NAME : ______________________ CLASS : ______________________

JURONG PIONEER JUNIOR COLLEGE
JC2 Preliminary Examinations 2023

BIOLOGY
Higher 2

9744/03
18 September 2023

Paper 3 Long Structured and Free-response Questions

2 hours

Candidates answer on the Question Paper.

Additional Materials: Answer Booklet

READ THESE INSTRUCTIONS FIRST

Write your class and name in the spaces at the top of this page.
Write in dark blue or black pen.
You may use an HB pencil for any diagrams or graphs.
Do not use staples, paper clips, glue or correction fluid.

Section A
Answer **all** questions in the spaces provided on the Question Paper.

Section B
Answer any **one** question on the separate Answer Booklet provided.

The use of an approved scientific calculator is expected, where appropriate.
You may lose marks if you do not show your working or if you do not use appropriate units.

The number of marks is given in brackets [ ] at the end of each question or part question.

For Examiner's Use	
1	
2	
3	
Section B	
Total	

This document consists of **20** printed pages.

[Turn over

Section A

Answer **all** the questions in this section.

1 Reindeer are semi-domesticated ruminants that have adapted to challenging environment characterised by long winters and marked annual fluctuations in daylight. Comparative genome analyses revealed several genes that may have promoted the adaptation of reindeer, such as those involved in vitamin D metabolism (*POR*), circadian rhythm (*GR1A1*), and tolerance to cold-triggered pain (*SCN11A1*).

(a) A study was carried out to examine the gene involved in vitamin D metabolism (*POR*) and the POR enzyme, which is an important enzyme in the vitamin D metabolic pathway. Vitamin D is made in the skin under the influence of UV light and is important in promoting calcium absorption and the mineralisation of bone for the rapid and robust growth of the antlers, which are important for various aspects of reindeer behaviour and reproductive success.

Samples were taken from the reindeer, as well as roe deer and goats to examine for POR enzyme activity in a reconstituted system consisting of the enzyme and substrate.

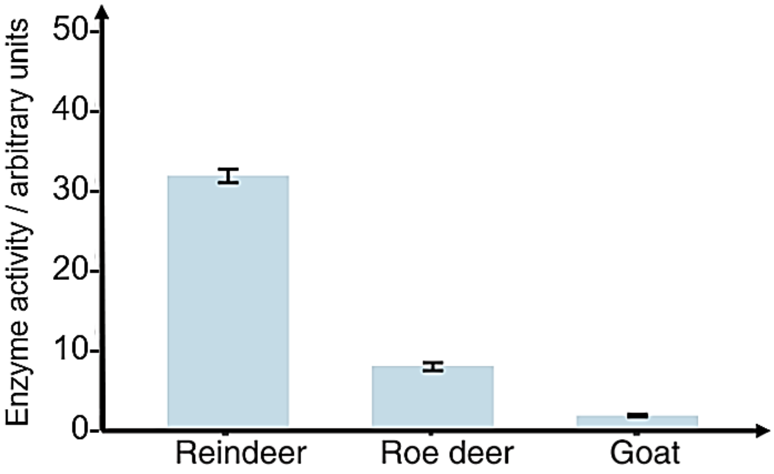

Fig. 1.1

With reference to Fig. 1.1, suggest how reindeer are able to produce sufficient vitamin D for their antler growth despite long winters with low amount of sunlight.

....[2]

1. **Reindeer has high enzyme activity of 32 arbitrary units, (25 a.u. more than roe deer, 30 a.u. more than goat) ;**
2. **Idea of reindeer has evolved / adapted +**
   - **(a) efficient vitamin D metabolism pathway /**
   - **(b) enzymes with high catalytic activity to <u>maximise</u> (OWTTE) the amount of vitamin D produced /**
   - **(c) procure/obtain <u>high</u> (OWTTE) levels of vitamin D with low levels of sunlight ;**

(b) The reindeer do not exhibit 24-hour activity rhythms, and evidence suggests absent circadian activity, which is a useful adaptation in Arctic conditions.

Explain how DNA methylation and histone modification had altered the gene expression of *GR1A1*.

....[4]

DNA methylation [2]

1. **physically blocks the binding of general transcription factors (GTFs) / RNA polymerase to the promoter of *GR1A1* ;**
2. **preventing formation of the transcription initiation complex, preventing transcription of *GR1A1* ;**
   OR
3. **leads to recruitment of transcriptional repressors / histone deacetylases / other repressive chromatin remodelling complexes, resulting in more compact chromatin and tighter nucleosomes / DNA more tightly coiled around nucleosomes, preventing transcription of *GR1A1*;**

histone modification [2]

4. **Histone deacetylation results in DNA winding more tightly around the nucleosomes / the chromatin condenses ;**
5. **GTFs and RNA polymerase are unable to recognise and bind to the promoter (of *GR1A1*), preventing formation of the transcription initiation complex, preventing transcription of *GR1A1* ;**

Two subspecies of reindeer, *Rangifer tarandus*, live in North America. Members of the different subspecies belong to the same species but have some morphological differences and are found in different geographical locations.

Table 1.1 compares the features of the two North American reindeer subspecies.

Table 1.1

feature	woodland subspecies, *R. tarandus caribou*	barren ground subspecies, *R. tarandus groenlandicus*
habitat	southern woodland (warmer)	northern tundra (colder)
type of food	tree leaves, grass	lichens, moss
summer and winter feeding grounds overlap	yes	no
carry out long migrations	no	yes
body size	large	small
colour of fur	dark	light

(c) During the last ice age, an ice sheet separated southern and northern populations of *R. tarandus* to result in the two different subspecies.

Explain how this ice sheet affected the evolution of *R. tarandus* to result in the two different subspecies.

....[4]

Selection

1. **The (sub)populations were exposed to <u>different environments</u> and were thus subjected to <u>different selection pressures</u> e.g. environment / habitat / climate / food / vegetation ;**
2. **Since there was <u>variation within the (sub-)populations</u> due to different mutations, <u>individuals with favourable characteristics were at a selective advantage (or vice versa)</u> and <u>evolutionary changes/changes in allele frequency</u> occurred <u>independently</u> in each (sub)population ;**
3. **Giving rise to morphological / ecological / behavioural differences ;**

Isolation

4. **The (sub)populations become <u>geographically isolated</u> leading to allopatric speciation ;**
5. **The (sub)<u>populations</u> <u>did not interbreed</u> (reproductive isolation) and thus <u>gene flow was disrupted</u> between populations (resulting in different subspecies) ;**

(d) Assess the relative importance of natural selection and genetic drift in producing:

(i) the different colours of fur of the two subspecies of reindeer

....[2]

1. **natural selection was more important than genetic drift ;**
2. **reindeer with dark colour / fur was selected for in the woods / warm / shade ; OR**
3. **reindeer with light colour / fur was selected for in the barren ground / cold / tundra;**
4. **act as camouflage to protect against (named) predators ;**

(ii) the different body sizes of the two subspecies of reindeer.

....[2]

1. **genetic drift was more important than natural selection ;**
2. **as small size in north was not adaptive / beneficial ;**
3. **small animals lose heat faster / harder to keep warm ;**
4. **Smaller fat reserves are unfavourable with unstable food supply ;**
5. **Different body sizes are due to food shortage in the tundra and plentiful food supply in the south ;**

(e) Hybridisation has occurred between individuals of the two subspecies which now live in the area previously covered by the ice sheet.

Comment on how the hybrid populations compare to the pure subspecies in terms of genetic variation and potential to adapt to climate change.

....[4]

1. **Hybrid populations have more genetic variation / alleles ;**
2. **As the gene pool contains genes / alleles from both (sub)species ;**
3. **More potential to adapt / can adapt better to climate change (in future) ;**
4. **Genes / alleles for migration may let some individuals find new habitats ;**
5. **They may have genes / alleles to allow them to survive in warm and cold / different temperatures ;**

(f) Outline how molecular techniques could be used to test the hypothesis that migratory behaviour in reindeer has a genetic basis.

....[3]

1. **Obtain blood / tissue / DNA from both (sub)species / migratory and non-migratory ;**
2. **Use PCR to amplify the DNA ;**
3. **Use gel electrophoresis / DNA fingerprinting and compare results / to see genetic differences / changes ;**
4. **Compare DNA sequences and count / identify differences / changes ;**
5. **Check / test for correlation between DNA / genetic profiles / alleles and migratory behaviour ;**

(g) Reindeer are currently listed as a vulnerable species by the International Union for Conservation of Nature (IUCN). Over the past 200 years, many species of animals and plants have become extinct.

Fig. 1.2 shows the changes between the years 1800 and 2000 in:

- the number of species becoming extinct
- the size of the world human population.

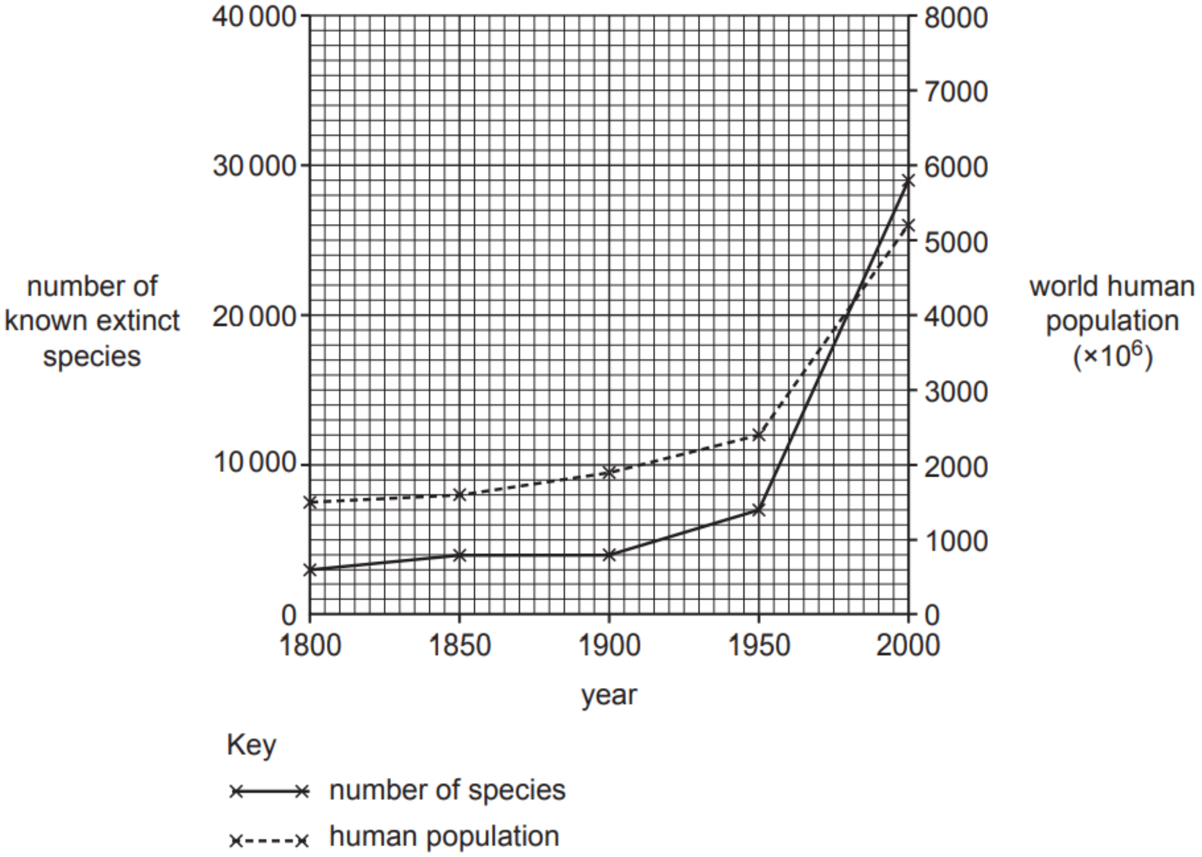

Fig. 1.2

(i) It has been suggested that there is a correlation between the number of species becoming extinct and the size of the world human population.

Suggest reasons for this possible correlation.

....[3]

1. **Deforestation for agriculture / development has led to habitat loss ;**
2. **Burning of fossil fuels linked to increasing energy usage / food choices linked to increasing consumption of meat has resulted in increased greenhouse gas emissions, global warming and thus extinction of species that cannot adapt to the higher temperatures ;**
3. **Due to humans hunting / fishing / collecting plants ;**
4. **Humans aid spread of (animal / plant) disease OR alien / invasive / competing species ;**
5. **Humans cause (named) pollution / use of pesticides ;**

(ii) Calculate the rate of species extinction per year between 1950 and 2000.

Show your working.

1. **Rate of species extinction per year = $\frac{29000 - 7000}{2000-1950}$ or $\frac{29000 - 7000}{50}$;**

2. **440 ;**

answer =………………… species per year [2]

(h) Extinction of animal and plant species reduces biodiversity.

Outline why it is important to maintain biodiversity.

………………………………………………………………………………………………[4]

1. **Maintain rich reservoir for biomedicines ;**
2. **Maintain genetic diversity for food ;**
3. **Maintain / protect food chains / food webs ;**
4. **Source of resources such as wood / fibres / paper / rubber ;**
5. **For science / technology / research / education ;**
6. **For aesthetics / wellbeing / (eco)tourism / attract visitors ;**

[Total: 30]

2 Yeast cells respond to changes in glucose concentration in their environment by using transcription factors to switch off genes.

When glucose is present:

- Mig1 transcription factors bind to the promoters of five genes
- Mig1 binding to the promoters stops transcription of these genes. The genes that are repressed by Mig1 code for five enzymes that allow yeast cells to metabolise the sugar galactose when glucose is absent.

(a) Mig1 binds to Mig1-binding promoter sites with these features:

- 17 base pairs long
- includes a region of five repeating adenine-thymine pairs
- includes a region of six repeating cytosine-guanine pairs.

Bioinformatic techniques were used to analyse the yeast genome to look for sections of DNA that match these features. Bioinformatics involves utilising computer technology to manage biological information. The information obtained for four chromosomes is shown in Table 2.1.

Table. 2.1

yeast chromosome	chromosome size /base pairs	number of Mig1-binding promoter sites per chromosome
A	230018	1
B	813184	10
C	316620	2
D	1531933	14

(i) Suggest why bioinformatic techniques were used to obtain the information in Table 2.1.

.... [1]

1. (because) sequences already known ;
2. (because) large, number of base pairs / quantity of data, to search ;

(ii) Identify, with a reason, the yeast cell chromosome that is most likely to include genes that code for enzymes that metabolise galactose.

.... [1]

1. chromosome D, as it contains the most (possible) Mig1-binding promoter sites ;

(iii) Mig1 binds to 27 promoters on these four chromosomes. Yeast cells also have other chromosomes where Mig1 binds to additional promoters.

Five different enzymes, coded by five genes, must be made for yeast cells to metabolise galactose.

Suggest why a diploid yeast cell has a larger number of Mig1-binding promoter sites than the expected number of ten.

.... [1]

1. **Mig 1 (also) regulates genes involved in other pathways ;**
2. **there could be several copies of these five genes ;**

(b) The repression of genes involved in galactose metabolism in yeast is similar to events at the *lac* operon in the bacterium *Escherichia coli*.

Explain how *E. coli* represses the production of proteins needed to metabolise lactose.

.... [3]

1. **regulatory gene / lacI codes for a lac repressor (which regulates the expression of lacZ, lacY and lacA) ;**
2. **lac repressor is synthesised in its active conformation ;**

3. **Absence of lactose/allolactose is not bound to lac repressor, lac repressor recognises and binds to the operator ;**
4. **the operon is turned off ;**
5. **RNA polymerase is unable to bind to the promoter, and unable to transcribe the (structural) genes of the lac operon ;**
6. **mRNA is not synthesised / β-galactosidase, lac permease and β-galactoside transacetylase are not produced ;**

Pt 1 – 5: max 2

(c) In an investigation into the growth of *E. coli*, a sample of the bacterium was grown in a medium that contained limited concentrations of glucose and lactose. The population size of *E. coli* was measured at regular intervals.

Fig. 2.1 shows the population growth curve obtained for this investigation.

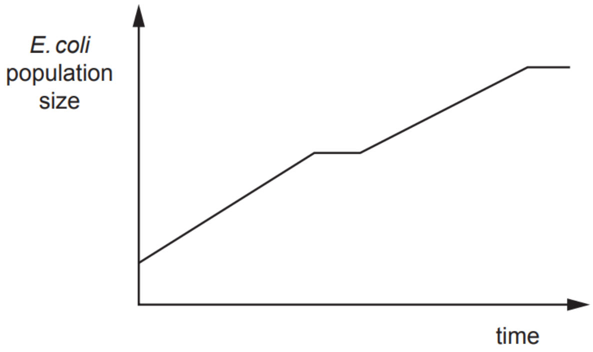

Fig. 2.1

Describe and suggest explanations for the population growth curve shown in Fig. 2.1.

.... [4]

Describe (compulsory)

1 As time increases, the *E.coli* population size increases, then levels off, increases, then levels off / AW ;

Explanation (max 3):

(first increase)

2 glucose, metabolised / respiration, ATP released for binary fission ;

(first levelling off)

3 glucose has run out (OWTTE) ;

4 idea of time delay + any 1 of the following
  - **a) for, expression of structural genes**
  - **b) for, lactose permease / beta galactosidase, to work**
  - **c) for, lactose, hydrolysed / broken down, into, glucose / galactose ;**

(second increase)

5 glucose / galactose, metabolised / respired, ATP released for binary fission (mark once);

(second levelling off)

6 lactose / glucose / galactose, has run out ;

[Total: 10]

3 Fig. 3.1 shows the seaweed *Laminaria hyperborea*. This is a photosynthetic protoctist found in the coastal waters around Norway. The seaweed is grown commercially to obtain the glucose polysaccharide called alginate. This is used in certain food products.

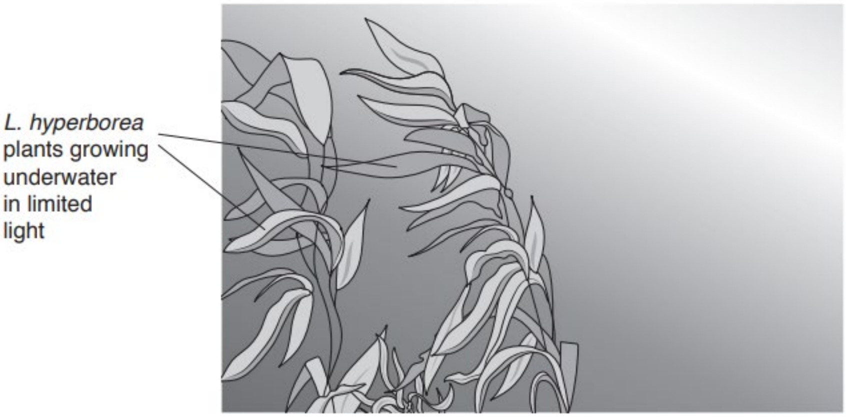

Fig. 3.1

An increase in carbon dioxide concentration in the atmosphere has resulted in higher concentrations of carbon dioxide in the ocean. This has caused a decrease in the pH of the ocean and has resulted in ocean acidification.

Scientists are studying seaweeds such as *L. hyperborea* because they absorb a large quantity of carbon dioxide during photosynthesis. This may help to increase the pH of the ocean and reverse ocean acidification.

(a) Outline the reactions occurring in the stroma that lead to the production of a polysaccharide, such as alginate.

.... [4]

1. **During CO_2 fixation in Calvin cycle, carbon dioxide is fixed by combining with ribulose bisphosphate (RuBP) to form a 6C unstable intermediate, catalysed by rubisco ;**
2. **The 6C unstable intermediate breaks down immediately to form 2 molecules of glycerate phosphate (GP) ;**
3. **The (2 molecules of) GP are phosphorylated by ATP and reduced by NADPH to form triose phosphate (TP) ;**
4. **Some TP (exits the Calvin cycle to) produce glucose, polymerisation / condensation / formation of glycosidic bonds between glucose molecules to form polysaccharide / alginate ;**

(b) Laboratory experiments were carried out to investigate the effect of day length on the rate of photosynthesis in another marine autotroph, *Zostera marina*.

- The temperature was controlled at 4°C.
- A low concentration of carbon dioxide dissolved in the water was used.
- The light exposure period (day length) was different for five groups of *Z. marina*.
- This was maintained for 10 days to allow *Z. marina* to adapt to these conditions.
- After 10 days, the rate of photosynthesis was measured for each group under the same controlled conditions.
- The experiment was repeated using five groups of *Z. marina* with a high concentration of carbon dioxide dissolved in water.

Table 3.1 shows the rate of photosynthesis for each group.

Table 3.1

day length / hours	rate of photosynthesis / arbitrary units	
	low carbon dioxide concentration	high carbon dioxide concentration
12	2.0	2.5
14	3.0	5.0
16	4.0	7.0
18	5.5	11.0
20	7.5	18.0

(i) With reference to Table 3.1, explain the difference in the rate of photosynthesis at high carbon dioxide concentration compared to low carbon dioxide concentration.

.... [3]

1. **Rate of photosynthesis at high carbon dioxide concentration is higher than at low carbon dioxide concentration + data e.g. 18.0 arbitrary units v.s. 7.5 arbitrary units at day length of 20 hours ;**
2. **<u>More</u> carbon dioxide react with RuBP / <u>more</u> CO_2 fixation / <u>more</u> carbon dioxide available to bind to rubisco ;**
3. **<u>More</u> reduction of CO_2 (using ATP and NADPH produced by the light-dependent reactions) to produce sugars , <u>increasing rate</u> of Calvin cycle / light independent reaction ;**

(ii) With reference to Table 3.1, describe and explain the effect of increasing day length on the rate of photosynthesis for the *Z. marina* in high carbon dioxide concentration.

.... [2]

1. **As day length increases from 12 hours to 20 hours, rate of photosynthesis increases from 2.5 arbitrary units to 18.0 arbitrary units at high carbon dioxide concentrations ;**
2. **<u>More</u> light is absorbed by photosystems / photosynthetic pigments resulting in <u>more</u> photophosphorylation / light dependent reaction (and <u>more</u> oxygen / reduced NADP / ATP / glucose / starch produced) ;**

(c) In the laboratory, a seaweed was grown in water with different pH values. All other variables, including temperature and light, were standardised. The mean rate of photosynthesis was calculated over a 24 hour period for each pH value. The results are shown in Fig 3.2.

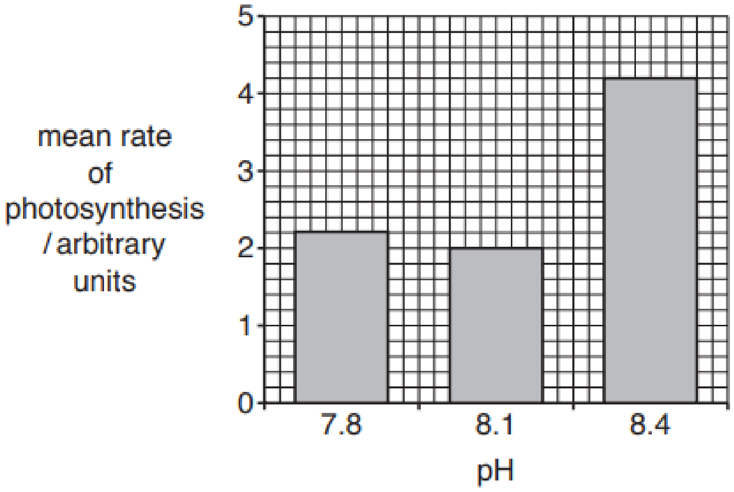

Fig. 3.2

The lower pH values on Fig. 3.2 represent ocean acidification.

Suggest why the results for the lower pH values do not fully support the idea that seaweeds can help to reduce ocean acidification.

.... [1]

1. **Mean rate of photosynthesis is lower than at higher pH, meaning less carbon dioxide absorbed / fixed (so ocean acidification not reduced) ;**

[Total: 10]

Section B

Answer **one** question in this section.

Write your answers on the Answer Booklet provided.

Your answers should be illustrated by large, clearly labelled diagrams, where appropriate.

Your answers must be in continuous prose, where appropriate.

Your answers must be set out in parts **(a)** and **(b)**, as indicated in the question.

4 **(a)** Describe the roles of enzymes in the synthesis of a functional protein in eukaryotic cells. [15]

1. **enzymes are required in chromatin modification, transcription, post-transcriptional modification, translation and post-translation modifications (any three) to synthesise a functional protein ;**
2. **3 correct enzymes named ;**

a) chromatin modification			
3.	**histone acetyltransferase**	**adds acetyl groups to lysine residues on histone tails, affinity of histone for DNA is therefore reduced. (DNA coils less tightly around the nucleosomes and the chromatin decondenses)**	**;**
4.		**increase accessibility of the general transcription factors and RNA polymerase / transcription machinery to the promoter**	**;**
5.	**DNA demethylase**	**methyl groups removed (demethylated) from cytosine residues at the CpG islands (thereby forming a less tightly coiled euchromatin structure)**	**;**
6.		**enables general transcriptional factors and RNA polymerase / transcription initiation complex, to recognise and bind to the promoter to initiate transcription**	**;**
b) transcription			
7.	**RNA polymerase**	**unwinds and unzips the DNA molecule over the region of the gene**	**;**
8.		**breaking hydrogen bonds between complementary bases (and starts transcribing the DNA template strand)**	**;**
9.		**catalyses the formation of phosphodiester bonds between RNA nucleotides, resulting in the synthesis of RNA**	**;**

c) post-transcriptional modification			
10.	enzymes / endonuclease and ligase, in spliceosomes	removes introns and splice exons together to form a continuous coding strand / mature mRNA	;
11.	5’ / RNA, capping enzyme	adds a 5' 7-methylguanosine cap	;
12.	ribonuclease	recognises the polyadenylation signal sequence and cleaves the mRNA at the 3’ end	;
13.	poly-A polymerase	adds (50-250) adenine nucleotides to the 3’ end of the mRNA, forming a poly-A tail (to stabilize and protect the mRNA)	;
d) translation			
14.	aminoacyl-tRNA synthetase	catalyses attachment of a specific amino acid to the 3’ end of a specific tRNA, forming an aminoacyl-tRNA	;
15.	peptidyl transferase	catalyses the formation of peptide bonds between adjacent amino acids during elongation	;
e) post- translation modification			
16.	kinases	catalyses phosphorylation of / the transfer of phosphate groups from ATP to, proteins (to activate them)	;
17.	enzymes / glycosyltransferases	catalyses glycosylation / the addition of a short carbohydrate chains, to proteins (to target the protein for association with membranes)	;
18.	(thiol) oxidase / (sulfhydryl) oxidase	catalyses the formation of disulfide bonds through the oxidation of cysteine and SH-containing peptides / proteins (leads to formation of the three-dimensional structure of functional proteins)	;
19.	protease	catalyses the hydrolysis of peptide bonds in zymogen/proenzymes (e.g. trypsinogen and chymotrypsinogen) to activate zymogens	;
f) other relevant points			
20.	ATP synthase	synthesises ATP required for (state 1 function of ATP in ptn synthesis) via oxidative phosphorylation	;
21.	glyceraldehyde-3-phosphate dehydrogenase	catalyses the conversion of TP to G1,3P and by the production of NADH	;
22.	phosphoglycerate kinase	catalyses the (reversible) phosphoryl transfer between G1,3P and ADP to form G3P and ATP	;

QWC: At least one named enzyme and role described from at least three category (a) to (e) ;

(b) Compare the interaction between a hormone and a cell surface receptor with the interaction between a substrate and an enzyme. [10]

Similarities

1. **Both receptor and enzyme have sites with specific 3D conformation which only molecules of complementary shape will fit into / Both hormone and substrate bind to specific sites / receptor site and active site, on receptor and enzyme respectively ;**
2. **Both showed high specificity in their interactions ;**
3. **Both receptor and enzyme can be reused / do not change 3D conformation after interaction / remain unchanged at the end of the interaction ;**
4. **Both interactions require molecules to be chemically compatible ;**
5. **Temporary weak bonds such as ionic bonds, hydrogen bonds and hydrophobic interactions (any 2) are formed between hormone-receptor and enzyme-substrate during the interactions ;**

Differences

	feature	hormone and cell surface receptor interaction	substrate and enzyme interaction	
6.	enable reactions to proceed faster by lowering activation energy	no	yes	;
7.	site for binding	binding site	active site	;
8.	conformational changes in site for binding	receptor changes shape upon binding of hormones	active site does not change shape upon binding of substrates (lock & key hypothesis)	;
9.	induced fit	no	yes, as the substrate enters and binds to the active site, it induces a conformational change in the shape of the enzyme such that the substrate can fit even more snugly into the active site	;
10.	cofactors	cofactors not required	cofactors may be required	;
11.	complex formed	hormone–receptor complex	enzyme-substrate complex	;
12.	formation of product	no changes to hormones after binding hormones dissociate from receptor after activation of other proteins	changes to substrate after binding, products formed substrate is broken down / converted to product after reaction	;
13.	function	cell signalling	catalysing biological reactions	;

QWC: Clearly expressed using the correct terminology and communicated without ambiguity, with at least 1 similarity and 1 difference addressed ;

5 **(a)** Explain why variation is important in natural selection and outline the sources of variation in eukaryotes. [15]

Why variation is important

1. **Genetic variation describes the differences in characteristics / presence of different characteristics shown by individuals belonging to the same species ; A: phenotype**
2. **due to presence of different alleles in the individuals ;**
3. **it is the raw material for natural selection to act on ;**
4. **Variations in characteristic are subjected to selection pressure from the environment / environment would exert different selection pressure on the different phenotype ;**
5. **variants who are better adapted to the environment will be at selective advantage ;**
6. **These variants with favourable characteristics (higher fitness) will survive to maturity, reproduce and pass down their favourable alleles to their offspring ;**
7. **Those with unfavourable characteristics (lower fitness) die and fail to do so ;**
8. **Example of characteristic that influences survival ; e.g. beak size affecting type of seeds birds can eat ;**
9. **Variation can be due to interaction of genotype and environment ;**
10. **Ref continuous/discontinuous variation ; e.g. two forms of variation occurs: continuous (many, additive genes control a characteristic) and discontinuous (one or a few genes control a characteristic) ;**

Sources of genetic variation

Genetic variations arise via:

11. **Gene mutations such as base-pair substitution / base-pair addition / base-pair deletion ;**
12. **Gene mutation is defined as a change in the sequence of DNA nucleotides in the gene ;**
13. **Due to errors occurring during semi-conservative DNA replication/DNA repair ;**

14. **Chromosomal aberrations include numerical aberration / change in chromosome number or structural aberration / alteration in chromosome structure ;**
15. **numerical aberration e.g. aneuploidy (in the case of trisomy 21 / Down syndrome) ;**
16. **occurs due to non-disjunction / failure of homologous chromosomes / chromatids to separate during anaphase I of meiosis I / anaphase II of meiosis II ;**
17. **structural aberrations such as translocation, duplication, inversion and deletion (any 2) ;**

18. **Crossing over between non-sister chromatids of homologous chromosomes during prophase I of meiosis I ;**
19. **to give new combination of alleles in gametes/recombinant chromatids ;**
20. **Independent assortment/segregation of homologous chromosomes during metaphase I/anaphase I of meiosis I ;**
21. **Independent assortment/segregation of (recombinant) chromatids during metaphase II/anaphase II of meiosis II ;**
22. **Results in independent assortment of paternal and maternal chromosomes between the nuclei of daughter cells producing new combinations of alleles in gametes ;**

23. **Random fusion of gametes/fertilisation during sexual reproduction ;**
24. **results in new combinations of alleles in the zygote and adds to genetic variation in the genotype and phenotype of offspring ;**
    Award once for new combi of alleles (pt 19, pt 22, pt 24)

QWC [1]

At least two reasons why variation is important and two sources of variation mentioned AND both parts of the question addressed in separate paragraphs ;

(b) Outline the main differences between prokaryotes and eukaryotes in terms of their cell structure and outline their evolutionary relationship. [10]

<u>Differences</u>

	feature	prokaryotic	eukaryotic	
1.	**Ribosome**	**70s**	**80s**	**;**
2.	**Organelles**	**No membrane bound organelles**	**Have membrane bound organelles**	**;**
3.	**Nucleus**	**Absence of nucleus** **OR** **DNA not enclosed by nuclear membrane** **OR** **DNA found in the cytoplasm and aggregated as supercoil in the <u>nucleoid</u>**	**Presence of nucleus** **OR** **DNA found in the <u>nucleus</u>, enclosed by the nuclear membrane**	**;**
4.	**Size**	**Smaller than eukaryotic cells**	**Larger than eukaryotic cells**	**;**
5.	**Cell wall**	**Have peptidoglycan cell wall**	**Have cellulose cell wall in plant cells**	**;**
6.	**Number of chromosomes**	**Genome is usually found on <u>1 main chromosome</u> (excluding plasmids)**	**Genome is divided into <u>many different chromosomes</u>.** ***(Number of chromosomes is species-dependent)***	**;**
7.	**DNA linearity/ circularity**	**<u>Circular / Looped</u> chromosome**	**<u>Linear</u> chromosomes**	**;**
8.	**DNA association with proteins**	**DNA <u>naked</u> / <u>associated with H-NS proteins</u> (nucleoid-associated proteins)**	**DNA <u>associate with histones forming nucleosomes</u> and scaffolding proteins**	**;**

<u>Evolutionary relationship</u>

9. **According to the <u>endosymbiotic theory</u>, the first eukaryotic cells evolved from a <u>symbiotic relationship</u> between two or more prokaryotic cells ;**

10. **Smaller prokaryotic cells were engulfed by larger prokaryotic cells. The small cells (now called endosymbionts) <u>benefited from the relationship</u> by getting nutrients from the larger cells ;**
11. **The large cells (now called hosts) <u>benefited from the relationship</u> by getting some of the organic molecules or energy released by the endosymbionts ;**

12. **Eventually, the <u>endosymbionts evolved into organelles of the host cells</u> ;**
13. **Some of the endosymbionts were aerobic bacteria (specialised to break down chemicals and release energy) and evolved into the <u>mitochondria</u> of eukaryotic cells;**
14. **Some of the endosymbionts were cyanobacteria (specialised for photosynthesis) and evolved into the <u>chloroplasts</u> of eukaryotic cells ;**

QWC – At least two main difference between prokaryotes and eukaryotes in terms of their cell structure described and one endosymbiotic relationship e.g. chloroplast or mitochondrion described ;