TAMPINES MERIDIAN JUNIOR COLLEGE

JC2 PRELIMINARY EXAMINATION

CANDIDATE NAME

CIVICS GROUP

H2 BIOLOGY

9744/01

Paper 1 Multiple Choice Questions

19 September 2024

1 hour

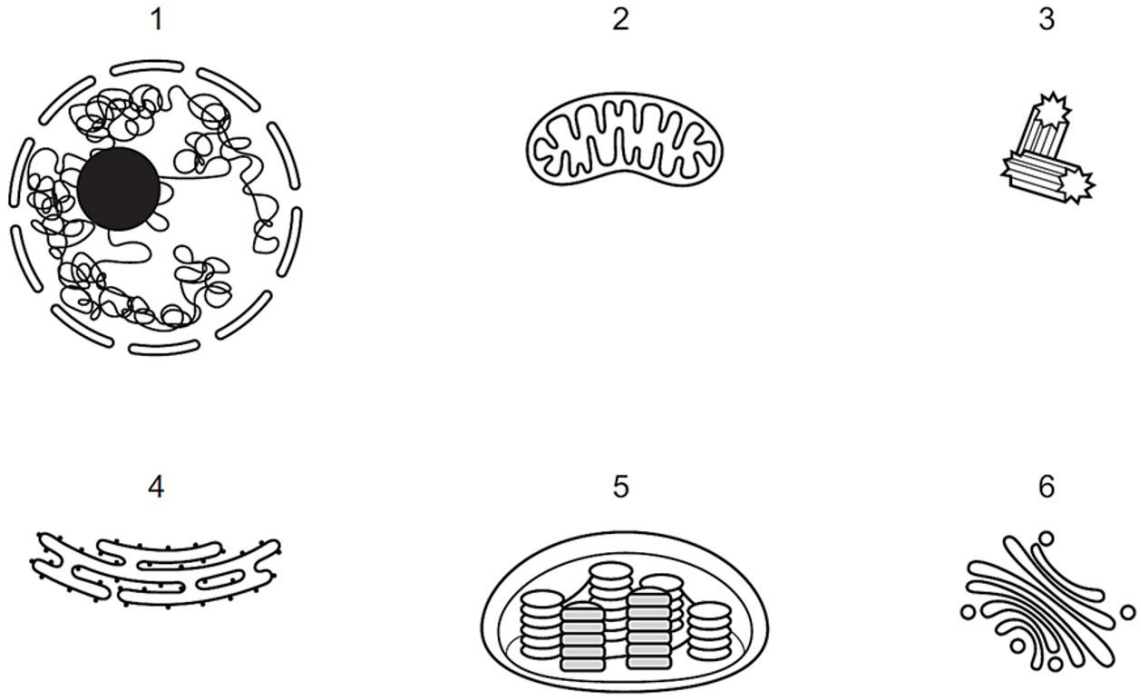
Additional material: Multiple Choice Answer Sheet

ANSWERS WITH EXPLANATION

QUESTION	ANSWER	QUESTION	ANSWER
1	B	16	A
2	C	17	B
3	C	18	C
4	D	19	A
5	A	20	D
6	C	21	D
7	A	22	C
8	D	23	C
9	D	24	B
10	A	25	C
11	B	26	D
12	B	27	D
13	D	28	D
14	C	29	B
15	A	30	C

[Cell 1/2, KU-1]

1. Six organelles found in eukaryotic cells are shown. They are not drawn to scale.



Which organelles are involved in the synthesis and secretion of a glycoprotein?

A. 1, 2, 3 and 4 **B.** 1, 2, 4 and 6 **C.** 2, 3 and 5 **D.** 3, 4, 5 and 6

Explanation

- 1 = nucleus, 2 = mitochondria, 3 = centrioles, 4 = RER, 5 = chloroplast, 6 = Golgi apparatus
- Nucleus carries gene coding for the protein. It is also where transcription takes place.
- RER is where translation takes place. The protein enters the ER lumen where folding and glycosylation occurs.
- Golgi further modifies the glycoprotein and packages them into a secretory vesicles.
- Mitochondria synthesizes ATP needed for protein synthesis and movement of vesicles along microtubules.

[Cell 2/2, KU-1]

2. What is present in **all** viruses, prokaryotes and eukaryotes?

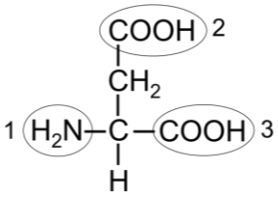
A. thymine **B.** deoxyribose **C.** adenine **D.** phospholipid

Explanation

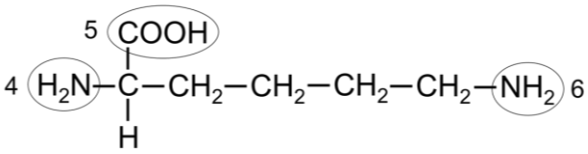
- Thymine is present in DNA. Some viruses are RNA viruses (hence no thymine).
- Deoxyribose is present in DNA. Some viruses are RNA viruses (hence no DNA).
- Some viruses are non-enveloped, hence no phospholipids.

[BioMol 1/2, KU-1]

3. The diagrams show the structures of two amino acids, aspartic acid and lysine.



aspartic acid



lysine

Which groups form the bonds that maintain the primary, secondary and tertiary structures of proteins?

	primary structure	secondary structure	tertiary structure
A.	2, 6	1, 3, 4, 5	1, 3, 4, 5
B.	1, 3, 4, 5	2, 6	2, 6
C.	1, 3, 4, 5	1, 3, 4, 5	2, 6
D.	2, 6	2, 6	1, 3, 4, 5

Explanation:

- 1 and 4 are the amino group, and 3 and 5 are the carboxylic acid group. They form peptide bonds that link amino acids together to form the primary structure (sequence of amino acids).
- The C=O group and –NH groups of the peptide bond regions are needed to form hydrogen bonds in alpha helices and beta pleated sheets.
- The R-groups, which are CH_2COOH in aspartic acid and $CH_2CH_2CH_2CH_2NH_2$ in lysine forms bonds with other R-groups to maintain the globular (tertiary) structure of proteins.

[BioMol 2/2, HI-2]

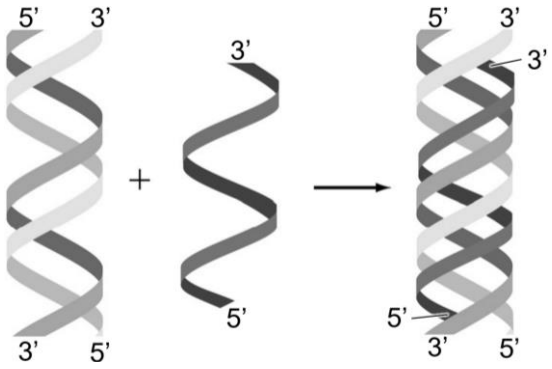
4. DNA can form a triple helix, but such structures are extremely rare in nature.

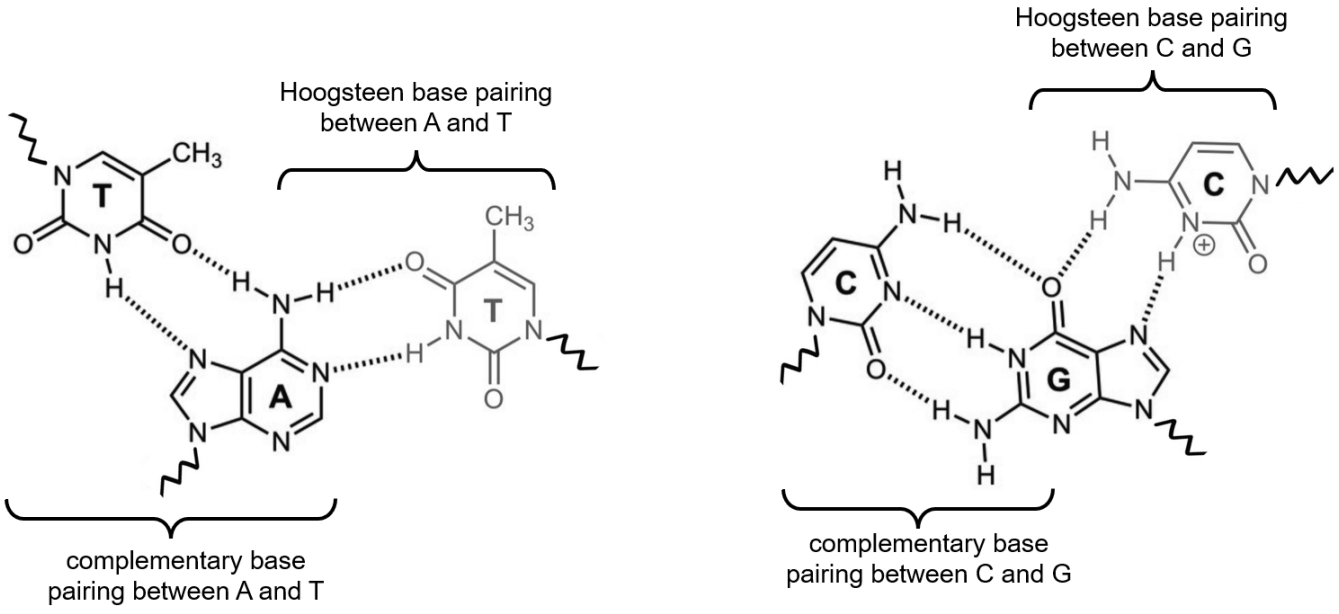
Base pairing within a normal double-stranded DNA is termed complementary base pairing.

Base pairing of the third DNA strand with one of the two strands of the double-stranded DNA is termed Hoogsteen base pairing.

The diagrams illustrate

- how a third strand can bind to a double-stranded DNA molecule
- how bases from the third strand can interact with the double-stranded DNA molecule.





Which statements are correct regarding the formation of DNA triple helix?

1. Both major grooves and minor grooves of the double-stranded DNA are accessible to the third DNA strand for binding.
2. Complementary base pairing between adenine and thymine and Hoogsteen base pairing between guanine and cytosine are equally strong.
3. DNA triple helices can exhibit greater thermal stability than DNA double helices.
4. Synthetic oligonucleotides can be designed to bind to the target gene through triple helix formation, leading to gene silencing.

A. 1 and 2 **B.** 1 and 4 **C.** 2 and 3 only **D.** 2, 3 and 4

Explanation

1. Only the bases along the major grooves are exposed for interaction with the third DNA strand, as shown in the diagram. In fact, all DNA-binding proteins interact with DNA via the major grooves as well.
2. Both CBP between A and T and HBP between G and C form two hydrogen bonds, hence equally strong.
3. Because there are more hydrogen bonds in triple helix, it takes a higher temperature to denature the three strands into single strands, hence exhibits greater thermal stability.
4. When a third strand is bound to a gene, RNA polymerase will be unable to unwind the original double helix for transcription, terminating transcription prematurely, leading to gene silencing.

[Enzymes 1/1, HI-2]

5. CYP3A4 is an important enzyme in the human digestive system where it is needed to break down a range of different toxins. The activity of CYP3A4 has been shown to be reduced by substances called furanocoumarins. Furanocoumarins are found in some fruits and so dangerous concentrations of toxins may develop in the human digestive system when fruits containing furanocoumarins are eaten.

From the information provided, what can be concluded about molecules of the enzyme CYP3A4?

A. They lower the activation energy of the toxin breakdown reactions.

B. They bind specifically through the active site to a substrate found in some fruits.

C. They change permanently when acted upon by furanocoumarin molecules.

D. They resume normal activity when concentrations of furanocoumarins decrease.

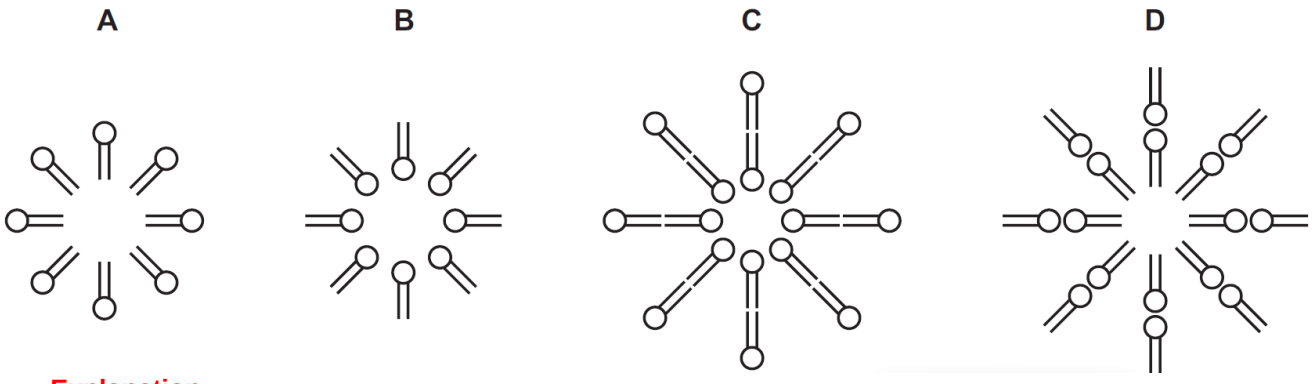
Explanation

A. The substrates of CYP3A4 are the toxin molecules. Hence, the activation energy of the breaking down of toxin is lowered by the enzyme CYP3A4.
B. The toxins (substrates) are not specifically stated to be found in fruits.
C. This option suggests that furanocoumarin binds permanently to and change the conformation of CYP3A4 . How furanocoumarin binds and inhibits CYP3A4 is not stated in the question stem.
D. This option suggests that furanocoumarin binds reversibly to CYP3A4 . How furanocoumarin binds and inhibits CYP3A4 is not stated in the question stem.

[Transport 1/1, KU-1]

6. When a small quantity of phospholipid is added to a test-tube of water and then shaken vigorously, an emulsion is formed by small droplets called liposomes.

Which diagram shows the arrangement of phospholipid molecules in a cross-section of a liposome? **ANSWER: (C)**

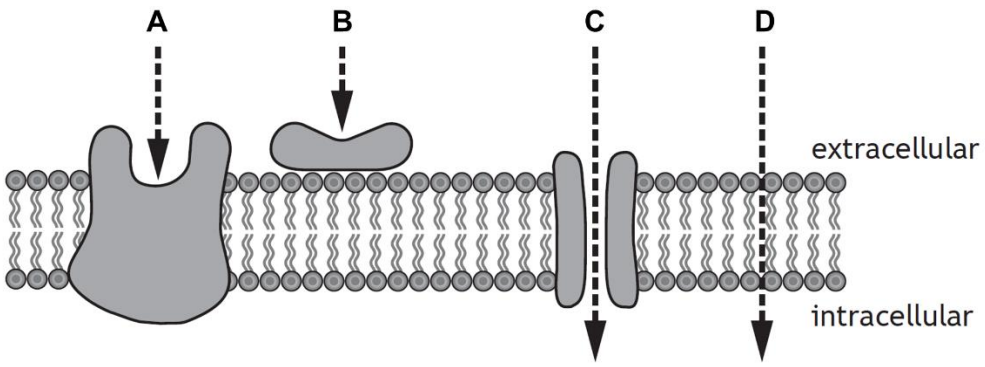


Explanation

Water is present outside the liposome and within the liposome. The hydrophilic phosphate heads must face the water molecules.

[Transport 2/2, KU-1]

7. Which letter in the diagram represents the first step in cell signalling for a protein ligand molecule? **ANSWER: (A)**



Explanation

- Protein ligands are too big to enter the cell via a channel (C) or directly through the bilayer (D). They bind to transmembrane protein receptor (A) at the extracellular domain (signal reception), transducing the signal to the inside of the cell.

[Transformation of Energy 1/2, HI-2]

8. Cyanobacteria are photosynthetic prokaryotes.

A scientist exposed cyanobacteria to light of different colours and intensities and made the following observations:

- Most cyanobacteria are blue in colour.
- At low light intensities, glucose production in cyanobacteria is low.
- When light intensity reaches a certain level the rate of glucose production in cyanobacteria stops increasing.

Which of the following statements correctly explains these observations?

A. The pigments in cyanobacteria absorb blue light and light intensity is a limiting factor for the rate of photosynthesis.

B. The pigments in cyanobacteria absorb red light and light intensity is not a limiting factor for the rate of photosynthesis.

C. The pigments in cyanobacteria absorb blue light and light intensity is not a limiting factor for the rate of photosynthesis.

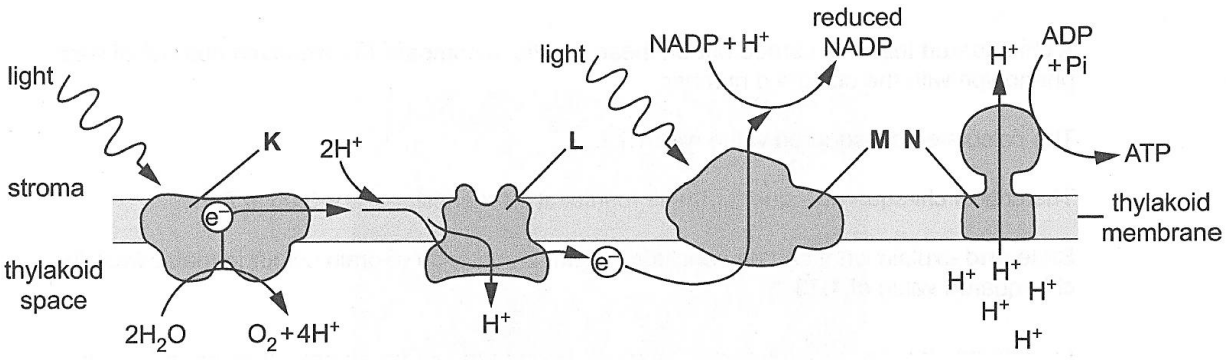
D. The pigments in cyanobacteria absorb red light and light intensity is a limiting factor for the rate of photosynthesis.

Explanation

- Cyanobacteria appear blue because they **reflect** blue wavelength, which then enters our eyes.
- Light intensity **is** a limiting factor since rate of glucose production levels off when light intensity reaches a certain level.

[Transformation of Energy 2/2, KU-1]

9. The diagram represents the arrangement of some of the large protein complexes, labelled K to N, involved in the light-dependent reactions in photosynthesis.



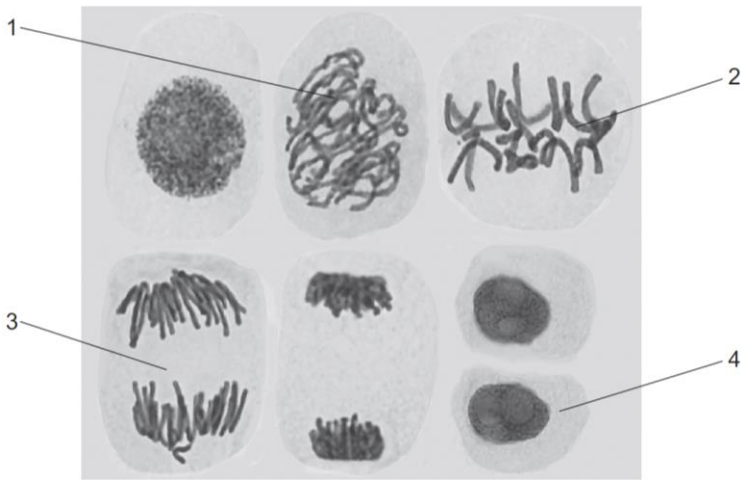
Which of the following most accurately describes K, L, M and N?

	K	L	M	N
A.	photosystem I	proton channel	photosystem II	ATP synthase
B.	photosystem I	proton pump	photosystem II	ATP synthase
C.	photosystem I	proton channel	NADP reductase	proton pump
D.	photosystem II	proton pump	photosystem I	ATP synthase

[Cell Cycle 1/1, KU-2]

10. Vinca alkaloids are potential cancer drugs that bind to tubulin proteins to prevent their polymerization into microtubules.

The photomicrograph shows cells in different phases of mitosis.



In a population of cancer cells that have been treated with vinca alkaloids, which stage(s) of mitosis will the majority of cells be at?

A. 1 only **B.** 2 only **C.** 2 and 3 **D.** 4 only

Explanation

- Formation of microtubules are required to move the chromosomes to the metaphase plate through a 'tug-of-war' pulling forces from the opposite poles.
- Cells will hence be arrested at prophase (cannot proceed on to metaphase and beyond).

[DNA Rep & Gene Exp 1/2, KU-2]

11. Which enzymes are involved in the replication of DNA in bacterial cells?

1. DNA-dependent DNA polymerase
2. RNA-dependent DNA polymerase
3. DNA-dependent RNA polymerase
4. RNA-dependent RNA polymerase

A. 1 only **B.** 1 and 3 only **C.** 3 and 4 only **D.** 1, 2, 3 and 4

Explanation

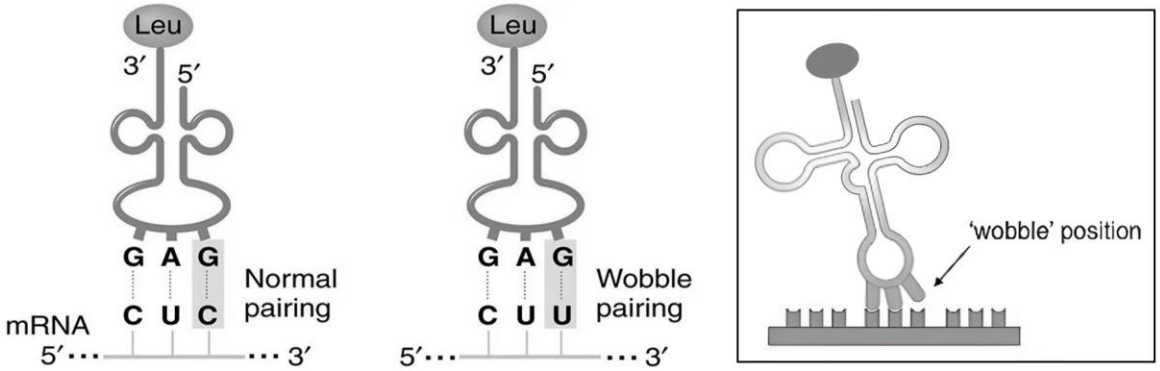
- DDDP = DNA polymerase III and DNA polymerase I
- DDRP = RNA primase (synthesizes the RNA primer using DNA as the template)

[DNA Rep & Gene Exp 2/2, HI-3]

12. In 1966, Francis Crick proposed the Wobble Hypothesis. According to this widely proven hypothesis, only the first two bases of the codon undergo precise pairing with the bases of the anticodon of tRNA, while the pairing between the third bases of codon and anticodon may wobble (to sway or move unsteadily).

For example, both the codons CUC and CUU code for the amino acid leucine. The same tRNA with the anticodon GAG can bind to both codons.

The diagram below illustrates the Wobble Hypothesis.



How many of the following statements can be concluded regarding the Wobble Hypothesis?

- It may allow the same amino acid to be coded for despite a mutation that changes the third nucleotide of a codon.
- It reduces the number of different tRNA molecules needed for translation.
- Some tRNAs can bind to stop codons (UAG, UAA or UGA) to terminate translation.
- Some codons may act as the start codon.
- It contributes to the degeneracy of the genetic code.

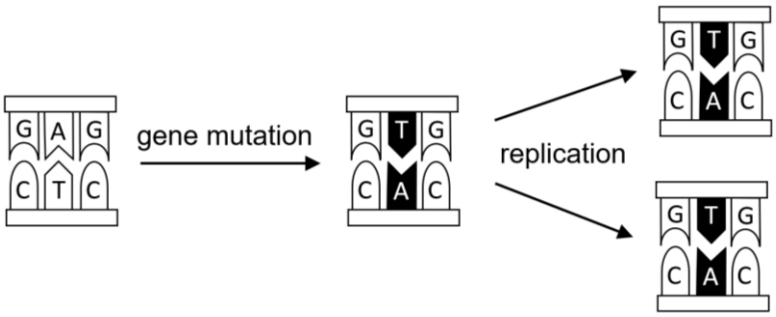
A. 2 **B.** 3 **C.** 4 **D.** 5

Explanation

- Statement 3 (incorrect): Only release factors (proteins) can bind to the stop codon.
- Statement 4 (incorrect): The only start codon is AUG, which binds to tRNA with the anticodon UAC. If AUU, AUC, AUA can act as the start codon, that would lead to many abnormal/nonfunctional proteins.

[Mutation & Conseq 1/1, KU-2]

13. DNA mutation is defined as a change in base pair(s) in DNA and can be inherited by the next generation of cells. The β-globin gene mutation that causes sickle cell anaemia is illustrated below.



Which of the following is correct about gene mutations?

A. Gene mutations can be repaired by DNA repair enzymes.

B. Some antibiotics bind to the 30S ribosome and cause a base on a normal mRNA to be not read during translation, leading to a frameshift mutation.

C. A gene mutation that occurs on the stop codon of DNA can lead to an abnormally short polypeptide.

D. A gene mutation on the promoter sequence can result in either under-expression or over-expression of the gene.

Explanation

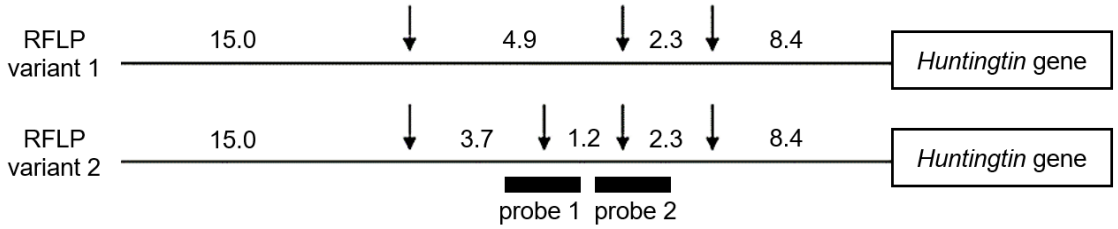
1. Gene mutation follows the complementary base pairing rule. DNA repair enzymes only repair base mismatches, base damage, or DNA lesions (e.g. thymine dimers).
2. The mRNA being synthesized is normal, which means that the gene is normal. The shift in reading frame is due to the effect of kanamycin at the translational level.
3. Abnormally long polypeptide, since the ribosome will translate past the abolished stop codon as a result of the mutation (e.g. UAA becomes UAU).
4. Mutations on the promoter can either decrease or increase the binding affinity of transcription factors / RNA polymerase, resulting in under-expression or overexpression, respectively.

[Molecular Techniques 1/1, HI-2]

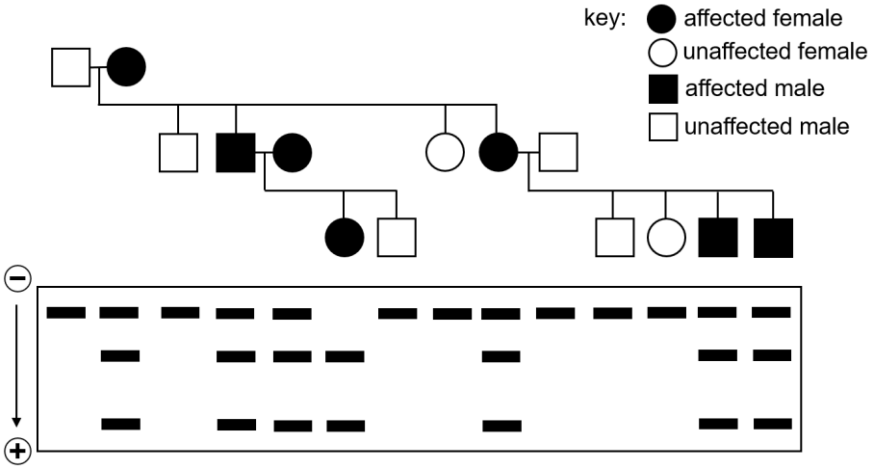
14. Restriction fragment length polymorphism (RFLP) refers to differences among people in their DNA sequences at sites recognized by restriction enzymes. Such differences result in different lengths of DNA fragments produced when digested with a restriction enzyme.

An RFLP variant is found to be tightly linked to the mutated *Huntingtin* allele that causes Huntington's disease, an autosomal dominant disease. This RFLP variant can be used to detect the presence of the mutated allele after digestion with *Hind*III restriction enzyme.

One of the two probes shown below can be used to detect the presence of the mutated *Huntingtin* allele. The arrows represent *Hind*III restriction sequence. The numbers represent the length of the restriction fragments in kilobase pairs.



A family is screened for the presence of the mutated *Huntingtin* allele. The Southern blotting results are shown below.



Which RFLP variant is associated with Huntington's disease and which probe is used?

	RFLP variant associated with Huntington's disease	probe used
A.	RFLP variant 1	probe 1
B.	RFLP variant 1	probe 2
C.	RFLP variant 2	probe 1
D.	RFLP variant 2	probe 2

Explanation

- If probe 2 is used, unaffected individuals would have produced 2 bands (4.9 kbp and 2.3 kbp), since probe 2 can bind partially to these two fragments. Hence, probe 1 is used.
- RFLP variant 2 is tightly linked to the mutant allele, since probe 1 detects only one band on unaffected individuals. If it is RFLP variant 1, probe 1 would have detected two bands on unaffected individuals.

[OCGE in Euk 1/3, KU-1]

15. The following statements are about eukaryotic control elements:

1. Attachment of RNA polymerase at the TATA box is facilitated by a group of specific transcription factors.
2. General transcription factors and specific transcription factors contain DNA-binding sites that comprise different nucleotide sequences.
3. The control elements of a gene are more easily accessible when the surrounding histones are acetylated.
4. Proteins known as silencers bind to DNA sequences known as repressors to downregulate transcription.

Which of the above statements are true?

A. 3 only **B.** 1 and 2 **C.** 3 and 4 only **D.** 2, 3 and 4

Explanation:

A. Incorrect: attachment of RNA Pol II involves **general** transcription factors instead.
B. Incorrect: transcription factors are made of proteins and not DNA. Hence, these transcription factors have DNA-binding sites that comprise different **amino acid** sequences.
C. Correct: acetylation removes positive charges of lysine and arginine on histone N-terminal tails, hence disrupting the ionic bonds that keep DNA tightly interacted with histones. Such loosening enables that access of transcription factors and/or RNA polymerase to the control elements.
D. Incorrect: **Silencers are DNA**. **Repressors are protein**.

[OCGE in Euk 2/3, KU-1]

16. Non-coding sequences make up a significant portion of mammalian DNA. Estimates suggest that about 98% of the human genome consists of non-coding DNA.

How many of the following are non-coding DNA?

- centrosome
- telomerase
- introns
- poly(A) tail
- enhancer

A. 2 **B.** 3 **C.** 4 **D.** 5

Explanation:

- A centrosome is a protein-rich region comprising a pair of centrioles, and is found at the two poles of a cell during cell division. **Centromere** is a non-coding DNA.
- Telomerase is an enzyme comprising of protein and RNA. **Telomere** is a non-coding DNA.
- A eukaryotic gene comprises exons that are interspersed by introns. While introns are transcribed together with exons, the introns on the mRNA are removed post-transcriptionally.
- Poly(A) tail is found on the 3' end of mature mRNA.
- Enhancer is a non-coding DNA that binds to activator proteins to upregulate transcription.

[OCGE in Euk 3/3, KU-1]

17. It has been found that stem cells transferred from the intestinal lining to the bone marrow are sometimes able to produce all of the different types of blood cells instead of intestinal cells.

Which statement explains this?

A. Intestinal stem cells are totipotent.

B. Interaction with cells and molecules in the bone marrow changes the DNA methylation pattern of intestinal stem cells.

C. Genes that are specific to intestinal functions are excised by restriction endonucleases.

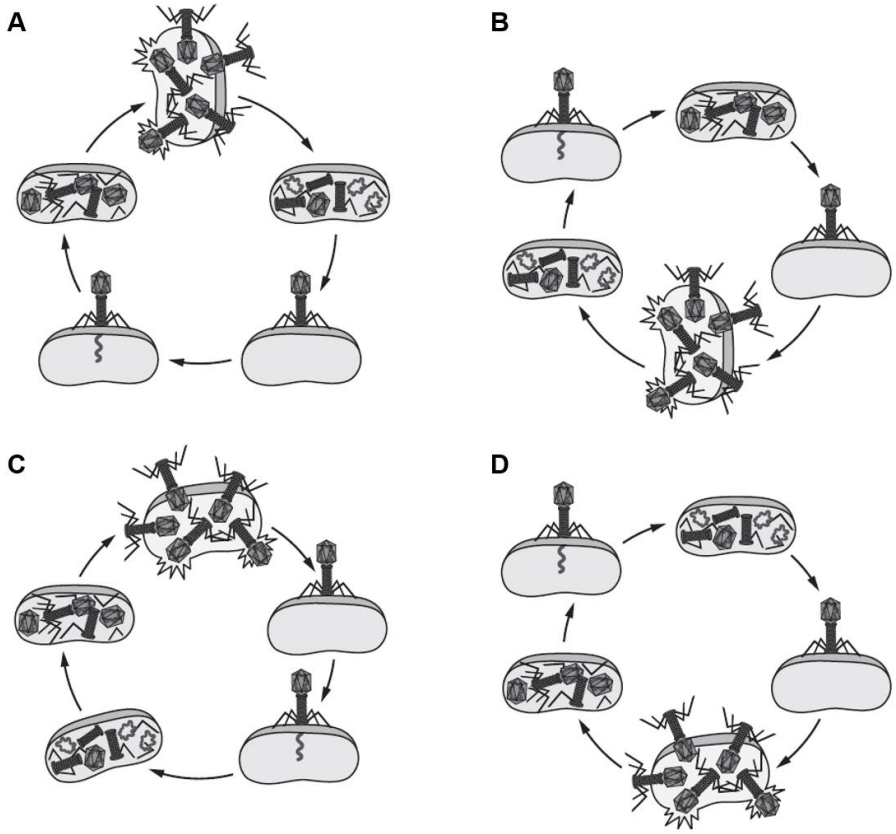
D. Intestinal stem cells undergo reprogramming to become induced pluripotent stem cells.

Explanation:

- Adult stem cells sometimes exhibit plasticity.
- Interaction with specialized cells and molecules of another tissue/organ type can change the cell signalling pathways of the stem cell, leading to the methylation and demethylation of specific genes.
- This allows the stem cell to differentiate into other cell types that it does not usually become.

[Viruses 1/1, KU-1]

18. Which sequence represents the order of stages in the reproductive cycle of a lytic bacteriophage? **ANSWER: (C)**



Explanation:

- Attachment → injection of DNA → synthesis of viral proteins and DNA → assembly → release

[OCGE in Prok 1/2, KU-1]

19. A culture of *Escherichia coli* bacterial cells that contained an F plasmid conferring resistance to the antibiotic ampicillin was grown for several generations in nutrient broth containing ampicillin.

A small volume of this culture of *E. coli* cells was then inoculated into a large volume of sterile nutrient broth, containing all of the requirements for optimal bacterial growth and without ampicillin. After incubating at 37°C for several hours, the number of bacterial cells present had increased by a factor of more than 4,000. Most, but not all, of these cells were found to be ampicillin resistant when tested.

Which method of gene transfer from one bacterial cell to another is responsible for the large increase in the number of bacterial cells that were resistant to ampicillin?

A. binary fission

B. conjugation

C. transduction

D. transformation

Explanation:

- *E. coli* divides by binary fission once every 20 minutes. There are three 20-min in one hour.
- Assuming the initial small volume of bacterial cells contains 5,000 cells, and the incubation time was 4 hours, there will be 5,000 x 2^{12} = 20.48 million.
- 20.48 million ÷ 5000 = 4,096 fold increase.

[OCGE in Prok 2/2, HI-1]

20. What do the *lac* operon and the *trp* operon have in common?

A. Both are regulated by a regulatory gene, whose product is an active repressor that binds to the operator to switch off the expression of the structural genes.

B. Their structural genes code for proteins and enzymes involved in the same metabolic pathway that synthesizes an essential metabolite.

C. Both are subject to feedback inhibition, where the end product of the metabolic pathway act as an allosteric activator to the inactive repressor protein that switches off the expression of the structural genes.

D. Both contain multiple structural genes that are under the control of a single promoter and a single operator, hence are transcribed together as a single mRNA molecule.

Explanation:

A. The *lacI* regulatory gene codes for an **active repressor**, while the *trpR* regulatory gene codes for an **inactive repressor**.

B. This is true only for *trp* operon. The *lac* structural genes codes for proteins and enzymes in the same metabolic pathway that **breaks down lactose**.

C. This is true only for *trp* operon. Once sufficient tryptophan is synthesized, they bind to the inactive repressor to activate it, which then binds to the operator to shut down the *trp* operon.

[Inheritance 1/3, HI-2]

21. In humans, a gene on chromosome 19 is responsible for the synthesis of a glycolipid found in red blood cell surface membranes. This glycolipid is known as antigen H. The gene has two alleles, H and h. The product of allele h is non-functional.

A second gene on chromosome 9 codes for an enzyme that modifies antigen H. There are three alleles of this gene:

- I^A which results in the conversion of antigen H to antigen A
- I^B which results in the conversion of antigen H to antigen B
- I^O which does not produce a functional product so does not modify antigen H.

Two parents, who are both blood group AB, have a son who is blood group O.

Which phenomena are illustrated by the above descriptions?

1. multiple alleles
2. epistasis
3. codominance
4. dihybrid inheritance

A. 1 and 3 only **B.** 2 and 4 only **C.** 1, 3 and 4 only **D.** 1, 2, 3 and 4

Explanation

1. The ABO blood group has three alleles. **Multiple alleles** = more than 2 alleles.
2. Both parents' genotype is HhI^AI^B. Their son's genotype is hhI^AI^B or hhI^BI^B or hhI^AI^B. Since antigen H is needed for conversion to antigen A or antigen B, this is a case of **recessive epistasis**, where the genotype hh masks the effect of allele I^A or allele I^B.
3. Allele I^A and allele I^B are equally expressed (**codominant**) in both parents (who are blood group AB).
4. Both parents' genotype is HhI^AI^B. This is a case of **dihybrid inheritance**, where both parents are heterozygous at both gene loci.

[Inheritance 2/3, HI-3]

22. In *Primula*, the dominant allele A of a gene for anthocyanin pigment production gives magenta-coloured flowers. The recessive allele a gives yellow-coloured flowers.

The dominant allele B of another unlinked gene inhibits the effect of allele A, while the recessive allele b has no effect.

Plants in which allele A is inhibited by allele B have yellow flowers.

A yellow-flowered plant is known to be homozygous recessive at the A/a locus. The genotype at the B/b locus is unknown.

A cross with a plant of known genotype is performed to reveal the genotype of this yellow-flowered plant.

Which of the following plant genotypes will reveal the genotype of the yellow-flowered plant?

A. aabb **B.** AABB **C.** AAbb **D.** aaBB

Explanation:

- magenta = A−bb yellow = A−B− yellow = aa−−
- The genotype of the yellow flowered plant must be either aaBB, aaBb or aabb

A. If aabb is used:
- aaBB x aabb → aaBb → all yellow
- aaBb x aabb → 1 aaBb, 1 aabb → all yellow
- aabb x aabb → aabb → all yellow

B. If AABB is used:
- aaBB x AABB → AaBB → all yellow
- aaBb x AABB → 1 AaBB, 1 AaBb → all yellow
- aabb x AABB → AaBb → all yellow

C. If AAbb is used:
- aaBB x AAbb → AaBb → all yellow
- aaBb x AAbb → 1 AaBb (yellow), 1 Aabb (magenta)
- aabb x AAbb → Aabb → all magenta

D. If aaBB is used:
- aaBB x aaBB → aaBB → all yellow
- aaBb x aaBB → 1 aaBB, 1 aaBb → all yellow
- aabb x aaBB → aaBb → all yellow

[Inheritance 3/3, KU-3]

23. There are two hypotheses to explain the production of white, pale pink or dark pink flowers in a species of plant.

hypothesis 1: There are two codominant alleles.

hypothesis 2: There are three alleles, one for each flower colour.

Which approach is the best way to test these hypotheses?

A. Analysis of the flower pigments in several different flowers by chromatography to find whether some plants contain more than one pigment.

B. Controlled cross-pollination of all the different colour varieties available, in all possible combinations, and recording the colours shown by the offspring.

C. Controlled self-pollination of several individuals of each of the colour varieties and recording the colours shown by the offspring of each individual plant sampled.

D. Surveying large wild populations and finding the ratios of the different colours in these.

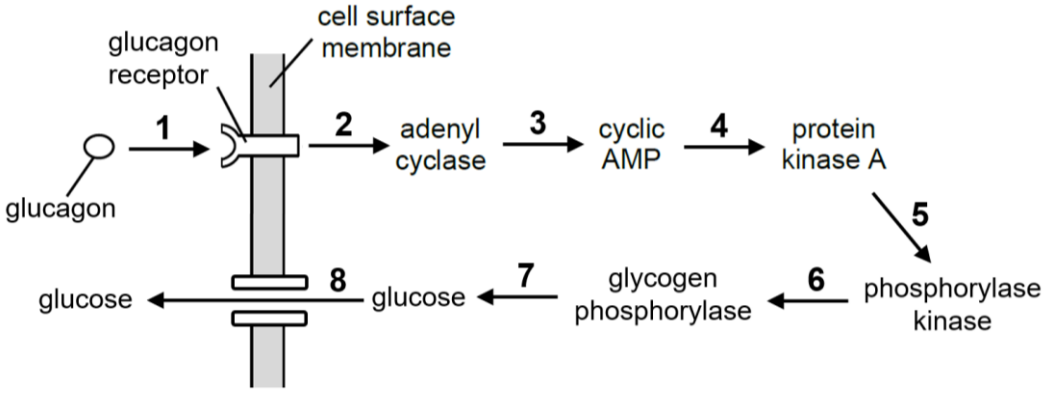
Explanation:

- Option A: number of pigments identified does not show reflect the types of inheritance.
- Option B: cross pollination will give rise to different possibilities and is difficult to make conclusions.
- Option D: inconclusive as there's no fixed parental cross. Hence ratios of wild population sampled may be skewed.
- Option C can be used:

If hypothesis 1 is true:	**If hypothesis 2 is true**, the 3 alleles will have different level of dominance: dark (C^A) **>** pale (C^B) **>** white (C^C)
Selfing dark pink: C^AC^A x C^AC^A → all dark pink	Selfing dark pink: C^AC^A x C^AC^A → all dark pink C^AC^B x C^AC^B → 3 dark : 1 pale C^AC^C x C^AC^C → 3 dark : 1 white
Selfing pale pink: C^AC^B x C^AC^B → 1 dark : 2 pale : 1 white	Selfing pale pink: C^BC^C x C^BC^C → 3 pale : 1 white
Selfing white: C^BC^B x C^BC^B → all white	Selfing white: C^BC^B x C^BC^B → all white

[Communication 1/1, KU-2]

24. The diagram shows several steps during glucagon signalling in a liver cell.



Which row correctly identifies the numbered steps?

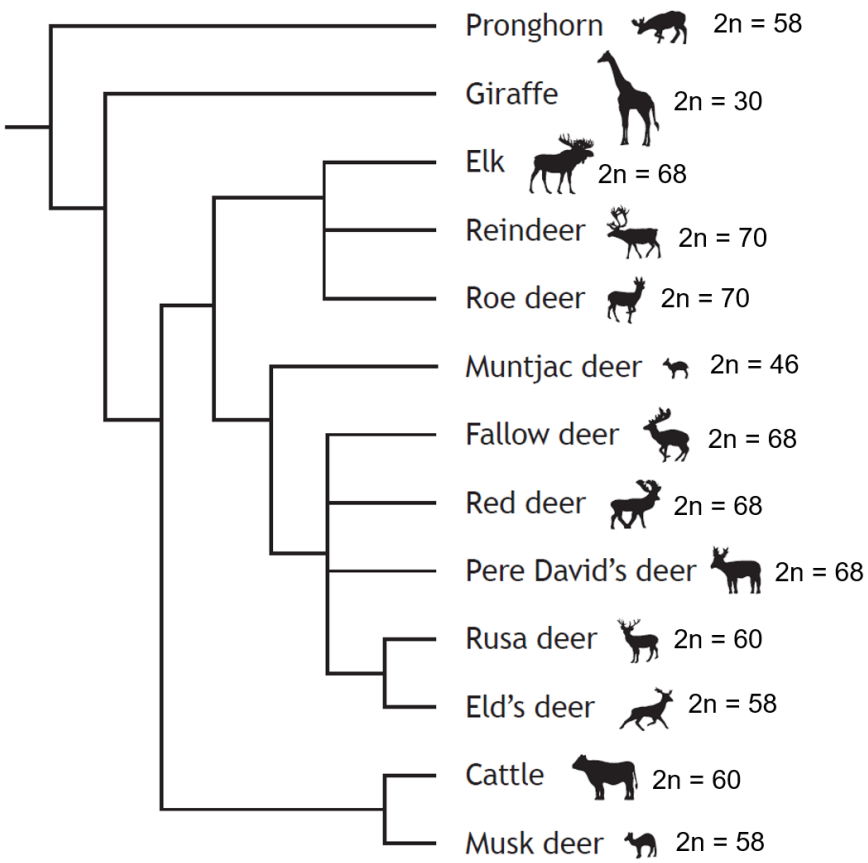
	signal amplification	enzyme activation	facilitated diffusion	hydrolysis
A.	3, 4, 5, 6	1, 2, 4, 5, 6	8	7, 8
B.	3, 5, 6	2, 4, 5, 6	8	7
C.	3, 4, 5, 6	1, 2, 4, 5, 6	1, 8	7, 8
D.	3, 5, 6	2, 4, 5, 6	1, 8	7

Explanation:

- Signal amplification:
  - One adenyl cyclase can catalyze the formation of many cAMP.
  - One protein kinase A can phosphorylate and activate many phosphorylase kinase.
  - One phosphorylase kinase can phosphorylate and activate many glycogen phosphorylase.
- Enzyme activation:
  - Adenyl cyclase is activated by the receptor via activation of G protein (not shown).
  - PKA is activated by the binding of cAMP.
  - Phosphorylase kinase is phosphorylated and activated by PKA.
  - Glycogen phosphorylase is phosphorylated and activated by phosphorylase kinase.
- Facilitated diffusion:
  - Glycogen breakdown by glycogen phosphorylase results in an increase in cytosolic glucose, which then diffuse out of the cell via glucose transporter.
- Hydrolysis:
  - Breakdown of glycogen to glucose involves hydrolysis of glycosidic bonds.

[Evolution 1/3, HI-2]

25. The figure is a phylogenetic tree showing the evolutionary history and relationships of a number of mammalian species. Their diploid numbers are also shown.



What conclusion can be drawn from the phylogenetic tree?

A. Diploid number is a good indicator of evolutionary relationships.

B. Red deer are more closely related to reindeer than elk.

C. Cattle are closer relatives of fallow deer than giraffes.

D. Pere David's deer and red deer have evolved at the same rate.

Explanation

A. The diploid number of musk deer and pronghorn are both 58, yet they are distantly related.
B. Red deer are equally closely related to reindeer and elk.
C. Cattle share a more recent common ancestor with fallow deer than with elk.
D. Even though Pere David's deer and red deer (and fallow deer) share a most recent common ancestor, it does not mean they have evolved at the same rate. In the context of molecular evolution, "evolving at the same rate" implies that mutations occur at a constant rate for both Pere David's deer and red deer, which is not true. They accumulate mutations at different rate.

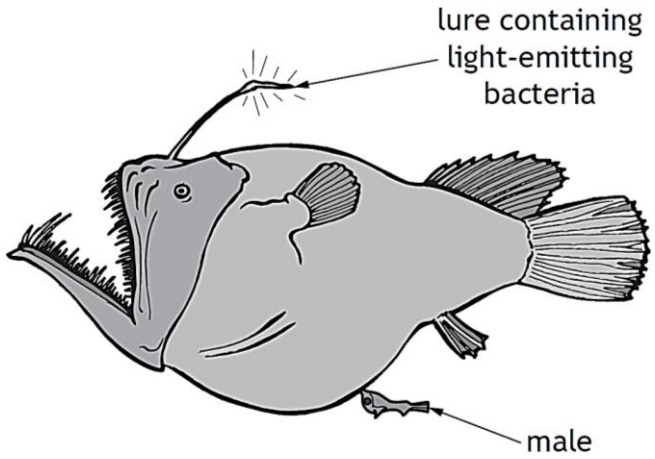
[Evolution 2/3, HI-2]

26. The diagram shows the triplewart seadevil, *Cryptopsaras couesii*, a deep-sea anglerfish that lives over 1000 m below sea level in total darkness.

Two striking evolutionary features of the anglerfish are:

- Females possess a glowing lure that attracts prey as well as mates. The light from inside the lure is made by light-emitting bacteria that live in extracellular skin grooves of the fish lure. The light-emitting lure bacteria have lost most of the genes associated with synthesising amino acids and breaking down nutrients.

- Males are at least ten times smaller than females and have an underdeveloped digestive system. Males lack jaws strong enough to catch prey. When a male finds a female, he bites into her skin and releases an enzyme that digests the skin of his mouth and her body, fusing the pair down to blood vessel level. This attached male is then available to fertilise eggs when the female releases them.



What terms could be used to describe
- the relationship between the female and the light-emitting bacteria
- the relationship of the male to the female?

	relationship between the female and the light-emitting bacteria	relationship of the male to the female
A.	predatory	parasitic
B.	symbiotic	predatory
C.	parasitic	symbiotic
D.	symbiotic	parasitic

Explanation
- Between the female and the light-emitting bacteria:
  - ❑ Bacteria gains nutrients from the female.
  - ❑ The female gains a light source to attract preys and mates.
- Of the male to the female:
  - ❑ The male absorbs nutrients from the female, hence the male is parasitic to the female.
  - ❑ However, parasitism is not entirely accurate, since both are the same species and both benefit from the availability of mates.

[Evolution 3/3, HI-3]

27. Hardy-Weinberg equilibrium is a principle in population genetics that states that allele and genotype frequencies in a population will remain constant from generation to generation in the absence of evolutionary forces such as mutation, genetic drift, gene flow, and natural selection.

The key assumptions of Hardy-Weinberg equilibrium include a large population size, random mating, no mutation, no gene flow, and no natural selection.

The equations used to describe Hardy-Weinberg equilibrium are:

$$p + q = 1$$

$$p^2 + 2pq + q^2 = 1$$

- p represents the frequency of the dominant allele in the population.
- q represents the frequency of the recessive allele in the population.
- p^2 represents the frequency of the homozygous dominant genotype.
- q^2 represents the frequency of the homozygous recessive genotype.
- 2pq represents the frequency of the heterozygous genotype.

In humans, the allele (T) for the ability to taste the bitter chemical phenylthiocarbamide is dominant over the allele (t) for the inability to taste the chemical.

400 biology students were tested and 64 were found to be non-tasters.

What percentage of students are heterozygous?

A. 16% **B.** 27% **C.** 32% **D.** 48%

Explanation

- 64 students are homozygous recessive tt (non-tasters).
- Proportion of non-taster = 64 ÷ 400 = 0.16 = q^2
- Hence, q = 0.4 (square-root of 0.16)
- Hence, p = 1 – q = 1 – 0.4 = 0.6
- Hence, proportion of heterozygote = 2pq = 2 × 0.4 × 0.6 = 0.48 = 48%

[Immunity 1/2, HI-2]

28. Some animals have genes that code for small peptides called cathelicidins. These peptides kill a wide range of bacteria by attaching to lipids in bacterial membranes, hence weakening or disrupting them.

Scientists have produced a synthetic version of the cathelicidin that kills bacteria that are resistant to a number of antibiotics such as tetracycline.

Which pair of statements explains how this synthetic cathelicidin might help with the problem of antibiotic resistance?

1. Cathelicidin is synthetic so bacteria can never become resistant to it.
2. Cathelicidin could be used instead of tetracycline, allowing tetracycline resistance to be reduced.
3. The only way a bacterium could develop resistance to cathelicidin is by altering all the lipids in its membranes.
4. Cathelicidin could be used to kill multidrug-resistant strains of bacteria for which there is no effective antibiotic.

A. 1 and 3 **B.** 1 and 4 **C.** 2 and 3 **D.** 2 and 4

Explanation

1. Synthetic version is still a polypeptide. Bacteria can still gain resistance.
2. By replacing tetracycline with cathelicidins, bacteria that are resistant to tetracycline will not be selected for, and non-resistant bacteria can continue to divide. The proportion of tetracycline-resistant bacteria hence is reduced.
3. Bacteria gain resistance to drugs as a result of random mutations that create new alleles that code for proteins/enzymes/transporters that renders that drug ineffective. While mutations could have resulted in some bacteria being able to synthesize enzymes that modify their lipids, it is not the only way to develop resistance. For example, some mutations could confer the bacteria the ability to secrete certain enzymes that break down cathelicidin.
4. Since cathelicidin is a new drug, many bacteria would be sensitive to it. Hence, cathelicidin can be used to kill off bacteria which have developed resistance to many different antibiotics.

[Immunity 2/2, KU-2]

29. A successful vaccination programme provides a level of immunity where the majority of a population is protected.

There are several factors that can hinder the success of a vaccination programme.

Which row correctly shows the factors that can hinder the success of a vaccination programme?

	frequent mutation of the pathogen	vaccination from eight weeks old	pathogen is able to invade T-cells	booster vaccinations needed frequently
A.	✓	✓	✗	✓
B.	✓	✗	✓	✓
C.	✗	✓	✓	✗
D.	✓	✗	✓	✗

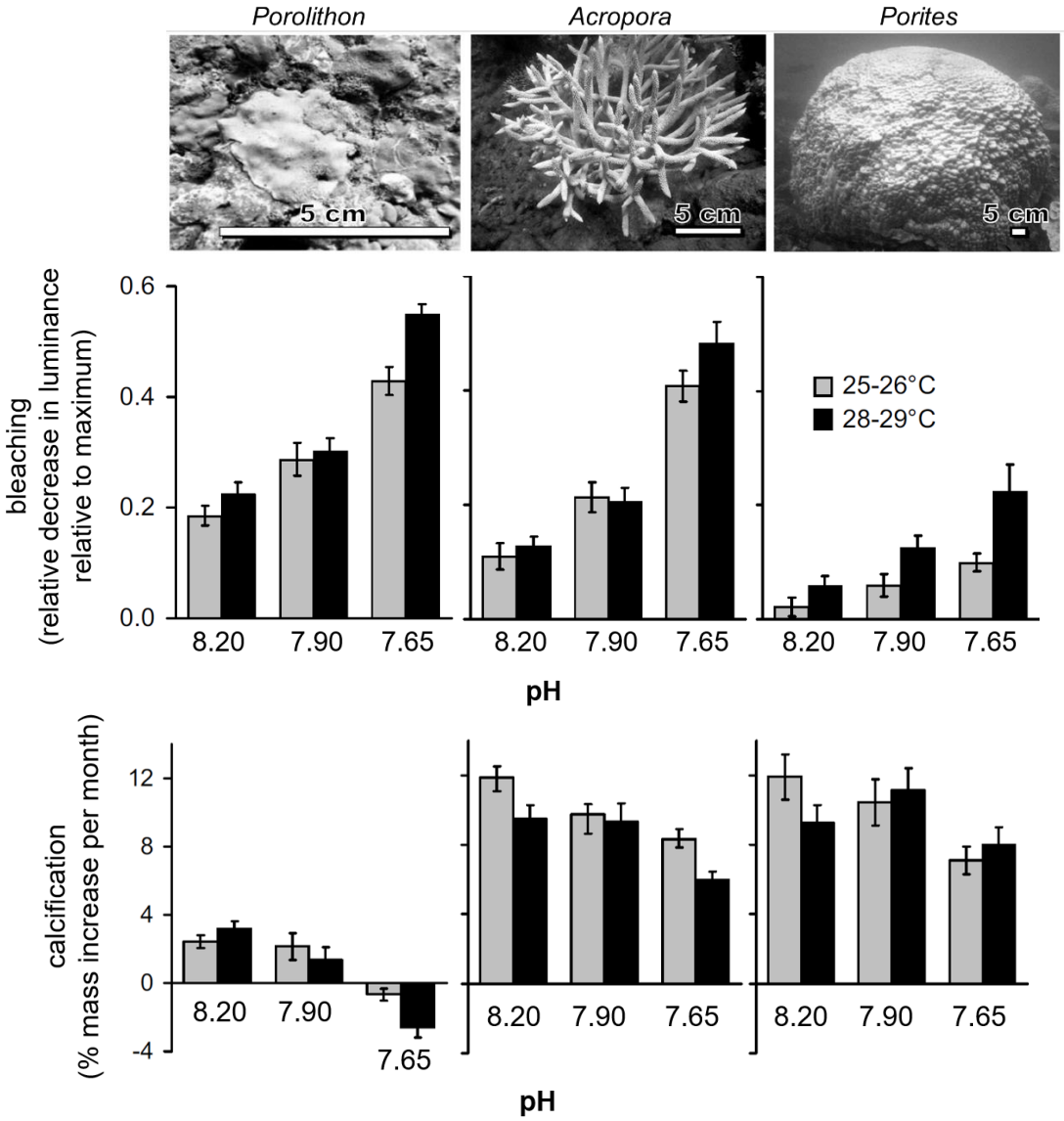
key: ✓ = hinders, ✗ = does not hinder

Explanation

- Frequent mutation of the pathogen can change their antigen conformation, which are no longer recognized by the antibodies raised from the previous vaccine.
- Vaccination from eight weeks old will allow majority of population to achieve immunity, which can also lead to herd immunity. This increases the success of a vaccination programme.
- If the pathogen invades T-cells (e.g. helper T cells), it may reduce the body's ability to produce antibodies, since the activation of B cells requires helper T cell.
- It may be difficult to get the individuals in a population to return multiple times for booster shots (e.g. inconvenience, accessibility, time, cost etc.)

[Climate Change 1/1, HI-3]

30. An 8-week study was conducted in 2007 in Heron Island (Southern Great Barrier Reef, Australia) to compare bleaching and calcification in three species of coral (*Porolithon*, *Acropora* and *Porites*) in response to ocean acidification and ocean warming.



What can be concluded from the study?

1. In *Porolithon* and *Acropora*, the effect of acidification on bleaching is stronger than the effect of warming. In *Porites*, the effect of acidification and warming are equally strong.
2. Warming amplifies acidification-induced bleaching in *Porites* more strongly than it does on *Porolithon* and *Acropora*.
3. Compared to *Acropora* and *Porites*, *Porolithon* calcification is highly sensitive to the highest acidity, but the effect was reversed by warming.
4. Calcification in *Porites* in response to acidification is similar to that in *Acropora*, but calcification in *Porites* did not show a clear response to warming.

A. 1 and 2 only **B.** 3 and 4 only **C.** 1, 2 and 4 only **D.** 1, 2, 3 and 4

☺ End of Paper 1 ☺