

# **BIOLOGY TOPICAL:**

## **Molecular Biology Test 1**

Time: 25 Minutes\*  
Number of Questions: 19

\* The timing restrictions for the science topical tests are optional. If you are using this test for the sole purpose of content reinforcement, you may want to disregard the time limit.

**DIRECTIONS:** Most of the questions in the following test are organized into groups, with a descriptive passage preceding each group of questions. Study the passage, then select the single best answer to each question in the group. Some of the questions are not based on a descriptive passage; you must also select the best answer to these questions. If you are unsure of the best answer, eliminate the choices that you know are incorrect, then select an answer from the choices that remain. Indicate your selection by blackening the corresponding circle on your answer sheet. A periodic table is provided below for your use with the questions.

**PERIODIC TABLE OF THE ELEMENTS**

1 <b>H</b> 1.0																2 <b>He</b> 4.0	
3 <b>Li</b> 6.9	4 <b>Be</b> 9.0											5 <b>B</b> 10.8	6 <b>C</b> 12.0	7 <b>N</b> 14.0	8 <b>O</b> 16.0	9 <b>F</b> 19.0	10 <b>Ne</b> 20.2
11 <b>Na</b> 23.0	12 <b>Mg</b> 24.3											13 <b>Al</b> 27.0	14 <b>Si</b> 28.1	15 <b>P</b> 31.0	16 <b>S</b> 32.1	17 <b>Cl</b> 35.5	18 <b>Ar</b> 39.9
19 <b>K</b> 39.1	20 <b>Ca</b> 40.1	21 <b>Sc</b> 45.0	22 <b>Ti</b> 47.9	23 <b>V</b> 50.9	24 <b>Cr</b> 52.0	25 <b>Mn</b> 54.9	26 <b>Fe</b> 55.8	27 <b>Co</b> 58.9	28 <b>Ni</b> 58.7	29 <b>Cu</b> 63.5	30 <b>Zn</b> 65.4	31 <b>Ga</b> 69.7	32 <b>Ge</b> 72.6	33 <b>As</b> 74.9	34 <b>Se</b> 79.0	35 <b>Br</b> 79.9	36 <b>Kr</b> 83.8
37 <b>Rb</b> 85.5	38 <b>Sr</b> 87.6	39 <b>Y</b> 88.9	40 <b>Zr</b> 91.2	41 <b>Nb</b> 92.9	42 <b>Mo</b> 95.9	43 <b>Tc</b> (98)	44 <b>Ru</b> 101.1	45 <b>Rh</b> 102.9	46 <b>Pd</b> 106.4	47 <b>Ag</b> 107.9	48 <b>Cd</b> 112.4	49 <b>In</b> 114.8	50 <b>Sn</b> 118.7	51 <b>Sb</b> 121.8	52 <b>Te</b> 127.6	53 <b>I</b> 126.9	54 <b>Xe</b> 131.3
55 <b>Cs</b> 132.9	56 <b>Ba</b> 137.3	57 <b>La</b> * 138.9	72 <b>Hf</b> 178.5	73 <b>Ta</b> 180.9	74 <b>W</b> 183.9	75 <b>Re</b> 186.2	76 <b>Os</b> 190.2	77 <b>Ir</b> 192.2	78 <b>Pt</b> 195.1	79 <b>Au</b> 197.0	80 <b>Hg</b> 200.6	81 <b>Tl</b> 204.4	82 <b>Pb</b> 207.2	83 <b>Bi</b> 209.0	84 <b>Po</b> (209)	85 <b>At</b> (210)	86 <b>Rn</b> (222)
87 <b>Fr</b> (223)	88 <b>Ra</b> 226.0	89 <b>Ac</b> † 227.0	104 <b>Unq</b> (261)	105 <b>Unp</b> (262)	106 <b>Unh</b> (263)	107 <b>Uns</b> (262)	108 <b>Uno</b> (265)	109 <b>Une</b> (267)									

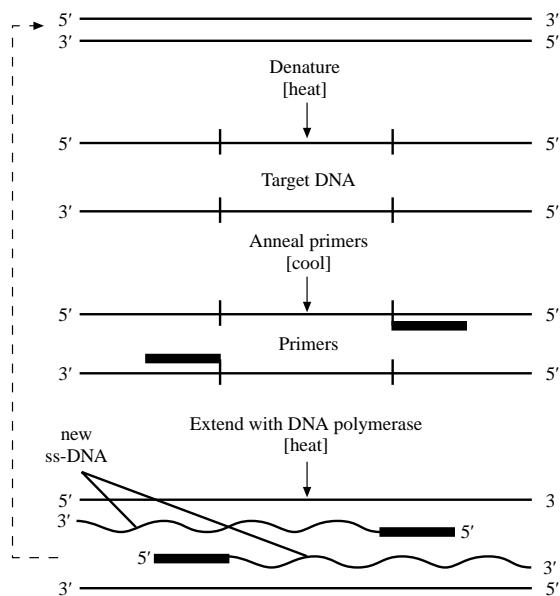
* 58 <b>Ce</b> 140.1	59 <b>Pr</b> 140.9	60 <b>Nd</b> 144.2	61 <b>Pm</b> (145)	62 <b>Sm</b> 150.4	63 <b>Eu</b> 152.0	64 <b>Gd</b> 157.3	65 <b>Tb</b> 158.9	66 <b>Dy</b> 162.5	67 <b>Ho</b> 164.9	68 <b>Er</b> 167.3	69 <b>Tm</b> 168.9	70 <b>Yb</b> 173.0	71 <b>Lu</b> 175.0
† 90 <b>Th</b> 232.0	91 <b>Pa</b> (231)	92 <b>U</b> 238.0	93 <b>Np</b> (237)	94 <b>Pu</b> (244)	95 <b>Am</b> (243)	96 <b>Cm</b> (247)	97 <b>Bk</b> (247)	98 <b>Cf</b> (251)	99 <b>Es</b> (252)	100 <b>Fm</b> (257)	101 <b>Md</b> (258)	102 <b>No</b> (259)	103 <b>Lr</b> (260)

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### Passage I (Questions 1–8)

The *Polymerase Chain Reaction* (PCR) is a widely utilized technique in molecular biology that allows investigators to amplify segments of genomic (chromosomal) DNA or complementary DNA (DNA derived from reverse transcription of cellular RNA). PCR requires investigators to know the sequences bracketing the target region to be amplified.

The first step of PCR is to design *oligonucleotide primers*. These are short sequences of single-stranded DNA that are complementary to the sequences bracketing the target region. A preparation of DNA is heated so that the strands of the double helix separate (denature), and then the temperature is lowered, enabling the primers to anneal to their complementary DNA sequences. At this point, the temperature is raised slightly, and a thermostable DNA polymerase synthesizes new single strands from the 3' end of each primer.



Thus, the amount of target DNA is doubled in the fast round of temperature cycling. The entire cycle can be repeated by denaturing the DNA preparation and starting again. In fact, the number of copies of target DNA doubles with each cycle; after 30 cycles, one target DNA segment will have given rise to  $2^{30}$  daughter segments.

PCR has enabled researchers to isolate and amplify a gene from one species using the primers for the corresponding gene in another species. Altering the primer annealing temperature enables the primers to hybridize to the target DNA (although there may be a few base pair mismatches between the two species' DNA), and amplification proceeds. In this manner, PCR has enabled scientists to characterize a given gene from several species in a very short time.

- The advantage of using a thermostable DNA polymerase in the PCR amplification is that:
  - heat-labile DNA polymerases are unable to synthesize DNA at the annealing temperature.
  - heat-labile DNA polymerases are not as efficient at DNA synthesis as thermostable polymerases.
  - heat-labile DNA polymerases do not remain active throughout the temperature cycles.
  - heat-labile DNA polymerases have a higher error rate than thermostable polymerases.
- It can be inferred from the passage that:
  - the PCR preparation must contain free nucleotides.
  - all of the DNA in the initial PCR preparation is amplified.
  - PCR amplification using DNA and primers from the same species require the lowest annealing temperatures.
  - PCR amplification is not practical when only a few segments of the target DNA are present in a sample.
- A researcher has three segments of target DNA in a PCR preparation. After 40 rounds of temperature cycling with DNA polymerase and the appropriate primers, how many segments of target DNA will be present?
  - 120
  - $(3)(2^{40})$
  - $(3)(2)(40)$
  - $(3)(2)\log 40$

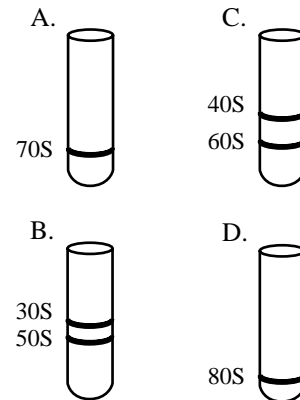
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4. Reverse transcription involves the conversion of:
- A. protein to DNA.
  - B. RNA to protein.
  - C. DNA to RNA.
  - D. RNA to DNA.
5. A molecular biologist attempts to use PCR primers derived from the DNA sequence of the bovine *apoE* gene to amplify the corresponding gene from within a sample of human DNA. The experiment fails, and no amplified product is observed. In order for this experiment to amplify the human version of the gene, the scientist should:
- A. lower the annealing temperature in the cycle, in order to enable interspecies' DNA hybridization.
  - B. lower the annealing temperature in the cycle, in order to prevent interspecies' DNA hybridization.
  - C. raise the annealing temperature in the cycle, in order to enable interspecies' DNA hybridization.
  - D. raise the annealing temperature in the cycle, in order to prevent interspecies' DNA hybridization.
6. In which environment would you expect to find the organism responsible for the production of the thermostable DNA polymerase?
- A. Polar ocean waters
  - B. Tropical rain forest
  - C. Geothermal hot springs
  - D. Glaciers
7. In the PCR technique, the high temperature (95–100°C) required for the denaturation of the DNA helix breaks which of the following chemical bonds?
- A. Covalent bonds between phosphate groups along the DNA backbone
  - B. Hydrogen bonds between base pairs in the double helix
  - C. Ionic bonds between salt groups in the double helix
  - D. Polar bonds between the sugar moieties along the DNA backbone
8. A scientist believes that the *c-fos* gene may be involved in the development of the human sense of taste. To test this hypothesis, she will attempt to amplify the gene through PCR using *c-fos* primers. In order for this experiment to be successful the DNA preparation to be amplified should be:
- A. genomic DNA from taste bud cells.
  - B. genomic DNA from any somatic cell.
  - C. complementary DNA from taste bud cells.
  - D. complementary DNA from germ-line cells.
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Questions 9 through 13 are **NOT** based a descriptive passage.

9. In the cells of brown fat tissue, the inner membrane of the mitochondrion is completely permeable to  $H^+$ . For each molecule of glucose that is metabolized under aerobic conditions by these cells, how many molecules of ATP are produced?
- A. 2  
B. 4  
C. 18  
D. 36
10. When a researcher heated the segment of the DNA helix containing the five histone genes, only the DNA sequences between these genes were denatured, revealing the location of the histone-coding regions. Which of the following best accounts for this observation?
- A. Histones protect the DNA helix from denaturation.  
B. Packaging of the DNA with histones strengthens base pair bonding.  
C. The genes coding for histones are rich in adenine and thymine, while the DNA sequences between them are rich in guanine and cytosine.  
D. The genes coding for histones are rich in guanine and cytosine, while the DNA sequences between them are rich in adenine and thymine.
11. Suppose that a peptide has the sequence val-ser-met-pro, and the tRNA molecules used in its synthesis have the following corresponding sequence of anticodons: 3'-CAG-5', 3'-UCG-5', 3'-UAC-5', 3'-UUU-5'. What is the sequence of the DNA that codes for this peptide?
- A. 5'-GACGCTCATTTT-3'  
B. 5'-UUUCAUGCUGAC-3'  
C. 5'-CAGTCGTACTTT-3'  
D. 5'-TTTCATGCTGAC-3'
12. Which of the following observations proves that the anticodon of a tRNA molecule, and not the amino acid that it carries, recognizes and binds to the mRNA codon at the ribosome?
- A. A tRNA carrying a valine but with an isoleucine anticodon does not place any amino acid onto a growing peptide chain when an isoleucine mRNA codon is present.  
B. A tRNA carrying a valine with a valine anticodon places a valine onto a growing peptide chain when only the first two bases of the anticodon pairs with the mRNA codon.  
C. A tRNA carrying a valine with a valine anticodon does not place any amino acid onto a growing peptide chain when only the first two bases of the anticodon pairs with the mRNA codon.  
D. A tRNA carrying a valine but with an isoleucine anticodon places a valine onto a growing peptide chain when an isoleucine mRNA codon is present.
13. Ribosomal subunits were isolated from bacteria grown in a "heavy" medium of  $^{13}C$  and  $^{15}N$ . These ribosomal subunits were added to an *in vitro* system actively engaged in protein synthesis. After translation had ceased, a sample was removed and analyzed by centrifugation. Which of the following best represents the results of this centrifugation?



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## Passage II (Questions 14–19)

*Neurospora* is a bread mold that is haploid throughout most of its life cycle. A wild-type and four mutant strains of *Neurospora* are used in an experiment to study the biosynthesis of arginine. The mutant strains have specific mutations that affect their ability to synthesize arginine. The mutations affect the enzymes that convert one intermediate to the next along the arginine synthesis pathway. The mutant strains can only grow on minimal media when it is supplemented with the intermediate that they cannot produce. Growth results using some of the intermediates of the arginine pathway as media supplements, as well as arginine itself, are shown below. All of the media contained the precursor molecule of the arginine synthesis pathway.

Strain	Supplement added			
	None	Ornithine	Citrulline	Arginine
wild-type	+	+	+	+
1	–	–	–	+
2	–	–	+	+
3	–	+	+	+
4	–	+	+	+

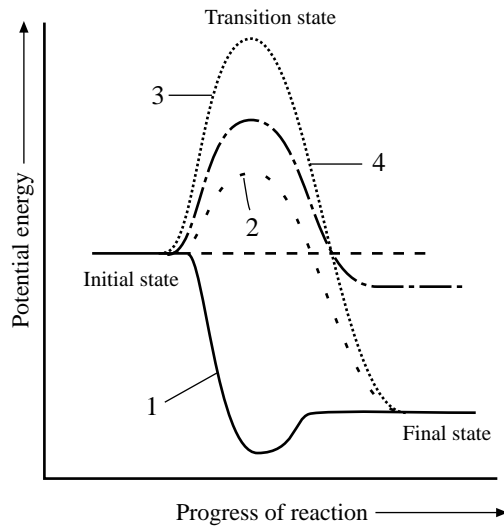
Table 1

A (+) sign indicates growth and a (–) sign indicates no growth.

14. Based on the data in Table 1, what is the sequence of these intermediates in the arginine synthesis pathway?
- precursor → arginine → citrulline → ornithine
  - precursor → citrulline → ornithine → arginine
  - precursor → ornithine → arginine → citrulline
  - precursor → ornithine → citrulline → arginine
15. *Neurospora* can also reproduce and form a diploid zygote that can remain dormant for extended periods of time. Which of the following would most likely cause *Neurospora* to produce diploid zygotes?
- Inadequate supply of nutrients
  - Excess supply of nutrients
  - Mutant arginine synthesis pathway
  - Contact between the wild-type strain and a mutant strain
16. This experiment does not yield enough information to differentiate between the nature of the mutations in Strain 3 and Strain 4. Which of the following would allow the exact nature of the mutations to be determined?
- Supplement the media of these strains with additional intermediates of the arginine pathway.
  - Repeat the experiment, adding a fifth mutant strain of *Neurospora*.
  - Supplement the media of these strains with twice the concentration of intermediates of the arginine pathway.
  - Remove arginine from the supplement for these strains.
17. In comparison to the wild-type strain, Strain 2 would most likely have a higher concentration of:
- phenylalanine.
  - ornithine.
  - citrulline.
  - arginine.
18. The mutation in Strain 4 that renders it incapable of synthesizing arginine occurred in:
- DNA.
  - mRNA.
  - protein.
  - the anticodon region of tRNA.

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19. The figure below shows the course of the reaction in the arginine synthesis pathway for which Strain 1 has a mutant enzyme. Which of the following lines would best represent this reaction as it would occur in Strain 1? [Note: This reaction in the wild-type strain is represented by Line 2.]



- A. Line 1
- B. Line 2
- C. Line 3
- D. Line 4

END OF TEST

**ANSWER KEY:**

- |             |              |              |              |
|-------------|--------------|--------------|--------------|
| 1. <b>C</b> | 6. <b>C</b>  | 11. <b>D</b> | 16. <b>A</b> |
| 2. <b>A</b> | 7. <b>B</b>  | 12. <b>D</b> | 17. <b>B</b> |
| 3. <b>B</b> | 8. <b>C</b>  | 13. <b>B</b> | 18. <b>A</b> |
| 4. <b>D</b> | 9. <b>B</b>  | 14. <b>D</b> | 19. <b>C</b> |
| 5. <b>A</b> | 10. <b>D</b> | 15. <b>A</b> |              |

## MOLECULAR BIOLOGY TEST 1 TRANSCRIPT

## Passage I (Questions 1-8)

**1. Choice C is the correct answer.** This question is asking you to infer from the passage why a thermostable DNA polymerase is used in PCR instead of a heat-sensitive, or heat-labile, polymerase. In order to answer this question correctly, you had to understand one key aspect of the PCR reaction--the high temperature used to denature the DNA helix, or duplex. Without the elevated temperature, the helix would not separate and the PCR reaction would not occur. This heat also inactivates any heat-labile polymerases in the reaction mixture. Remember, enzymes work only in a limited range of temperature and pH. Therefore, using a thermostable polymerase would be an advantage over a heat-labile polymerase, and so choice C is the correct answer. In fact, PCR was originally performed using heat-labile polymerases, but fresh enzyme had to be added during each cycle. This proved extremely cumbersome, so the developers of the technology began to seek out thermostable polymerases, eventually discovering one from an organism called *Thermophilus Aquatus*. This polymerase, called Taq, is now the industry standard for PCR amplification.

Let's look at the other choices. Choice A is incorrect, because the annealing temperature is the temperature at which two strands of DNA will anneal, or come together. Although this temperature varies slightly depending on the composition of the DNA, heat-labile polymerases can synthesize at these usually moderate temperatures; it is the high temperature required for DNA denaturation that they cannot survive. Similarly, choice B is incorrect because the two types of polymerases are equally efficient at synthesizing DNA. The advantage of the thermostable polymerase is that it remains active at the higher temperatures used in PCR. Finally, choice D is also incorrect since the error rates for the two types of polymerases are comparable. Besides, you're not told anything about the error rates in the passage, so you would not be expected to know anything about the error rates to answer the question. Again, choice C is the correct answer.

**2. Choice A is the correct answer.** From the question stem you know that this is an inference question. This means that you will not find the answer directly in the passage, but must base your answer on information from both introductory biology and the passage. Well let's see what the passage does tell us. You know that PCR is a technique that selectively amplifies DNA; it does NOT amplify all of the DNA in a sample. The specific oligonucleotide primers used in PCR promote the replication of the DNA sequence that lies between them. Thus, choice B is incorrect. Choice C is also incorrect. If the primer and gene are both from the same species, you would expect 100% homology between their sequences. This means that the two pieces of DNA will anneal strongly. However, if the primer and gene are from different species, they will not have perfectly complementary sequences, which means that these two pieces of DNA will NOT anneal very strongly. As a result, the annealing temperature must be lowered. Decreasing the temperature, and hence, the overall molecular motion in solution, will serve to stabilize duplexes with mismatches. Therefore, primer and DNA from the same species do NOT require as low an annealing temperature as primer and DNA from different species. Choice D is also incorrect. From the passage you know that one of the major advantages of PCR over other techniques is its ability to amplify extremely small amounts of DNA. And since choice D states the opposite, it is incorrect. Well, by the process of elimination you know that choice A must be the correct answer. Let's see why. Nucleotides serve as the building blocks of the nucleic acids, DNA and RNA, much as amino acids serve as the building blocks of proteins. There can be no synthesis of DNA (called replication) or RNA (called transcription) without the presence of free nucleotides. In addition, all four nucleotides need to be present in saturating concentrations, since the absence of any one will cause the polymerase to halt when it needs to add that particular nucleotide to the growing nucleic acid chain. And since PCR involves the replication of DNA, free nucleotides must be present. And so, choice A is the correct answer.

**3. The correct answer is choice B.** The passage states that, after 30 cycles, one target DNA segment produces  $2^{30}$  daughter segments. To gain a mental picture of the process, imagine the first few rounds of the PCR amplification of one DNA target molecule. After cycle number one, there will be  $2^1$ , or 2 identical daughter DNA molecules. After 2 cycles, there will be  $2^2$  or 4 DNA molecules. After 3 rounds, there will be  $2^3$  or 8 molecules, and so on... Thus, after 40 rounds, there will be  $2^{40}$  daughter segments per starting segment, or  $2^{40} + 2^{40} + 2^{40}$  daughter segments, which is  $3 \cdot 2^{40}$ . Thus, choice B is the correct answer. Most of the other answer choices played off these three numbers: 3, 2, and 40, in the hopes of distracting you. This is a case where solving the question first and looking at the answer choices second would have definitely prevented a test-taking error.

**4. The correct answer is choice D.** This is basically a really straightforward reading comprehension question. The passage states in the first paragraph that complementary DNA is derived from the reverse transcription of cellular RNA. Remember that forward transcription is the formation of messenger RNA molecules from DNA, choice C. Since choice C describes forward transcription, it must be incorrect. In eukaryotes, this conversion of genetic information from DNA to RNA is accomplished by the class of proteins known as the RNA polymerases. So reverse transcription must be the opposite. In other words, RNA must be converted into DNA. So choice D is the correct answer. Reverse transcription is carried out by very special proteins called reverse transcriptases. These proteins are unique because they do not occur naturally in eukaryotes. Reverse transcriptases are produced by a class of viruses, known as retroviruses, which include the Human Immunodeficiency Virus (HIV), the virus responsible for AIDS. These viruses store their genetic information and instructions as RNA

molecules instead of as DNA, and when they infect a cell, they must convert this RNA to DNA, which can then insert itself into the host cell's genome via homologous recombination.

Anyway, back to the question. Choice A is incorrect, as protein is never converted into DNA. Proteins are necessary for the formation of complex nucleic acids, but they do not serve as raw material or directional templates. Choice B is also incorrect. The conversion of RNA to protein occurs at the ribosome, a large complex of highly specialized proteins and nucleic acids. This process is known as translation. Again, choice D is the correct answer.

**5. The correct answer is choice A.** From the question stem you know that the experiment involved a primer and a DNA sample, or template, from different species--otherwise known as interspecies amplification. And you also know that the experiment did not work. Why? Well, from the passage you can infer that a lack of exact complementarity between a primer and a DNA sample often occurs when using primers from one species to amplify analogous genes from another species' DNA. If the primer and the DNA are NOT 100% complementary, they will not base pair with each other as strongly as a primer and template that ARE 100% complementary. And if the two pieces do not anneal, the PCR reaction will not occur. So what can be done to assure that the primer and template do anneal? From the passage and Figure 1, you know that altering the annealing temperature will allow the primer and template to hybridize. So should the temperature be raised or lowered? Since the primer and template do not form a very strong duplex because some of the bases in the primer do not pair with some of the bases in the template, which is known as mismatching, you need to make it easier for the two to hybridize. Raising the temperature will disrupt the hydrogen bonds, and since only a few bases are pairing in the first place due to the mismatches, the increased temperature will only disrupt the weak pairing and hence NOT promote hybridization. Lowering the temperature, on the other hand, will NOT disrupt the limited hydrogen bonding between the primer and template, and thus allow the primer to anneal to the template, thereby promoting interspecies DNA hybridization. Therefore, we must LOWER the annealing temperature. So choices C and D are incorrect. And all we have to do is decide between choices A and B. Well from our discussion we know that we are lowering the annealing temperature to promote hybridization, not prevent it. Thus, choice B is incorrect and choice A is the correct answer.

**6. The correct answer is choice C.** In order to survive the denaturation of the DNA duplex in the first step of the PCR reaction, the thermostable polymerases used must be able to withstand temperatures close to 100°C. So to answer this question correctly you need to pick the environment in which an organism would normally need to have its enzymes functional at such high temperatures. This means that the correct answer will be an organism that lives in a very hot environment. Obviously, polar ocean waters and glaciers, choices A and D, are very cold environments, and so these choices are incorrect. Organisms in these environments will have enzymes that are specially adapted to operate in extreme cold, not extreme heat. Choice B is also incorrect. Even in the hottest rain forests temperatures never reach 100°C. So an organism in the rain forest would not be expected to have special enzymes designed to function in extreme heat. So by the process of elimination, choice C is the correct answer. Let's see why. Geothermal hot springs, which do reach temperatures of 100°C, have been colonized mostly by microbial life forms. Many of these exhibit unique biological adaptations, including the use of sulfurous compounds as energy sources and the development of proteins that are highly resistant to heat. These heat resistant proteins enable these organisms to carry out enzymatic reactions in such high temperatures. So the polymerases from these organisms WOULD be expected to withstand the high temperatures used in PCR. So choice C is the correct answer.

**7. The correct answer is choice B.** This question cannot be answered from any information given in the passage. It requires that you have a basic understanding of the molecular structure of double-stranded DNA. You know that as base pairs form between complementary strands of DNA, adenine (A) pairs with thymine (T) and guanine (G) pairs with cytosine (C). There is a major difference between the two types of base pairs, since GC pairs possess 3 hydrogen bonds between them, while AT pairs possess two. A does not pair with C, because A can optimally form 2 hydrogen bonds whereas C can optimally form 3. Another crucial fact is that the breaking and forming of hydrogen bonds are reversible processes, and this allows for the repeated denaturation and renaturation of double-stranded DNA that occurs during PCR.

Choice A is incorrect because covalent bonds are neither broken nor formed during the denaturation and renaturation of DNA. Covalent bonds are also much stronger than hydrogen bonds, and require much more energy to break. Choice C is also incorrect. Among solids, ionic bonds are the strongest and require the most energy to break. Although salts in solution do promote duplex formation by allowing for closer proximity between negatively charged DNA molecules through a masking of the phosphate groups, these bonds are not broken by high temperature as DNA is denatured. Finally, choice D is wrong, because the sugar moieties along the backbone of DNA do not participate in base pair formation. Again choice B is the correct answer.

**8. The correct answer is choice C.** This question requires quite a bit of reasoning. For the c-fos gene to be involved in the development of the human sense of taste, it must be expressed in the taste bud cells. This means there must be mRNA for c-fos in the taste bud cells. Remember that all diploid cells of an individual organism possess identical genomic DNA, and that different cell types express different sets of genes from within the genome depending on their function within the organism. This is the end result of cell differentiation. That means there are different populations of mRNA transcripts within different cell types, and these mRNA transcripts can be converted to complementary DNA (cDNA) through reverse transcription. It is this new cDNA population that must be screened with PCR. A successful result from PCR amplification

of genomic DNA would only tell the investigator that the gene is present in the genome (which is already known), not whether the gene is expressed in that cell type. For this reason, choices A and B are incorrect. Finally, choice D is incorrect because even if the gene is expressed in germ-line cells, its expression may be repressed in the fully differentiated taste bud cell. So using cDNA from germ-line cells will not tell you if the gene is expressed in taste bud cells. Well, this leaves us with choice C as the correct answer. The cDNA from taste bud cells is made from taste bud cell mRNA. And if c-fos mRNA is present, this would mean that the gene was expressed, and would result in a PCR that supported the scientist's hypothesis. Therefore, choice C is the correct answer.

Discretes (Questions 9-13)

**9. Choice B is the correct answer.** From the question stem you know that the inner walls of the mitochondria found in the cells of brown fat tissue are completely permeable to  $H^+$ , or protons. This issue of permeability to  $H^+$  is the key to answering this question. What does this mean in terms of ATP production? Well, the inner membrane of the mitochondrion is the site of electron transport/oxidative phosphorylation. The process works by transferring electrons from NADH and  $FADH_2$  molecules produced during glycolysis and the Krebs cycle through the electron transport chain. This electron transfer leads to the pumping of protons from the mitochondrial matrix into the intermembrane space. This pumping produces a pH gradient due to the higher concentration of  $H^+$  in the intermembrane space than in the matrix. The pumping also produces a membrane potential due to the higher concentration of positive charges (from protons) in the intermembrane space than in the matrix. This pH gradient and membrane potential constitute a proton-motive force that is used to drive ATP synthesis. However, if the inner membrane is completely permeable to protons, which we're told is the case in brown fat cells, then no gradient or proton-motive force can be established, and thus no ATP can be synthesized from the NADH and  $FADH_2$  generated during glycolysis and the Krebs cycle. Therefore the only source of ATP must be from ATP molecules that are formed directly in glycolysis and the Krebs cycle. And as you should know from introductory biology, glycolysis yields a net of 2 ATP per molecule of glucose, and the Krebs cycle yields a total of 2 molecules of ATP per molecule of glucose. So, for each molecule of glucose, only 4 molecules of ATP will be produced in the cells of brown fat tissue. Therefore, choice B is the correct answer. As for the other answer choices: 2 ATP, choice A, is the amount of ATP generated by the glycolysis, or anaerobic respiration, of one molecule of glucose; choice D, 36 ATP, is the amount of ATP generated by the aerobic respiration of one molecule of glucose. Choice C, 18 ATP, is just your ordinary wrong answer. Again, choice B is the correct answer.

**10. Choice D is the correct answer.** In order to answer this question correctly you need to figure out which of the answer choices best explains why the segments of the DNA helix that code for histones did not separate upon heating, while the segments that did NOT code for histones DID separate during heating. Choice A and B can be eliminated because these choices discuss the functions of the histone proteins themselves; they do not address the structure of the DNA that codes for these proteins. So now we have narrowed it down to either choice C or D. Choice D suggests that the histone genes are rich in the bases guanine and cytosine, while the non-histone regions are rich in adenine and thymine. Well, G-C pairs have 3 hydrogen bonds, while A-T pairs have only 2 hydrogen bonds. What does this mean? The more hydrogen bonds, the more energy it will take to break apart the segment of double-stranded DNA. Therefore, if the histone coding DNA did not denature while the other regions did, then it makes sense that the histone coding regions must have been G-C rich, while the other regions must have been A-T rich. Therefore choice C is incorrect and choice D is the correct answer.

**11. Choice D is the correct answer.** This problem is a little bit more difficult than your standard "figure out the sequence" question. There are two ways to approach this problem--the long way, and the short way. Since most people probably did this question the long way, let's go over that first, and then I'll tell you a short cut. Here's the long way. From the question stem you know the order of the tRNAs that base paired with the mRNA. Whenever nucleic acids base pair, there is always a polarity associated with it. This means that the 3' end of the tRNA anticodon will correspond to the 5' end of the mRNA codon. And also remember that C pairs with G, and U pairs with A, since we're talking about RNA. This means that the corresponding sequence of mRNA is 5'--GUCAGCAUGAAA--3'. And now all you have to do is figure out what the complementary sequence of DNA is. Well this could have been a little tricky if you forgot that A pairs with T in DNA, not U, as in RNA. And as we just said, whenever you base pair nucleic acid, the polarities must be antiparallel. Therefore, the 3' end of the RNA will base pair with the 5' end of the DNA. This means that the correct DNA sequence must be 5'--TTTCATGCTGAC--3', which is choice D. Therefore choice D is the correct answer.

Now for the short cut. Since both the 3' end of the tRNA and the 3' end of DNA both base pair to the 5' of mRNA, the DNA sequence that base pairs to the mRNA is identical to the tRNA sequence that pairs with it, EXCEPT that the U's in the tRNA are replaced with T's. So reading the tRNA sequence with T's in place of U's, you get 5'--TTTCATGCTGAC--3', which is also choice D. Remember that, by convention, nucleic acids are always read in the 5' to 3' directions. Again, choice D is the correct answer.

**12. Choice D is the correct answer.** From introductory biology you know that the anticodons on tRNA base pair with mRNA codons being translated into a sequence of amino acids. As you can imagine, scientists did not always know this.

Some initially thought that it was the amino acid that the tRNA molecule was carrying that interacted with the mRNA codon. So to figure out how the genetic code was actually translated, a series of experiments were performed. And in this question, you're asked to determine which of the answers proves that it is the anticodon and not the amino acid itself that interacts with the mRNA codons during translation. So let's look at the answer choices. In choice A and choice D you have a tRNA molecule with an anticodon that is complementary to the isoleucine codon of mRNA, but with a valine amino acid attached to it. Now if the amino acid on the tRNA interacted with mRNA, no amino acid would be placed onto the growing peptide chain, since a valine would not recognize an isoleucine codon. On the other hand, if the anticodon interacted with the mRNA, the isoleucine anticodon would pair with an isoleucine codon, thus allowing the amino acid on the tRNA to be placed onto the growing peptide chain. Therefore choice A supports the interaction of the amino acid with the anticodon, while choice D supports the interaction of the anticodon with the codon. Thus choice A is incorrect and choice D is the correct answer.

Let's look at choices B and C quickly. Both of these choices are about the wobble hypothesis of the genetic code. The wobble hypothesis accounts for the ability of a tRNA anticodon to recognize more than one codon for a given amino acid by unusual, non-G-C or A-T, pairing with the third base of a codon. The wobble hypothesis has nothing to do with whether the tRNA molecule of the amino acid it carries interacts with the mRNA codons. Therefore choices B and C can be eliminated. Again, choice D is the correct answer.

**13. Choice B is the correct answer.** From the question stem you know that bacterial ribosomal subunits were used in this experiment. The subunits, which are radio-labeled with "heavy" carbon and nitrogen, were placed in a test tube that was actively engaged in protein synthesis. During translation, the subunits come together to form a complete ribosome. After translation has ceased, the complete ribosome dissociates back into its two constituent subunits. Since the sample used in centrifugation was taken after translation had ceased, you would expect to find ribosomal subunits, and not whole ribosomes. And since the subunits are different sizes, you would expect two different bands in your centrifuge tube, since centrifugation separates subcellular components based on their size and density. Based on this fact, you can eliminate choices A and D, since they both show only one band, representing the complete ribosome. To decide between choices B and C, you have to know the sizes of the two ribosomal subunits in bacteria. Bacteria have two subunits of weights 50S and 30S, which come together to form a 70 S complex, while eukaryotes have two subunits of weights 60s and 40S, which come together to form an 80S complex. This means that choice C represents the eukaryotic ribosomal subunits, and choice B represents the bacterial (prokaryotic) ribosomal subunits. Therefore choice C is wrong and choice B is the right answer.

Passage II (Questions 14-19)

**14. The correct answer is choice D.** To answer this question you need to have an understanding of biosynthetic pathways, as well as be able to interpret the data in Table 1. Biosynthetic pathways are series of chemical reactions that result in the formation of end products. Along the way from precursor to end product, stable intermediates are created. The intermediates are converted stepwise by specific enzymes until the end product is produced in sufficient quantity. No end product will be synthesized if there is a mutation in one enzyme of the pathway. However, if the media that the mutant strain is grown in is supplemented with the product that the defective enzyme is supposed to produce, the enzymatic block will be bypassed and an end product WILL be produced.

Now that we understand biosynthetic pathways a little bit better, let's apply this information to the data in Table 1. From the passage you know that the arginine pathway involves at least two intermediates, citrulline and ornithine, and that obviously, arginine is the end product. Therefore, choices A and C can be immediately eliminated. Now all we have to do is decide between choices B and D. According to the table, the wild-type strain can grow on all media, as expected. All strains can grow on arginine, which is expected if the mutations only affect the arginine pathway. Three of the four mutants can grow when supplemented with citrulline in the arginine pathway. This implies that citrulline is the intermediate directly before arginine. Thus, the order of the arginine pathway must be: precursor molecule, ornithine, citrulline, arginine. So choice B is incorrect and choice D is the correct answer.

**15. Choice A is the correct answer.** From the question stem you know that after *Neurospora* forms a zygote it will remain dormant for an extended period of time. So all you have to do to answer this question is decide what would cause the organism to enter a state of dormancy. Well to do this let's look at the answer choices. Choice A implies that a lack of adequate food for the organism to live on would cause this. Well, if this were the case, the organism WOULD die unless it went into a state of dormancy. So choice A is the correct answer. Let's look at the other choices quickly. If there is an excess of food there would be no need for the organism to become dormant. So choice B is incorrect. Choice C is also incorrect: The strains in the passage have mutant arginine synthesis pathways, but none of them enters a state of dormancy as a result. Finally, there is no reason to assume that contact between the wild-type strain and the mutant strains would induce the production of diploid zygotes that enter a period of dormancy. Therefore choice D is also incorrect. Again, choice A is the correct answer.

**16. The correct answer is choice A.** From Table 1 you can see that both Strains 3 and 4 can grow when supplemented with each of the intermediates used in this set of experiments, but can't grow when only the precursor molecule

is present. This implies that the mutations that these strains have lie in enzymes that catalyze reactions that occur somewhere in the pathway PRIOR to the synthesis of ornithine. And according to the passage, ornithine and citrulline are just a couple of the intermediates in the pathway. In other words, there are additional intermediates and additional enzymes in the pathway. Now, if Strains 3 and 4 were supplemented with these additional intermediates and one of them grew on a new intermediate while the other strain did not, then you would be able to differentiate between the nature of the mutations in Strains 3 and 4. Therefore, choice A is the correct answer. Adding a fifth mutant would not help differentiate between Strains 3 and 4; this would only allow you to determine the nature of the mutation in the fifth mutant. So choice B is incorrect. Doubling the concentration of intermediates would also not help. If an enzyme is defective it will not be able to convert any concentration of intermediate. Besides, we just decided that the intermediates used in Table 1 do not provide enough information, so adding more of the same would not help to differentiate between the mutations. So choice C is also incorrect. And removing the end product of the pathway, which is arginine, would not help differentiate between the strains either. The defective enzymes are involved with the production of ornithine, not arginine. Thus choice D is also incorrect. Again, choice A is the correct answer.

**17. The correct answer is choice B.** The wild-type strain can grow without being supplemented with any intermediates. Its arginine biosynthesis pathway is normal and you would expect to see low levels of all of the intermediates and a high level of arginine. To answer the question you need to figure out which of the compounds would be found in higher concentration in Strain 2 relative to the wild-type strain, which serves as our control for these experiments. To do this you need to figure out where the mutation lies in Strain 2. Well, let's examine where Strain 2 can grow when supplemented. You can see from Table 1 that it can grow when supplemented with arginine or citrulline, but not with ornithine or just the precursor molecule, which is the starting point for the pathway. Therefore, its mutated enzyme cannot convert ornithine to citrulline. The rest of the pathway appears fine. So Strain 2 will convert precursor molecule to ornithine, but will then be unable to convert ornithine into citrulline. Therefore, in comparison to the wild-type strain, Strain 2 will have a higher concentration of ornithine. Thus, choices C and D are incorrect and choice B is the correct answer. Choice A, phenylalanine, is an amino acid not related to the arginine biosynthesis pathway. Since it is unrelated to the information in the passage, you should assume that this pathway is normal in both strains. Thus, both strains would be expected to have the same concentration of phenylalanine, and so choice A is incorrect. Again choice B is the correct answer.

**18. The correct answer is choice A.** To answer this question all you have to do is determine where a mutation that would be passed on to all future generations, which would be necessary for a strain to be established, would occur. Although the question stem asks about Strain 4, I hope you didn't waste time looking at the table. This was just put in to throw you off the track a bit. It really doesn't matter which strain we're talking about. By definition, a mutation is an inheritable change in DNA sequence. It's inheritable because DNA is the genetic material that replicates and is passed on to daughter cells during cell division. Therefore choice A is the correct answer. It's not even appropriate to refer to errors in transcription or translation as mutations. If a mistake occurred during transcription, only those proteins translated from that piece of mRNA would be defective, and when a new strand of mRNA was transcribed the normal protein would again be produced. So an error in the mRNA would not produce a mutant strain. Thus choice B is incorrect. The same thing would also happen if an error occurred during translation. The protein synthesized would be defective, but as soon as new protein was translated, the problem would be fixed. Therefore choice C is also incorrect. Finally, an error in transcription that resulted in a defective anticodon region of tRNA would also result in a transitory error that would affect all proteins that were translated using that tRNA. But again, as soon as this defective molecule was replaced, the cell would return to normal and a mutant strain would not be created. Thus choice D is also incorrect. Again, choice A is the correct answer.

**19. Choice C is the correct answer.** This question is basically testing your understanding of enzyme function. You're told in the question stem that the graph represents the course of the reaction for which Strain 1 has a mutant enzyme. Enzymes are substances, typically proteins, that accelerate reactions by lowering the activation energy of the reaction. Enzymes do not change the equilibrium point of a reaction. In other words the overall free energy, initial state, and final state of the reaction are all unchanged. The overall free energy of a reaction is graphically represented by the vertical distance between the initial state and the final state. The activation energy of a reaction is graphically represented by the vertical distance between the initial state and the transition state. So basically the only difference between a catalyzed reaction and an uncatalyzed reaction will be that the uncatalyzed reaction will have a higher activation energy. Well, if this enzyme is mutant in Strain 1, then it will not catalyze the reaction. So basically, you need to pick the line on the graph that represents the uncatalyzed reaction. Although kinetically unfavorable, the uncatalyzed reaction is thermodynamically favorable and will eventually occur, but not in a biologically useful length of time. This is the same situation with diamond, which over time, turns into graphite. But this reaction, which is uncatalyzed, occurs so slowly that you'll never witness diamond turning into graphite. So for practical purposes, diamonds really are forever.

Anyway, back to the question. You know that Line 2 represents the course of the reaction in the wild-type strain, which does NOT have a mutant enzyme, and so you can use Line 2 as your point of reference for what a catalyzed reaction looks like. Therefore, choice B must be wrong. Line 4 must be incorrect because its final state differs from that of the wild-type reaction, and so choice D is incorrect. And choice A is also incorrect, because Line 1 has a lower, not a higher,

activation energy than Line 2. Only Line 3 has the same initial state and final state as Line 2 but a higher activation energy. Therefore choice C must be the correct answer.