15 | GENES AND PROTEINS

REVIEW QUESTIONS

1 What is the flow of information for protein synthesis according to the central dogma?

A DNA to mRNA to protein

B DNA to mRNA to tRNA to protein

C DNA to protein to mRNA to protein

D mRNA to DNA to mRNA to protein

Solution The solution is (A). DNA carries genetic information that is copied onto an mRNA template to make a particular protein.

2 The DNA of virus A is inserted into the protein coat of virus B. The combination virus is used to infect *E. coli*. The virus particles produced by the infection are analyzed for DNA and protein.

What results would you expect?

A DNA and protein from B

B DNA and protein from A

C DNA from A and protein from B

D DNA from B and protein from A

Solution The solution is (B). DNA is the genetic material, not protein. So when virus A is infected in the protein coat of virus B, the new virus produced will have DNA and protein of virus A. Protein is not the genetic material and cannot be inherited.

3 The AUC and AUA codons in mRNA both specify isoleucine. What feature of the genetic code explains this?

A Complementarity

B Degeneracy

C Nonsense codons

D Universality

Solution The solution is (B). The genetic code is a triplet code, with each DNA or RNA codon consisting of three nucleotides that encode one amino acid. It is degenerate, as most amino acids can be specified by more than one codon.

**********335***

4 How many nucleotides are in 12 mRNA codons?

A 12

B 24

C 36

D 48

Solution The solution is (C). Twelve mRNA codons would have 36 nucleotides, since each codon consists of three nucleotides.

5 Which molecule does NOT contain genetic information?

A DNA

B mRNA

C Protein

D RNA

Solution The solution is (C). Proteins are made up of amino acids and do not contain genetic information.

6 Which molecule in the central dogma can be compared to a disposable photocopy of a book kept on reserve in the library?

A DNA

B mRNA

C Protein

D tRNA

Solution The solution is (B). Messenger RNA is like a disposable photocopy of a book kept on reserve in the library. It carries a copy of the instructions from the nucleus to other parts of the cell and usually has a short half-life.

7 Which subunit of the *E. coli* polymerase confers specificity to transcription?

A α

B β

C β'

D σ

Solution The solution is (D). The σ subunit is involved in transcription initiation. It confers transcriptional specificity so that the polymerase begins to synthesize mRNA from an appropriate initiation site.

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8 Why are the -10 and -35 regions of prokaryotic promoters called consensus sequences?

A They are identical in all bacterial species.

B They are similar in all bacterial species.

C They exist in all organisms.

D They have the same function in all organisms.

Solution The solution is (B). At the -10 and -35 regions upstream of the initiation site, there are two promoter consensus sequences, or regions, that are similar across all promoters and across various bacterial species.

9 The sequence that signals the end of transcription is called the —

A promoter

B stop codon

C TATA box

D terminator

Solution The solution is (D). Transcription continues until RNA polymerase reaches a stop or terminator sequence at the end of a gene.

10 If the ρ protein is missing, will a prokaryotic gene be terminated?

A It depends on the gene.

B No, the rho protein is essential.

C Transcription termination is not required.

D Yes, the rho protein is not involved in transcription.

Solution The solution is (A). It depends on the sequence of the gene as to whether the transcription termination is rho dependent or independent. If the rho protein is missing, then termination can occur if the sequence consists of short strings of adenines.

11 Which feature of promoters can be found in both prokaryotes and eukaryotes?

A GC box

B Octamer box

C TATA box

D -10 and -35 sequences

Solution The solution is (C). The TATA box is a DNA sequence found in the promoter regions of both prokaryotes and eukaryotes.

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12 At what stage in the transcription of a eukaryotic gene would TFII factors be active?

A Elongation

B Initiation

C Processing

D Termination

Solution The solution is (B). The initiation of transcription in eukaryotes requires TFII. It binds to the promoter region and then recruits RNA polymerase II.

13 Which polymerase is responsible for the synthesis of 5S rRNA?

A Polymerase I

B Polymerase II

C Polymerase III

D Ribonuclease I

Solution The solution is (C). Polymerase III transcribes a variety of structural RNAs that includes the 5S pre-rRNA, transfer pre-RNAs (pre-tRNAs), and small nuclear pre-RNAs.

14 What transcripts will be most affected by low levels of α-amanitin?

A 18S and 28S rRNAs

B 5S rRNAs and tRNAs

C Other small nuclear RNAs

D Pre-mRNAs

Solution The solution is (D). Pre-mRNAs are transcribed by RNA polymerase II and are extremely sensitive to low levels of α-amanitin.

15 Which feature distinguishes eukaryotic transcription from bacterial transcription?

A Eukaryotic transcription does not start at a consensus sequence.

B Eukaryotic transcription does not require an initiation complex.

C Eukaryotic transcription and translation do not take place at the same time.

D Eukaryotic transcription does not require a termination sequence.

Solution The solution is (C). In prokaryotes, both transcription and translation takes place in the cytoplasm, while in eukaryotes, the transcription takes place in the nucleus and translation occurs in the cytoplasm.

16 A poly-A sequence is added at the —

A 5′ end of a transcript in the nucleus

B 3′ end of a transcript in the nucleus

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C 5′ end of a transcript in the cytoplasm

D 3′ end of a transcript in the cytoplasm

Solution The solution is (B). At the 3′ end of the transcript, a poly-A sequence is added. Polymerase A adds a string of approximately 200 A residues.

17 Which pre-mRNA processing step is important for initiating translation?

A Adding a poly-A tail

B RNA editing

C Splicing

D Adding the 7-methylguanosine cap

Solution The solution is (D). Capping occurs at the 5′ end while pre-mRNA synthesis is still going on. A 7-methylguanosine cap is added by a phosphate linkage at the 5′ end of the growing transcript.

18 Where are the RNA components of ribosomes synthesized?

A Cytoplasm

B Endoplasmic reticulum

C Nucleus

D Nucleolus

Solution The solution is (D). The nucleolus in the eukaryotic cell is a condensed region where ribosomes are formed. The ribosomal subunits are synthesized in the nucleolus, and then exported to the cytoplasm before use.

19 What processing step enhances the stability of pre-tRNAs and pre-rRNAs?

A Cleavage

B Methylation

C Nucleotide modification

D Splicing

Solution The solution is (B). Methylation is the addition of CH_3 moiety for the stability of pre-tRNAs and pre-rRNAs.

20 What are introns?

A DNA sequences to which polymerases bind

B Processed mRNA

C Translated DNA sequences in a gene

D Untranslated DNA sequences in a gene

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Solution The solution is (D). Untranslated DNA sequences that are transcribed in pre-mRNAs and consist of noncoding or intervening sequences are called introns. Until introns are removed, translation does not occur.

21 What is often the first amino acid added to a polypeptide chain?

A Adenine

B Leucine

C Methionine

D Thymine

Solution The solution is (C). AUG on an mRNA, where translation begins, always specifies methionine.

22 In any given species, there are at least how many types of aminoacyl tRNA synthetases?

A 20

B 40

C 100

D 200

Solution The solution is (A). Each tRNA molecule is linked to its correct amino acid by a group of enzymes called aminoacyl tRNA synthetases. At least one type of aminoacyl tRNA synthetase exists for each amino acid.

23 In prokaryotic cells, ribosomes are found in/on the —

A cytoplasm

B mitochondrion

C nucleus

D endoplasmic reticulum

Solution The solution is (A). Prokaryotic cells do not contain organelles. The ribosomes lie in the cytoplasm of prokaryotes.

24 Peptide bond synthesis in prokaryotic translation is catalyzed by —

A a ribosomal protein

B a cytoplasmic protein

C mRNA itself

D ribosomal RNA

Solution The solution is (D). Peptidyl transferase is an RNA-based enzyme that is integrated into the 50S ribosomal subunit and catalyzes the formation of peptide bonds.

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25 What would happen if the 5′-methyl guanosine was NOT added to an mRNA?

A The transcript would be degraded when the mRNA moves out of the nucleus to the cytoplasm.

B The mRNA molecule would be stabilized and start the process of translation within the nucleus of the cell.

C The mRNA molecule would move out of the nucleus and create more copies of the mRNA molecule.

D The mRNA molecule would not be able to add the poly-A tail onto its strand at the 5′ end.

Solution The solution is (A). Without 5′ capping, the pre-mRNA transcript would be degraded and initiation of translation would be compromised.

26 Which option is associated with the docking of mRNA on a ribosome in eukaryotic cells?

A Kozak's rules

B Poly-A sequence

C Shine-Dalgarno sequence

D TATA box

Solution The solution is (A). A Kozak consensus sequence is found in eukaryotic mRNA; the following consensus sequence must appear around the AUG:

5′-GCC(purine)CCAUGG-3′

CRITICAL THINKING QUESTIONS

27 If mRNA is complementary to the DNA template strand and the DNA template stand is complementary to the DNA non-template strand, why are the base sequences of mRNA and the DNA non-template strand not identical? Could they ever be?

A No, they cannot be identical because the T nucleotide in DNA is replaced by the U nucleotide in RNA, and AUG is the start codon.

B No, they cannot be identical because the T nucleotide in RNA is replaced by the U nucleotide in DNA.

C They can be identical if methylation of the U nucleotide in RNA occurs, yielding a T nucleotide.

D They can be identical if demethylation of the U nucleotide in RNA occurs, yielding a T nucleotide.

Solution The solution is (A). DNA is different from RNA in that T nucleotides in DNA are replaced by U nucleotides in RNA. The start codon, AUG, includes a U nucleotide. Therefore, they could never be identical in base sequence.

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28 Imagine if there were 200 commonly occurring amino acids instead of 20. Given what you know about the genetic code, what would be the shortest possible codon length?

A 4

B 5

C 2

D 3

Solution The solution is (A). For 200 commonly occurring amino acids, codons consisting of four types of nucleotides would have to be at least four nucleotides long, because 44 = 256. There would be much less degeneracy in this case.

29 What part of the central dogma is NOT always followed in viruses?

A The flow of information in HIV is from RNA to DNA, then back to RNA to protein. Influenza viruses never go through DNA.

B The flow of information is from protein to RNA in HIV, while the influenza virus converts DNA into RNA.

C The flow of information is similar, but nucleic acids are synthesized as a result of translation in HIV and influenza viruses.

D The flow of information is from RNA to protein. This protein is used to synthesize the DNA of the viruses in HIV and influenza.

Solution The solution is (A). The flow of information goes from RNA to DNA back to RNA to protein in HIV. Other viruses such as the influenza virus never go through DNA.

30 Suppose a gene has the sequence ATGCGTTATCGGGAGTAG. A point mutation changes the gene to read ATGCGTTATGGGGAGTAG. How would the polypeptide product of this gene change?

Solution It would change from MRYRE to MRYGE.

31 Explain the initiation of transcription in prokaryotes. Include all proteins involved.

A In prokaryotes, the polymerase comprises five polypeptide subunits, two of which are identical. Four of these subunits, denoted α, α, β, and β', compose the polymerase core enzyme. The fifth subunit, σ, is involved only in the initiation of transcription. The polymerase, which comprises all five subunits, is called the holoenzyme.

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B In prokaryotes, the polymerase comprises four polypeptide subunits, two of which are identical. These subunits, denoted α, α, β, and β', compose the polymerase core enzyme. There is a fifth subunit that is involved in translation initiation. The polymerase, which comprises all four subunits, is called the holoenzyme.

C In prokaryotes, the polymerase comprises five polypeptide subunits, two of which are identical. Four of these subunits, denoted α, α, β, and β', compose the polymerase holoenzyme. The fifth subunit, σ, is involved only in transcription initiation. The polymerase, which comprises all five subunits, is called the core enzyme.

D In prokaryotes, the polymerase comprises five polypeptide subunits, two of which are identical. Four of these subunits, denoted α, α, β, and β', compose the polymerase core enzyme. The fifth subunit, σ, is involved only in termination. The polymerase, which comprises all five subunits, is called the holoenzyme.

Solution The solution is (A). Refer to Figure 15.7 and add the additional subunits of the holoenzymes that are not in the figure.

32 How would you describe the difference between rho-dependent and -independent termination of transcription in prokaryotes?

A Rho-dependent termination is controlled by the rho protein, and the polymerase stalls near the end of the gene at a run of G nucleotides on the DNA template. In rho-independent termination, when the polymerase encounters a region rich in C-G nucleotides, the mRNA folds into a hairpin loop that causes the polymerase to stall.

B Rho-independent termination is controlled by the rho protein, and the polymerase stalls near the end of the gene at a run of G nucleotides on the DNA template. In rho-dependent termination, when the polymerase encounters a region rich in C–G nucleotides, the mRNA folds into a hairpin loop that causes the polymerase to stall.

C Rho-dependent termination is controlled by the rho protein, and the polymerase begins near the end of the gene at a run of G nucleotides on the DNA template. In rho-independent termination, when the polymerase encounters a region rich in C–G nucleotides, the mRNA creates a hairpin loop that causes the polymerase to stall.

D Rho-dependent termination is controlled by the rho protein, and the polymerase stalls near the end of the gene at a run of G nucleotides on the DNA template. In rho-independent termination, when the polymerase encounters a region rich in A–T nucleotides, the mRNA creates a hairpin loop that causes the polymerase to stall.

Solution The solution is (A). Rho-dependent termination is controlled by the rho protein, which tracks along behind the polymerase on the growing mRNA chain. Near the end of the gene, the polymerase stalls at a run of G nucleotides on the DNA template. The rho protein collides with the polymerase and releases mRNA from the transcription bubble. Rho-independent termination is controlled by specific sequences in the DNA template strand. As the polymerase nears the end of the gene being transcribed, it encounters a region rich in C–G nucleotides. This creates an

**********335***

mRNA hairpin that causes the polymerase to stall right as it begins to transcribe a region rich in A–T nucleotides. Because A–U bonds are less thermostable, the core enzyme breaks away.

33 What is the main structure that differentiates rho-dependent and -independent termination in prokaryotes?

A Rho-independent termination involves the formation of a hairpin.

B Rho-dependent termination involves the formation of a hairpin.

C Rho-dependent termination stalls when the polymerase begins to transcribe a region rich in A–T nucleotides.

D Rho-independent termination stalls when the polymerase begins to transcribe a region rich in G nucleotides.

Solution The solution is (A). Refer to Figures 15.7 and 15.8. Add the termination step, which may involve either the rho protein or a hairpin.

34 Which step in the transcription of eukaryotic RNA differs the most from its prokaryotic counterpart?

A The initiation step in eukaryotes requires an initiation complex with enhancers and transcription factors. Also, the separation of the DNA strand is different, as histones are involved.

B The initiation step in prokaryotes requires an initiation complex with enhancers and transcription factors. Also, the separation of the DNA strand is different, as histones are involved.

C The elongation step in eukaryotes requires an initiation complex with enhancers and transcription factors. Also, the separation of the DNA strand is different, as histones are involved.

D The initiation step in eukaryotes requires an initiation complex with enhancers and transcription factors. Also, the separation of the DNA strand is different, as histones are not involved.

Solution The solution is (A). The initiation step in eukaryotes requires an initiation complex with enhancers and transcription factors. The separation of the DNA strand is also different as histones are involved.

35 Would you be able to determine which RNA polymerase you isolated from a eukaryotic cell without analyzing its products?

A No, they have the same α-amanitin sensitivity in all products.

B No, quantitative analysis of products is done to determine the type of polymerase.

C Yes, they can be determined as they differ in α-amanitin sensitivity.

D Yes, they can be determined by the number of molecules that bind to the DNA.

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Solution The solution is (C). Yes, RNA polymerases differ in their sensitivity to α-amanitin.

36 Predict how alternative splicing may lead to an economy of genes. Do you need a different gene for every protein that the cell can produce?

A Alternative splicing can lead to the synthesis of several polypeptides from a single gene.

B Alternative splicing can lead to the synthesis of several forms of mRNA from a single gene.

C Alternative splicing can lead to the synthesis of several forms of codons from a set of genes.

D Alternative splicing can lead to the synthesis of several forms of ribosomes from a set of genes.

Solution The solution is (A). It is possible to synthesize several polypeptides from a single gene by alternative splicing.

37 What is the major challenge in the production of RNA in eukaryotes compared to prokaryotes?

A Exporting the mRNA across the nuclear membrane

B Importing the mRNA across the nuclear membrane

C Keeping the mRNA inside the nuclear membrane

D Translating the mRNA into proteins within seconds

Solution The solution is (A). The major challenge is exporting the mRNA across the nuclear membrane.

38 What would happen if the 5′ methyl guanosine was not added to an mRNA?

A The transcript would degrade when the mRNA moves out of the nucleus to the cytoplasm.

B The mRNA molecule would stabilize and start the process of translation within the nucleus of the cell.

C The mRNA molecule would move out of the nucleus and create more copies of the mRNA molecule.

D The mRNA molecule would not be able to add the poly-A tail on its strand at the 5′ end

Solution The solution is (A). Without the 5′ capping, the pre-mRNA transcript would degrade and initiation of translation would be compromised.

39 How should the following DNA sequence (non-template strand) be transcribed and translated?

5′-ATGGCCGGTTATTAAGCA-3′

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A The mRNA would be 5’-AUGGCCGGUUAUUAAGCA-3’ and the protein will be MAGY.

B The mRNA would be 3’-AUGGCCGGUUAUUAAGCA-5’ and the protein will be MAGY.

C The mRNA would be 5’-ATGGCCGGTTATTAAGCA-3’ and the protein will be MAGY.

D The mRNA would be 5’-AUGGCCGGUUAUUAAGCA-3’ and the protein will be MACY.

Solution The solution is (A). The mRNA would be 5’-AUGGCCGGUUAUUAAGCA-3’. The protein would be MAGY. Even though there are six codons, the fifth codon corresponds to a stop, so the sixth codon would not be translated

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40 The RNA world hypothesis proposes that the first complex molecule was RNA, and it preceded protein formation. Which major function of ribosomal RNA supports this hypothesis?

A rRNA has catalytic properties in the large subunit, and it assembles proteins.

B rRNA is a protein molecule that helps in the synthesis of other proteins.

C rRNA is essential for the transcription process.

D rRNA plays a major role in posttranslational processes.

Solution The solution is (A). The rRNA in the large subunit has catalytic properties. It synthesizes the peptide bond. The main idea is that the molecule that assembles proteins cannot itself be a protein. In other words, a protein could not have synthesized the first protein. RNA subunits can self-assemble.

41 A tRNA is chemically modified so that the bound amino acid is different than the one specified by its anticodon. Which codon in the mRNA would the tRNA recognize: the one specified by its anticodon or the one that matches the modified amino acid it carries?

A The anticodon will match the codon in mRNA.

B The anticodon will match with the modified amino acid it carries.

C The anticodon will lose the specificity for the tRNA molecule.

D The enzyme aminoacyl tRNA synthetase would lose control over the amino acid.

Solution The solution is (A). The anticodon matches the codon in mRNA.

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42 What characteristic of the genetic code points to a common ancestry for all organisms?

A The code is degenerate.

B The code contains 64 codons.

C The genetic code is almost universal.

D The code contains stop codons.

Solution The solution is (C). The code is universal.

43 What process transfers heritable material to the next generation?

A Replication

B Splicing

C Transcription

D Translation

Solution The solution is (A). Replication is the process by which two identical DNA molecules are produced from one DNA molecule.

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44 When comparing transcription of heritable information in prokaryotes and eukaryotes, which events are the same?

A The transcription by polymerase, the recognition of a consensus sequence in the promoter, and the termination by a hairpin loop are conserved.

B The translation by polymerase, the recognition of a consensus sequence in the promoter, and the termination by a hairpin loop are conserved.

C The transcription by polymerase, the recognition of a highly variable sequence in the promoter, and the termination by a hairpin loop are conserved.

D The transcription by polymerase, the recognition of a consensus sequence in the promoter, and the elongation by a hairpin loop are conserved.

Solution The solution is (A). Transcription by a polymerase, recognition of a consensus sequence in the promoter, and termination by a hairpin loop are conserved.

45 Which cell structure does NOT contain heritable information?

A Chloroplast

B Cytoplasmic membrane

C Mitochondria

D Nucleus

Solution The solution is (B). The cytoplasmic membrane separates the interior of the cell from the outside environment.

46 How does the enzyme reverse transcriptase violate the central dogma of molecular biology in HIV?

A The enzyme reverse transcriptase reverse-transcribes the RNA in the genome of HIV into DNA.

B The enzyme reverse transcriptase translates the RNA of the HIV into protein and then back into DNA.

C The enzyme reverse transcriptase transcribes the DNA straight into the protein molecules.

D The enzyme reverse transcriptase transcribes DNA into RNA, then again into DNA. There is no protein synthesis.

Solution The solution is (A). The genome of HIV is made of two molecules of RNA, which are reverse transcribed to DNA in the host. The enzyme reverse transcriptase is virally encoded and packaged in the virus particle.

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47 Radioactive deoxythymidine triphosphate is supplied to the protist *Euglena*. After an interval of time, the cells are homogenized, and different fractions are analyzed for radioactivity content in large nucleic acid molecules. Which fraction will not be labeled?

A Nucleus

B Mitochondrion

C Chloroplast

D Plasma membrane

Solution The solution is (D). The plasma membrane does not contain DNA.

48 You sequence a gene of interest and isolate the matching mRNA. You find that the mRNA is considerably shorter than the DNA sequence. Why is that?

A There was an experimental mistake. The mRNA should be the same length as the gene.

B The mRNA should be longer than the DNA sequence because the promoter is also transcribed.

C The processed mRNA is shorter because introns were removed.

D The mRNA is shorter because the signal sequence to cross the nuclear membrane was removed.

Solution The solution is (C). Introns are noncoding regions of an RNA transcript, which are spliced out before the RNA is translated into protein. Splicing decreases the length of mRNA in comparison to DNA molecule.

49 A mutation in the promoter region of the gene for beta-globin can cause beta-thalassemia, a hereditary condition that causes anemia. Why would mutations in the promoter region lead to low levels of hemoglobin?

A The globin chains produced are too long to form functional hemoglobin.

B The globin chains are too short to form functional hemoglobin.

C Fewer globin chains are synthesized because less mRNA is transcribed.

D Globin chains do not fold properly and are nonfunctional.

Solution The solution is (D). Protein folding is determined by the amino acid sequence. Mutations in the promoter region do not affect the amino acid sequence of the protein.

50 You are given three mRNA sequences:

1. 5′-UCG-GCA-AAU-UUA-GUU-3
2. 5′-UCU-GCA-AAU-UUA-GUU-3′
3. 5′-UCU-GCA-AAU-UAA-GUU-3′

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Using the table, write the peptide encoded by each of the mRNA sequences.

Codon on mRNA	Amino Acid
GCA	alanine
AAG	lysine
GUU	valine
AAU	asparagine
UGC	cysteine
UCG	serine
UCU	serine
UUA	leucine
UAA	stop

A (i) Serine-alanine-asparagine-leucine-valine; (ii) serine-alanine-asparagine-leucine-valine; (iii) serine-alanine-asparagine(-stop)

B (i) Serine-phenylalanine-asparagine-leucine-valine; (ii) serine-alanine-asparagine-leucine-valine; (iii) serine-alanine-asparagine(-stop)

C (i) Serine-alanine-asparagine-leucine-valine; (ii) serine-alanine-asparagine(-stop); (iii) serine-alanine-asparagine-leucine-valine

D (i) Serine-alanine-asparagine-leucine-valine; (ii) serine-arginine-asparagine-leucine-valine; (iii) serine-alanine-asparagine(-stop)

Solution The solution is (A). The three mRNA sequences are (i) serine-alanine-asparagine-leucine-valine; (ii) serine-alanine-asparagine-leucine-valine; (iii) serine-alanine-asparagine(-stop).

51 Refer to the table.

Codon on mRNA	Amino Acid
GCA	alanine
AAG	lysine
GUU	valine
AAU	asparagine
UGC	cysteine
UCG	serine
UCU	serine
UUA	leucine
UAA	stop

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You are given three mRNA sequences:

1. 5′-UCG-GCA-AAU-UUA-GUU-3
2. 5′-UCU-GCA-AAU-UUA-GUU-3′
3. 5′-UCU-GCA-AAU-UAA-GUU-3′

Using the peptide encoded by each sequence, compare the three peptides obtained. How are peptides 2 and 3 different from 1? What would the consequence be for the cell in each case?

A There is a silent mutation in peptide 2, and peptide 3 has a stop codon due to a mutation.

B There is a silent mutation in peptide 3, and peptide 2 has a stop codon due to a mutation.

C There is a different amino acid in peptide 2, and peptide 3 has a stop codon due to a mutation.

D There isn't a mutation in peptide 2, and peptide 3 has a stop codon due to a mutation.

Solution The solution is (A). In the case of peptide 2, there is a silent mutation. Although the base has been substituted, the amino acid is the same because the code is degenerate. In peptide 3, the mutation introduced a stop codon. Translation stops at the asparagine.

SCIENCE PRACTICE CHALLENGE QUESTIONS

15.1 The Genetic Code

52 Gamow (1954) proposed that the structure of DNA deduced by Watson and Crick (1953) could be interpreted as a way of forming roughly 20 "words"" of the common amino acids from the four "letters" A, T, C, and G that represent DNA nucleotides.

Crick and coworkers (1961) used a method developed by Benzer to induce mutations in the DNA of a virus by the insertion of a single nucleotide. The mutant could not infect the bacterium *Escherichia coli* and neither could viruses with a second insertion of a second DNA nucleotide. However, a third nucleotide insertion restored the ability of the virus to infect the bacterium.

In 1961, Nirenberg and Matthaei conducted a series of experiments to better understand the flow of genetic information from gene to protein. They discovered that in solutions containing the contents of ruptured *E. coli* bacterial cells from which DNA had been removed, polymers containing only one repeating amino acid, phenylalanine, would be synthesized if synthetic mRNA composed of only the single nucleotide, uracil (U), was added to the solution in which phenylalanine was also present. In solutions containing mRNA with only adenine (A) or cytosine (C) and the amino acids lysine or proline, polymers containing only these amino acids would be synthesized. The researchers found

**********335***

that when ribosomes were removed by filtration, these polymers did not form. Nirenberg and Leder (1964) extended this work to include other nucleotides.

A. Summarize the conclusions regarding the encoding and decoding of heritable information supported by these studies. Explain how these studies provided evidence to support the triplet code.

Khorana (1960) developed a technique for synthesizing RNA composed of predictable distributions of repeated pairs or triplets of nucleotides. He found, for example, that RNA synthesized when A and U were present in relative concentrations of 4:1, respectively, will produce RNA sequences with these distributions determined by their relative probabilities: AAU:AAA, AUA:AAA, and UAA:AAA; $0.82 \times 0.2 / 0.83 = 1 / 4$ [calculated as follows: (i) 4/5 of the bases are A, so the likelihood of selecting A is 0.8; (ii) the selection is repeated to determine the second letter of the three-letter codon; (iii) the likelihood of selecting a U is 1 in 5; (iv) the probability of selecting the set AUU is the product; (v) similarly, the probability of AAA is (4/5)3; and (vi) the ratio of these probabilities is their relative likelihood]: AUU:AAA, UUA:AAA, and UAU:AAA; $0.8 \times 0.22 / 0.83 = 1 / 16$; and UUU:AAA; $0.23 / 0.83 = 1 / 64$.

B. Based on Khorana's findings, **calculate** the relative distributions of the following ratios of concentrations of RNA triplet sequences from mixtures in which the relative concentrations of guanine and cytosine, G:C, are 5:1.

Ratio	**Relative Probabilities**
GGC:GGG GCG:GGG CGG:GGG	
GCC:GGG CGC:GGG CCG:GGG	
CCC:GGG	

C. Based on the work of Nirenberg, Matthaei, Leder, and Khorana, the following table was constructed (taken from Khorana's Nobel Prize address):

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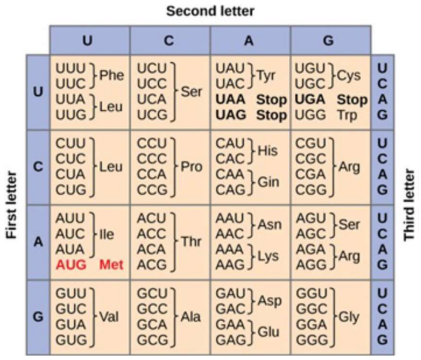
**********336**********



A solution containing the amino acids shown in the table and equal concentrations of the two nucleotides C and G is prepared. **Predict** the proteins that can be synthesized from this mixture in terms of each possible codon and their relative concentrations in terms of their amino acid repeat sequences.

D. Describe the effects of the codons UAA, UAG, and UGA on protein synthesis.

Solution Sample answer:

A. Gamow (a physicist) proposed that a sequence of three nucleotide letters could be used to make a single amino acid word. Crick and colleagues found that the length of the word was always three letters. Nirenberg, Matthaei, and Leder showed that DNA could be synthesized in the absence of a living cell and confirmed Gamow's idea.

B.

Ratio	**Relative Probabilities**
GGC:GGG GCG:GGG CGG:GGG	$\left[(5/6)^2 \times 1/6\right]/(5/6)^3 = 1/5 = 0.20$
GCC:GGG CGC:GGG CCG:GGG	$\left[(1/6)^2 \times 5/6\right]/(5/6)^3 = 1/25 = 0.04$
CCC:GGG	$(1/6)^3/(5/6)^3 = 1/125 = 0.08$

C. pro (CCC), ser (CCG), gly (CGG), arg (CGC), gly (GGG), gly (GGC), ala (GCC), and gly (GCG)

So, concentrations of alanine, proline, arginine, and serine are equal and each in concentrations that are one-quarter of the concentration of glycine. The specific names of the amino acids are not in scope.

D. These are the stop codons and do not encode amino acids.

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**********335***

15.2 Prokaryotic Transcription

53 The yeast life cycle is usually dominated by haploid cells, each with a single set of unpaired chromosomes. The cell propagates asexually, and the genetic material is replicated through mitosis. Cell division occurs every 2–4 h, leading to 60–100 generations in a single day. Yeast also reproduces sexually, particularly under adverse environmental conditions. When two haploid cells—with DNA containing complementary mating-type alleles—conjugate, a diploid zygote results. The diploid zygote can then complete the sexual segment of the life cycle through meiosis. After meiosis, four haploid spores are produced, which can germinate.

Researchers can grow yeast easily on nutrient-containing plates. Because both asexual and sexual reproduction is rapid, yeast has become an important organism for the experimental investigation of mutagenesis and evolution among eukaryotes. Environmental factors, such as chemicals or radiation, induce mutations. High-energy UV-c radiation of less than 1 min in duration will result in many mutated yeast cells. UV-c can be used to mutate a strain of yeast in which the synthesis of adenine is blocked. This mutation is observable because the *ade-2* mutant has a red color when cultured on nutrient-containing plates. Exposure to UV-c also can result in additional mutations. In particular, one mutant, *ade*-7, changes the color of the *ade-2* mutant to white.

A. You have a UV-c lamp, culture plates, and growth chambers at 23 °C and 37 °C. You also have available known haploid strains that are (*ade-2,+,+*), where *+* denotes the wild type. **Design** a plan to determine the rate of UV-c-induced mutations in nutrient-containing plates inoculated with yeast.

Earth's ozone layer removes high-energy ultraviolet radiation, UV-c, from the solar radiation received at the surface. Lower-energy ultraviolet radiation, UV-b, strikes Earth's surface. Damage to DNA induced by ultraviolet radiation occurs with the formation of bonds between an adjacent pair of pyrimidine nucleotides, thymine and cytosine, on the same strand of DNA. A repair enzyme, photolyase, which is activated by visible light, is present in plants and most animals, but not in humans. In characterizing the relationship between environmental mutagens and cell damage, a useful assumption is often made and referred to as the linear hypothesis. This assumption states that the extent of damage is proportional to the amount of radiation received.

Mutation rates for a strain (*preac*) that does not produce photolyase and a wild-type (*+*) strain were studied. Cultures of the two strains of yeast were diluted, and nutrient-containing plates were inoculated in triplicate at 23 °C. The plates were exposed to bright sunlight for varying time intervals. After exposure, the plates were incubated in the dark at 23 °C. After incubation between 1 and 8 h, data shown in the table were collected by counting the density of living cells relative to the control, and averaging these among replicates.

B. Using the data table, **graph** the average survival fraction, relative to the wild-type control. Predict the number of mutations in a sample of 1,000 cells of the *preac* type that are exposed to bright sunlight for 15 s.

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**********336**********

Incubation Time (h)	10-s Exposure	20-s Exposure	30-s Exposure	40-s Exposure	50-s Exposure
1	0.83	0.58	0.33	0.17	0.08
2	1.00	0.43	0.17	0.09	0.04
3	0.92	0.38	0.12	0.03	0.01
4	0.75	0.35	0.08	0.01	0.00
5	0.99	0.49	0.11	0.01	0.00
6	0.81	0.42	0.12	0.01	0.00
7	0.80	0.32	0.09	0.01	0.00
8	1.05	0.59	0.11	0.01	0.00
Mean	0.89	0.45	0.14	0.04	0.02
Standard Deviation	0.11	0.10	0.08	0.06	0.03

Yeast can also be used to study sexual reproduction, a somewhat puzzling phenomenon. Cloning of cells through mitosis is molecularly much less complex than meiosis, consumes less energy, and is less risky. Two alternative explanations for the evolution of sexual reproduction are popular. In one model, through assortment of genes, meiosis leads to an increase in the frequency of beneficial mutations. In the second model, detrimental mutations are purged from a population through sex. Studies using yeast (Gray and Goddard, *Evol. Biol*., 2012 and McDonald et al., *Nature*, 2012) have provided a mechanism to study these models. The graph shows the fitness (defined as the log of the ratio of the number of cells in successive generations) of yeast as a function of number of mitotic reproductions in yeast grown in low- and high-stress environments, and with and without alternating induction of sexual reproduction.

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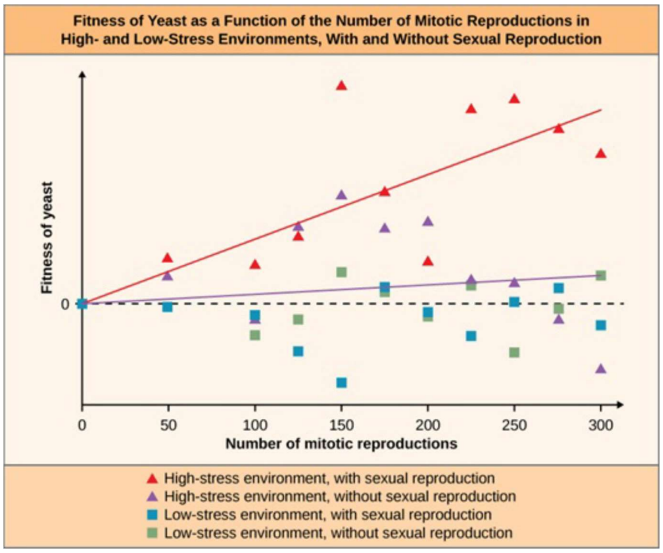
**********335***



C. Based on these data, **evaluate** the merits of the alternative theories of the adaptive advantage provided by sexual reproduction.

Solution Sample answer:

A. The main point should be that population measurements at multiple times after inoculation should be made with replicas at each time. Also, low to high dilutions will allow less uncertainty in the counts. Measurements of population density could count colonies or use a hemocytometer. It is essential that measurements of number are made. Triplets for each dilution are exposed to UV-c light for intervals such as 0, 10, 20, 30, 40, and 50 s. After exposure, each is incubated at 23° in the dark. Students should choose low temperature so yeasts will avoid sexual reproduction.

At intervals of time (guided by the statement that cloning occurs every few hours) such as 1, 2, 3, 4, 5 h, and so on, the plates are removed from the incubator and counts are made. In this first experiment, we are counting the number of cells that are red. Mutations in the *ade-2* will leave the cell white. Because we have a control and will be forming a fraction relative to the control Nred, exposed and mutated/Nred, no exposure we count either red or non-red.

Students who have done this or a similar lab may know that a mutation in ade-4 will counteract the effect of *ade-7*. They might then go on to propose a test to confirm that the mutation was at *ade-2*. In this case, after the plates have been used to obtain population density, a test cross should be made with (*ade-2*, *+*, *ade-7*) and perhaps also with (*+*, *ade-4*, *+*). This can be done by streaking a colony of non-red cells on a line down the middle of the plate. Then a test strain should be streaked

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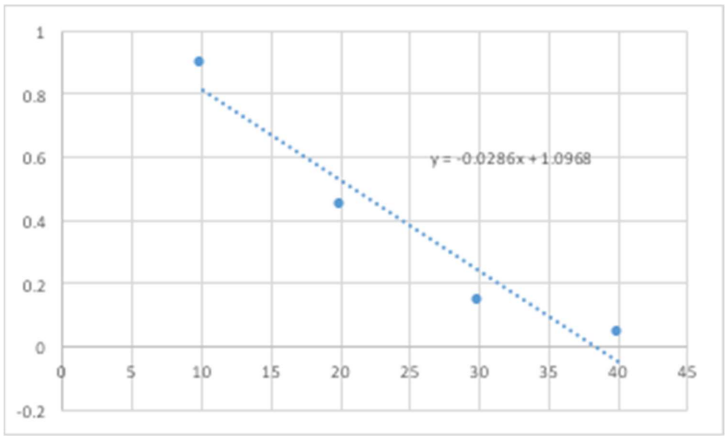
**********336**********

onto the plate in a series of lines perpendicular to the first streak. Where the streaks nearly intersect, there will be a region of sexually reproduced cells after they are shifted to incubation at the higher temperature. Observation of incubated cells is made over the next two days. If the products of sexual reproduction of the (*ade-2*, *+, ade-7*) test are red, we know that the *ade-2* allele was mutated. If the products of sexual reproduction of the (*+*, *ade-4*, *+*) test are red, we know that the ade-7 allele was mutated.

To determine the mutation rate, the ratio to the control is formed. This ratio should be approximately constant among samples taken at different times during incubation after exposure. Taking an average of this ratio (and standard deviation) and plotting that average against the period of exposure yields an approximately straight line (or so we assume) whose slope is the mutation rate in units of sec^{-1}.

B. This task is going to be daunting for students with weak backgrounds in math, or who are unfamiliar with graphing programs. Excel produced the graph shown below. Students should also have labels on the axes.



C. These results show that under low-stress conditions, there is no additional gain in fitness due to sexual reproduction. However, under stress, there is a dramatic gain in fitness.

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**********335***

15.3 Eukaryotic Transcription

54 **A. Describe** the storage and retrieval of genetic information with the following model. Use the list to fill in the blanks with the letter corresponding to the correct term.

A. amino acid
B. tRNA
C. DNA
D. transcription
E. mRNA
F. translation
G. protein
H. RNA polymerase
I. rRNA

Within the cytoplasm, __ is synthesized from __ bound to __ in a sequence that corresponds to information provided by __. This process is called __.

Within the nucleus, information originating in __ is encoded as a sequence of bases in __, which is synthesized by the enzyme __. This process is called __.

B. During development, cell differentiation occurs, and the expression of genes is permanently switched off. Using the model in (A), **explain** where information flow is most effectively blocked.

C. A chemical message is received by the cell regulating the timing of events controlled by gene expression. Using the model in (A), **explain** where information flow is most effectively managed.

Solution Sample answer:

A. Within the cytoplasm G is synthesized from A bound to B in a sequence that corresponds to the information provided by E. This process is called F.

Within the nucleus, information originating in C is encoded as a sequence of bases in I that is synthesized by the enzyme H. This process is called D.

B. Permanently blocking gene expression is accomplished by the irreversible modification of DNA, stopping transcription. This is often accomplished by methylation, a concept that is out-of-scope for the AP Biology Exam.

C. Posttranscriptional regulation is most efficient since the feedback loop has signals that vary in time, and the already transcribed information is available quickly.

55 Structure and function in biology result from both the presence of genetic information and the expression of that information. Some genes are continually expressed, whereas the expression of most genes is regulated, commonly at the level of transcription. At the initiation of transcription, the TATA-binding protein (TBP) provides access to the DNA strand to be transcribed. The 5'TATAAA3' sequence called the TATA box is found in prokaryotes, archaebacteria, and eukaryotes. Even among eukarya, when the TATA box is not present among eukaryotes, the initiation of transcription involves TBP. Scientists attribute this common characteristic to the relative thermostability of the A-T interaction. Hydrogen bonds hold the two strands of the DNA double helix together. This type of bond

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has the smallest interaction energy of all intermolecular forces; as temperature increases, these bonds are broken.

A. Explain the advantage, in terms of the energy required, which is provided by an AT-rich region in the sequence where transcription is initiated.

B. The fact that the TATA box or the associated TBP are common to all domains provides evidence of common ancestry among all life. **Pose a scientific question** that would need to be addressed by a valid alternative explanation of this fact.

C. A whole-genome survey of prokaryotes (Zheng and Wu, *BMC Bioinformatics*, 2010) showed that the relative amounts of guanine and cytosine in DNA poorly predicted the temperature range conditions that are suitable for an organism. **Refine the question** posed in (B), taking this result into account.

Solution Sample answer:

A. Because A and T interact with only two hydrogen bonds (rather than three in the C-G interaction), the energy required to open the helix is smaller in the AT-rich region.

B. Is the difference between the A-T and G-C interactions large enough that the TATA box would be the outcome for any DNA structure?

C. How can we know if an initiation region with CG-rich regions could not transcribe DNA? This result shows that the difference between CG-rich and AT-rich regions is small enough not to provide a robust prediction of temperature range. So the difference should not be expected to be sufficient to allow multiple evolutionary lines to all adopt the TATA box solution. There must be a common ancestor.

15.5 Ribosomes and Protein Synthesis

56 Only a fraction of DNA encodes proteins. The noncoding portion of a gene is referred to as the intron. The intron fraction depends upon the gene. Introns are rare in prokaryotic and mitochondrial DNA; in human nuclear DNA, this fraction is about 95 percent. The intron is transcribed into mRNA, but this noncoding mRNA is edited out before translation of the coding portion, or exon, of a gene. The edited exon segments are then spliced together by a spliceosome, a very large and complex collection of RNAs and proteins.

Although introns do not encode proteins, they have functions. In particular, they amplify the expression of the exon, although the mechanism is unknown. When introns are very long, which is common among mammalian genes with roles in development, they can significantly extend the time required to complete transcription. Analysis of genes common to different plant and animal species shows many shared intronic positions and base sequences, although in some organisms, such as yeast, many introns have been deleted. Because introns do not encode proteins, mutations can remain silent and accumulate.

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A. Introns are ancestral remnants that are replicated because they do not disadvantage the organism. Consider the claim that introns are "junk DNA." **Evaluate the claim** with supporting evidence.

B. Introns may be retained during transcription. **Explain** how the retention of a transcribed intron between two transcribed exons within a gene could do the following:

- Block expression of one polypeptide sequence.
- Increase expression of a polypeptide.
- Alter the polypeptide expressed.

Solution Sample answer:

A. The fact that such a significant burden is imposed and the risk (such as splicing errors) is so great imply that there has to be an advantage in maintaining the noncoding sequences. Reasonable arguments can be made that the introns are just artifacts and have been for the four decades since the discovery of the intron. The assessment here is of the student's ability to provide supporting evidence. This evidence is summarized in the stem.

B. Consider a linear sequence with exons on either side of a retained intron. If the intron contains a stop code the second exon will not translate to protein. If both exons encode the same protein, expression will be increased. If the intron has a length that is not a multiple of three, it can cause the mRNA to be translated with nonfunctional proteins at either or both of the exons.

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