sites along an intron, releasing the intron, and joins together the two exons that flanked the intron. the intron is rapidly degraded. Small nuclear RNA (snRNA) catalyzes these process and participates in spliceosome assembly and splice site recognition.

12. What is the relationship between exons and protein domains?

☒ **Domains** are proteins consisting of discrete structural and functional regions. One domain of an enzyme might include the active site while another might allow the enzyme to bind to a cellular membrane. Different exons code for the different domains of a protein.

13. What is a tRNA? What are it's most important parts? How does any tRNA know