RAFFLES INSTITUTION

2015 Year 6 Preliminary Examination Higher 2

CANDIDATE NAME									
CIVICS GROUP	1	5	S	0	3	INDEX NUMBER			

BIOLOGY Paper 2 Core paper

9648/02 16th SEPTEMBER 2015 2 hours

Additional materials: Answer Sheet

READ THESE INSTRUCTIONS FIRST	For Examiner's Use		
Write your index number, CT group & name on all the work you hand in. Write in dark blue or black pen on both sides of the paper.	Section A		
You may use a soft pencil for any diagrams, graphs or rough working. Do not use staples, paper clips, highlighters, glue or correction fluid.	1	/ 9	
Section A	2	/10	
Answer all questions.	3	/12	
Section B	4	/10	
Answer either ONE question.	5	/10	
At the end of the examination, hand in your essay SEPARATELY. The number of marks is given in brackets [] at the end of each question or part question.	6	/ 9	
	7	/ 9	
	8	/11	
	Section B		
	9 or 10	/20	
	Total	/100	

This document consists of 24 printed pages.

Raffles Institution

Internal Examination

Section A

Answer all the questions in this sec

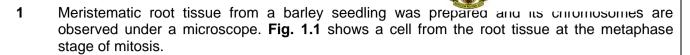
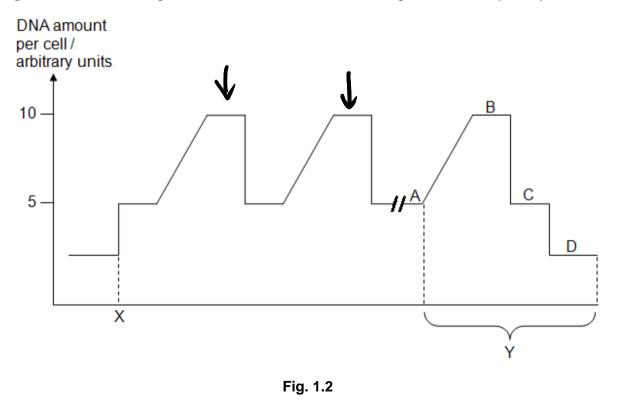




Fig. 1.1

Fig. 1.2 shows the changes in amount of DNA at different stages of the barley life cycle.



Mark out with an arrow $~\psi$ clearly on Fig 1.2 which part of the graph corresponds to the

(a)

stage shown in Fig. 1.1. [1]

Accept all part of line except the corners

- (b) From stages A to D in Fig. 1.2, state all stages
 - (i) that has/have the same number of chromosomes as shown in **Fig. 1.1**; [1]

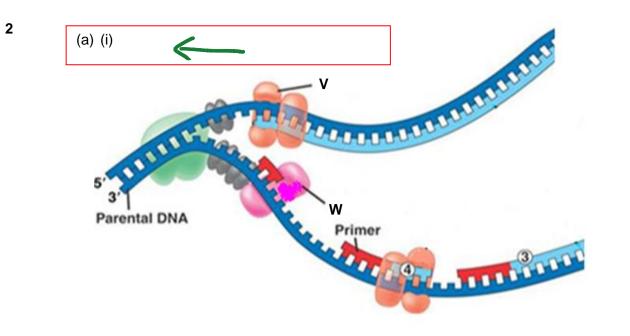
A and B;

(ii) has/have a different number of chromosomes as shown in Fig. 1.1. [1]

C and D;

- (c) Explain how stages in Y lead to variation. [4]
 - <u>Crossing over</u>* between <u>non-sister chromatids</u>* of <u>homologous</u> <u>chromosomes/bivalents/homologous pair</u> takes place during <u>prophase I</u>*; Or where <u>equivalent portions</u> of <u>non-sister chromatids</u>* of <u>homologous chromosomes</u> break and rejoin during **prophase I***
 - gives rise to <u>new combination of *alleles** / mixing of alleles</u> from both parental chromosomes which creates genetic variation in gametes;
 A: new linkage groups in place of new combination of alleles
 - 3. <u>Independent assortment*</u> of homologous chromosomes/bivalents/homologous pair at metaphase plate during <u>metaphase l</u>* and their subsequent separation during anaphase I OR <u>Homologous chromosomes are arranged independently of other homologous pairs</u> at metaphase plate during <u>metaphase l</u>* and their subsequent separation during anaphase I
 - results in <u>2ⁿ possible</u> (types of) <u>gametes</u> where <u>n</u> is the <u>number of homologous pairs</u> OR <u>Gametes</u> with <u>different combinations of parental (maternal and paternal)</u> <u>chromosomes</u>
- (d) Explain the significance of the event occurring at X. [2]
 - 1. X refers to *fertilization**;
 - (point 1 is essential)
 - <u>random fusion of gametes</u>* results in <u>greater variation/varied offspring</u> with different genotypes and phenotypes;
 - 3. <u>Restoration</u> of the <u>diploid number</u> of chromosomes;

[Total : 9]



4

Fig. 2.1

Fig. 2.1 shows DNA replication.

- (a) (i) Use an arrow to show the direction of replication of the leading strand in the box provided in **Fig. 2.1**. [1]
 - (ii) What do 5' and 3' on the DNA molecule represent? [2]
 - 1. 5' represents the end (of strand of nucleotide) with <u>carbon 5</u> on <u>deoxyribose/pentose</u> <u>sugar</u> having <u>free phosphate group</u>
 - 2. 3' represents end (of strand of nucleotide) with <u>carbon 3 on deoxyribose/pentose</u> sugar having <u>free hydroxyl group</u>
 - (iii) Name the following molecules. [1]
 - V: DNA polymerase
 - W: Primase R: RNA primase

Note: RNA primase forms DNA primer DNA primase forms RNA primer

- (iv) Describe the role of two named enzymes that are required for DNA replication. [2].
 - (role is needed, not description of how)
 1. Helicase

 <u>Unzips the DNA double helix/ separates the two DNA strands</u> by breaking hydrogen bonds between the complementary base pairs.
 - 2. Topoisomerase Breaking and rejoining DNA strands to <u>relieve overwinding</u> strain ahead of

replication fork

- 3. DNA Polymerase <u>Addition of free deoxyribonucleotides/elongation of the new DNA strand</u> by formation of phosphodiester bond between nucleotides.
- DNA ligase form phosphodiester bonds to join the Okazaki <u>fragments</u> sealing the nicks.
 Primase
 - to <u>synthesise the RNA primers</u> to <u>provide free 3'OH</u> for DNA Polymerase to elongate the new DNA strand
- (b) Fig. 2.2 shows transcription.

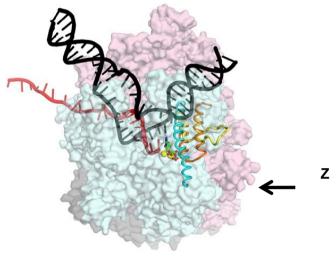


Fig. 2.2

Describe how the structure of molecule **Z** is adapted to its role in transcription. [2]

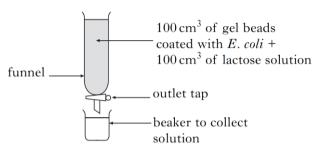
- 1. molecule Z = RNA polymerase,
- which has a specific <u>active site</u>* which is <u>complementary in shape/conformation</u>* and charge to <u>substrate</u> such as DNA template and ribonucleotides; / <u>DNA binding site</u>* that is complementary to <u>nucleotide sequences at the promoter</u>.
- 3. catalytic amino acids capable of catalyzing the <u>formation</u> of <u>**phosphodiester bond**</u>* elongating the RNA
- (c) Describe how a silent mutation can result in no change in protein structure. [2]
 - 1. <u>Single base substitution</u> mutation (involves a replacement of a DNA nucleotide with a different nitrogenous base)
 - 2. <u>Change in codon</u> resulting in <u>same amino acid</u> incorporated in polypeptide chain due to <u>degeneracy</u> of the <u>genetic code</u> (R: wobble)

OR

- 3. Any mutation (e.g. insertion, deletion, substitution) in introns
- 4. which will be spliced out in post-transcriptional modification
- (1 and 2 OR 3 and 4)
- 5. <u>Same primary structure</u> and hence no change in <u>secondary and tertiary</u> structure

[Total : 10]

- **3** The Jacob-Monod hypothesis describes lactose metabolism in the bacterium *Escherichia coli*. An investigation of this reaction in *E. coli* at 25 °C was carried out as described below.
 - 100 cm³ of gel beads coated with *E. coli* were placed into each of seven identical funnels fitted with outlet taps.
 - 100 cm³ of solution containing 2 grams of lactose was poured into each funnel at 0 min.
 - At each time shown in the table, the solution from the respective funnel was released and collected.
 - The mass of lactose in each solution was measured.



The results are shown in the table below.

Funnel	Time (min)	Mass of lactose collected in the solution (g)
1	0	2.00
2	10	2.00
3	20	1.48
4	30	0.92
5	40	0.40
6	50	0.12
7	60	0.04

With reference to **Table 3.1**

(a) (i) calculate the average mass of lactose broken down per minute in funnel 5. [1] (2.00 - 0.40)/40 = 0.04

g per minute

- (ii) explain the results from funnels 3 to 7. [4]
 - 1. As from 20 to 60 min/ time passes/ over 40 min, lactose digested increased from 0.52 g to 1.96 g

A: 1a: from 20 to 60 min, lactose collected decreased from 1.96 g to 0.04 g

- Lactose/ allolactose <u>binds</u> to and <u>inactivates/alters</u> tertiary structure of <u>repressor</u> such that <u>it fails to bind to **operator***</u>
- 3. <u>RNA polymerase is free to bind to</u> **promoter*** and initiate <u>transcription</u> of <u>structural</u> <u>genes/lac Z and Y</u> of the operon/switch on *lac* operon
- 4. Produces more *permease** which increases rate of uptake of lactose
- 5. Produces more *beta-galactosidase*^{*} which will <u>hydrolyse lactose</u>

Fig. 3.2 below shows an operon that controls a catabolic reaction in *E. coli*. Some information on how this operon functions is also provided.



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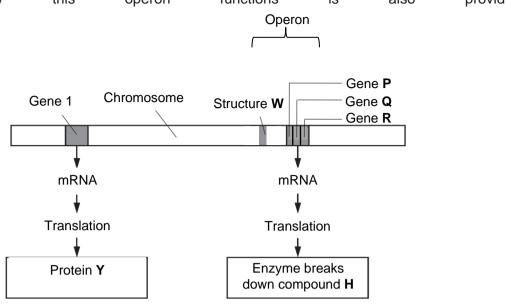


Fig. 3.2

- (b) (i) In the presence of inducer, protein Y cannot bind to structure W. Name W. [1] Operator
 - (ii) A mutation occurred in gene P. This resulted in the production of a truncated protein. Assuming that the inducer is present, explain if the proteins encoded by Gene Q and Gene R are produced. [2]
 - 1. Yes they will be produced;
 - 2. each cistron / protein has its <u>own start and stop codon</u> on the polycistronic mRNA; OR
 - 3. so an unexpected stop codon in <u>one does not affect the others / translated</u> <u>independently;</u>
 - [Note: 1. Must be present]
- (c) An *E. coli* cell can be infected by a bacteriophage. How does the bacteriophage differ from HIV (human immunodeficiency virus) in the way its genome enters the host cell? [1]

Phage <u>contracts its tail sheath</u> and punctures <u>cell wall</u> of bacterium to <u>introduce</u> DNA into cell whereas HIV enters host cell by <u>fusion</u>* of viral envelope with <u>cell membrane</u>.

(d) Bacteriophage lambda in an *E. coli* cell can replicate as a prophage or lytically. These two phases are controlled by the gene regulatory proteins cl and Cro, which are encoded by the virus (refer to **Fig. 3.3**).

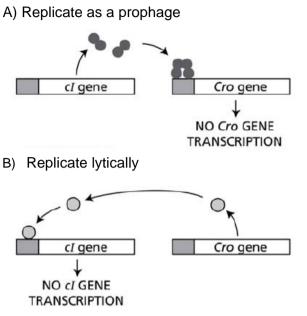


Fig. 3.3

When bacteria containing a lambda prophage are irradiated with ultraviolet light, the cl protein is degraded.

With reference to Fig. 3.3,

- (i) state which phase the bacteriophage enters upon UV irradiation, [1] Lytic stage
- (ii) describe the events following the degradation of the cl protein. [2]
 - 1. <u>cl protein no longer binds</u> (R: blocks) to operator of *Cro* gene, so *Cro* gene is <u>transcribed and translated / expressed</u> into <u>Cro protein</u>
 - 2. Cro protein turns off expression of cl gene
 - 3. so that <u>Crogene</u> will be <u>constitutively expressed / not repressed further</u>
 - 4. Phage genome excises itself and starts to <u>synthesize enzymes/phage components /</u> <u>list examples like capsid, contractile sheath</u>, and new virus particles are released/assemble into complete virions

Note: cl protein is also known as repressor

[Total : 12]

4 Glucocorticoids (S), are a class of steroid hormones that bind to the glucocorticoid receptor (GR), and are crucial in regulation of many genes. S binds to GR, activating GR. Activated GR binds to glucocorticoid response elements (GREs) within the promoter regions of target genes. This results in the recruitment of the chromatin remodelling complex, BRG1 complex.

Fig. 4.1 shows the effect of **GR**-mediated gene expression. Fig. 4.2 shows the effect of **BRG1** complex binding to the promoter region of the target gene.

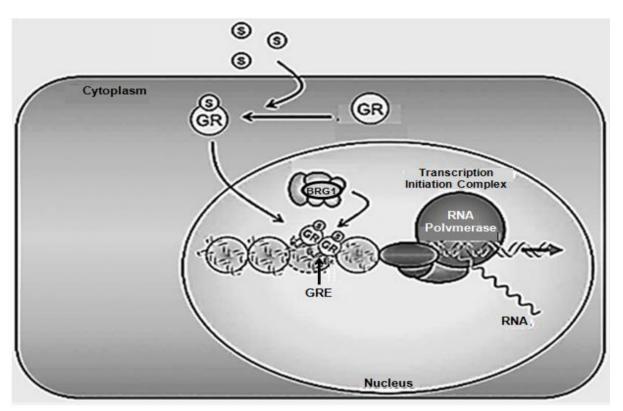


Fig. 4.1

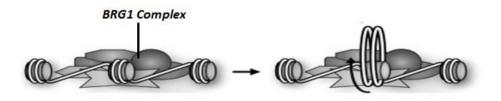


Fig. 4.2

(a) Explain how the steroid hormone is able to enter the cell. [1]

Steroid hormone being <u>hydrophobic</u> can easily diffuse through the <u>hydrophobic core</u> of <u>phospholipid bilayer</u>* of the cell surface membrane.

(b) **GR**s are known to have highly conserved regions which are structurally important for its function.

Describe 2 structural features of **GR** which allows it to carry out its role. [4]

- 1. DNA binding site,
- 2. which is <u>complementary* in shape</u> and charge to the sequences at the <u>GRE</u>*, allowing it to <u>bind</u> to GRE.
- 3. <u>Binding site for steroid hormones/GC</u> [R: protein binding site for steroid / receptor binding site]
- 4. <u>complementary to shape S</u>, to allow <u>change in conformation</u> of GR <u>to activate GR/allow</u> <u>binding to GRE</u> in promoter.
- 5. Binding site for BGR1 complex*
- 6. to allow binding / recruitment of BGR1 regulate gene expression
- 7. <u>GR-GR binding site</u>
- 8. To recruit RNA polymerase and transcription factors for the formation of the transcription initiation complex.

Reject : reference to active site.

NB: Points 1&2, 3&4, 5&6, 7&8 must be marked together. The structure must be mentioned before the mark for role is awarded.

- (c) (i) With reference to the information provided, describe the effect of the presence of **S** on gene expression. [3]
 - 1. Glucocorticoids increases the rate of transcription/gene expression.
 - <u>Glucocorticoids</u> binds* to/activates GR which then binds to <u>GRE</u>*, [R: presence of GC without mentioning GC binding]
 - Recruits <u>BRG1*/chromatin remodelling complex</u> which causes the <u>DNA to be</u> <u>less tightly coiled</u> around the <u>histones</u>;
 - <u>RNA polymerase*</u> and <u>transcription factors</u> can <u>access / bind to the</u> <u>promoter*</u> to initiate transcription OR To promote assembly of *transcription initiation complex** at the promoter*
 - (ii) Briefly describe one other mechanism that may bring about a similar effect on gene expression as described in (c)(i) [1]
 1. <u>De-methylation of DNA</u> at cytosine (C) nucleotides located <u>decondenses chromatin</u>;
 - 2. <u>Acetylation of histones</u> at lysine residues, decreases interaction between DNA and histones allows <u>chromatin to decondense;</u>
 - 3. <u>Activators*</u> binds to <u>enhancers*</u>, promoting <u>assembly of transcription initiation</u> <u>complex</u>.
 - R : enzyme inhibition

(d) Function and activity of **GR**s are known to be affected by different post-translational modifications.

Suggest one post-translational modification and its effect on the activity of GRs. [1]

- 1. <u>cleavage</u> / <u>glycosylation</u> / <u>disulfide bond formation</u>/ <u>attachment of prosthetic groups</u> etc to <u>form functional/activate or inactivate GRs</u>
- 2. <u>phosphorylation / addition of phosphate group</u> OR <u>dephosphorylation / removal of</u> <u>phosphate group</u> to <u>activate or inactivate GRs</u>.
- 3. Reference to ubiquitin for GR degradation.

R: enzyme inhibition

- **5** A researcher was investigating the inheritance of 3 gene loci in mice coat colour, skin colour, and tail shape.
- (a) In the first set of experiments, a pure breeding female mouse with agouti coat and fair skin was crossed with a pure breeding male mouse with albino coat and dark skin. All the F₁ offspring had agouti coat and dark skin. One of the male F₁ mouse was then testcrossed with a female mouse, and the result of the testcross was recorded in Table 5.1.

Phenotype	Male	Female			
Agouti coat, fair skin	18	20			
Agouti coat, dark skin	7	6			
Albino coat, fair skin	6	7			
Albino coat, dark skin	18	18			

Table 5.1.

- (i) Describe the inheritance of coat colour and skin colour in mice. [2]
 - 1. Two genes are *linked**/on the <u>same chromosome</u>
 - 2. Autosomal
 - 3. Agouti allele dominant to albino allele, and dark skin allele dominant to fair skin allele (ORA)

R: not sex-linked

(ii) Draw a genetic diagram to explain the results of the testcross. Use appropriate symbols to represent coat colour and skin colour. [5]

Let A represent the dominant allele for albino coat and a to represent the recessive allele for albino coat. Let D represent the dominant allele for dark skin and d to represent the recessive allele for fair skin. [1] Establishing of the appropriate symbols Phenotype of parents: Agouti coat, dark skin x albino coat, fair skin Genotype of parents: [1] for test cross (crossing with albino, fair) [1] for genotypes of parents in test cross matching phenotype + rep of linked genes using stick diagram (R: if genotypes are circled) (if no stick diagram only 2 marks for legend and parental phenotype) Gametes: а а d Ч Parental D d Recombinant [1] for circled and correct gametes Offspring genotypes: Offspring phenotypes: Agouti, fair; Albino, dark; Agouti, dark; Albino, fair %36%13%ParentalRecombina Offspring phenotypic %: 38% 13% **Recombinant types** [1] for correct offspring genotype linked to corresponding offspring phenotypes

[1] recombinants and parental types clearly labelled including percentages

(b) The researcher then looked into the trait of tail shape separately, and derived the following pedigree as shown in **Fig. 5.1**. Normal tails are denoted by shaded symbols, whereas bent tails are denoted by unshaded symbols.

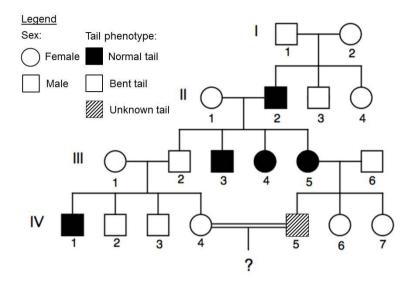


Fig. 5.1.

From the results, the researcher concluded that gene for tail shape lies on the X chromosome.

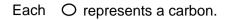
(b) (i) What is the probability of a cross between IV-4 and IV-5 (the phenotype of IV-5 is unknown) producing a female mouse with normal tail. [1]

P(female, with normal tail) = $\frac{1/8 \text{ or } 0.125}{1/8 \text{ or } 0.125}$

- (ii) Explain your answer in (b)(i). [2]
 - 1. <u>IV-5</u> has a <u>normal tail</u>, X^bY, as it would have <u>inherited the recessive allele for normal</u> <u>tail from III-5</u>.
 - 2. <u>IV-4</u> is has a bent tail, thus, there is <u>0.5</u> chance that it can be a <u>carrier $X^{B}X^{b}$ or <u>homozygous $X^{B}X^{B}$ </u>.</u>
 - Thus for it to be a female with normal tail, it has to be X^bX^b, it would need to inherit the allele X^b from IV-5 which is a probability of 0.5, and X^b from IV-4 which is a probability of 0.25 (0.5 x 0.5). (A: 0.5 chance female)

[Total : 10]

6(a) Fig. 6.1 shows a series of aerobic and anaerobic reactions.



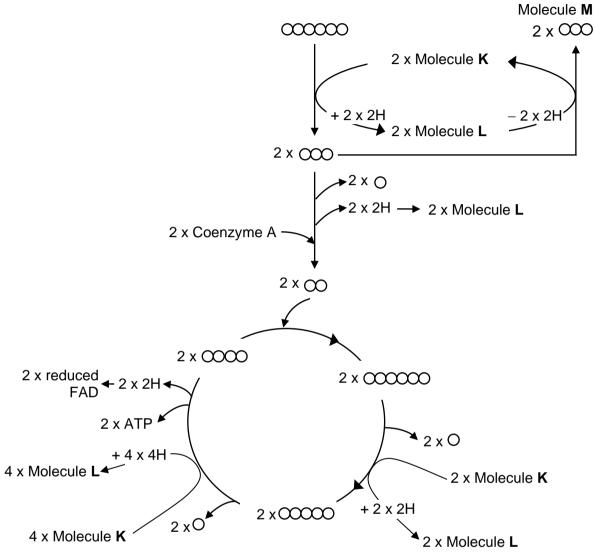


Fig. 6.1

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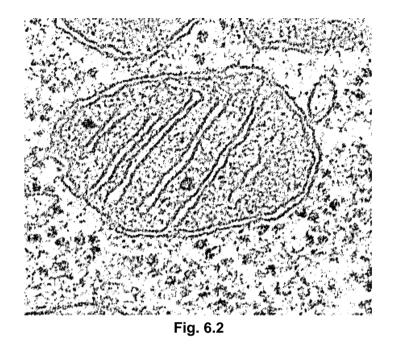


Fig. 6.2 shows an electron micrograph of a mitochondrion.

With reference to Fig. 6.1,

- (i) Using an 'X', mark a point on Fig. 6.2 clearly, showing where Molecule M is produced.
 [1] Mark 'X' anywhere outside the mitochondria (mitochondria) M = Lactate
- (ii) Name Molecule L. [1]

1. $\mathbf{L} = \mathbf{NADH} / \mathbf{reduced} \mathbf{NAD}^+$

- (iii) In aerobic conditions, explain how Molecule L is converted to Molecule K. [2]
 - 1. Oxygen is the <u>final electron acceptor</u> reoxidising the electron carriers of the <u>Electron</u> <u>Transport Chain*</u>
 - So NADH (Molecule L) can continue to <u>donate electrons</u> and protons the ETC, thus regenerating <u>NAD⁺</u> *(Molecule K)

- (iv) The mitochondrion has two major compartments. Suggest the significance of compartmentalisation within the mitochondrion. [1]
 - 1. <u>Enzymes and substrates</u> of <u>Krebs cycle</u> are kept in <u>close proximity/ confined</u> within the <u>matrix</u> increasing rate of reaction.
 - 2. <u>Optimal conditions</u> e.g. pH for <u>enzymes</u> of <u>Krebs cycle</u> can be maintained within <u>matrix</u> for higher rate of reaction.
 - 3. <u>Intermembrane space</u> has a high concentration of protons / a proton gradient can be set up <u>across inner membrane</u> so ATP can be produced via chemiosmosis.
- (b) Fig. 6.3 shows the absorption spectrum of one type of photosynthetic pigment from a plant and the rate of photosynthesis of the plant in different colours of light.

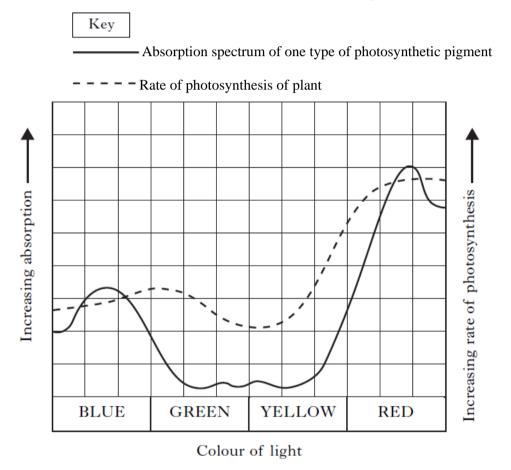


Fig. 6.3

- (i) Leaves of this plant contain more than one type of photosynthetic pigment. Use evidence from the graph to justify this statement. [1]
 - 1. Photosynthesis occurs in green and yellow light though little light is absorbed by the single photosynthetic pigment in these wavelengths (green and yellow).
 - 2. Photosynthesis occurs in all colours but the pigment absorbs mainly blue and red light.
- (ii) Plants typically have several photosynthetic pigments. Describe the role of accessory pigments in photophosphorylation. [1]
 - 1. Widen the absorption spectrum / widen action spectrum
 - 2. by <u>chanelling</u> light <u>energy</u> of <u>different wavelengths</u> to <u>chlorophyll a/main</u> <u>photosynthetic pigment/reaction centre</u>
- (c) *Spirogyra* is a photosynthetic green alga which grows as a long strand of cells. A strand of *Spirogyra* was placed into water containing aerobic bacteria. Different parts of the strand were exposed to different colours of light. After a period of time, the bacteria had moved into the positions shown in **Fig. 6.4**.

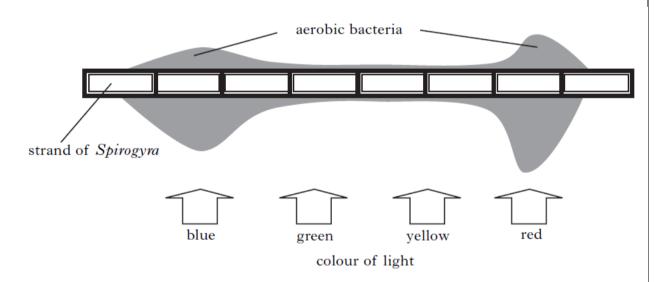


Fig. 6.4

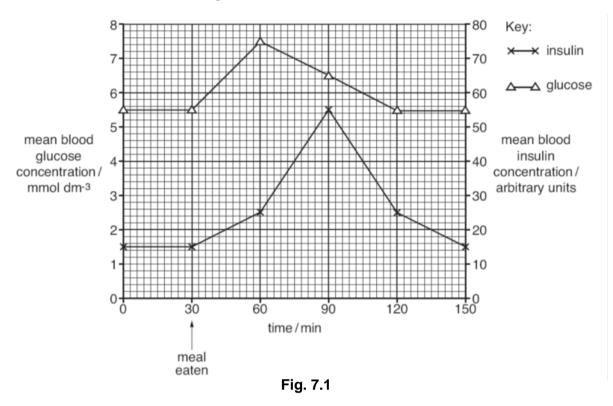
Explain the distribution of aerobic bacteria shown in the diagram. [2]

- 1. <u>Photosynthesis occurs at higher rates</u> in the regions with <u>red and blue light</u>
- 2. Producing more oxygen thus attracting aerobic bacteria

Accept reverse arguments Eq:

- 3. <u>Photosynthesis</u> occurs at <u>higher rates</u> as indicated by <u>more oxygen</u> produced
- 4. Thus at red, blue light thus attracting aerobic bacteria

7 A study was carried out to measure the concentrations of glucose and insulin in the blood. The results are summarised in **Fig. 7.1**.



- (a) Explain the relationship between the concentration of glucose and the concentration of insulin shown in **Fig. 7.1** after the meal. [3]
 - Rise in glucose concentration from <u>5.5 to 7.4 mmol/dm³</u> between <u>30 to 60min</u> is <u>detected</u> by <u>β cells islets</u>,
 - 2. results in the increase in insulin secretion into the blood from <u>15 to 55 arbitrary</u> <u>units</u> between <u>30 to 90min;</u>
 - Insulin binds to receptors on the <u>liver / muscle/ adipose cells</u> results in <u>increased</u> <u>uptake of blood glucose</u>; OR

results in <u>increased respiration of glucose/ conversion of glucose fat / glycogen/</u> <u>amino acids</u>;

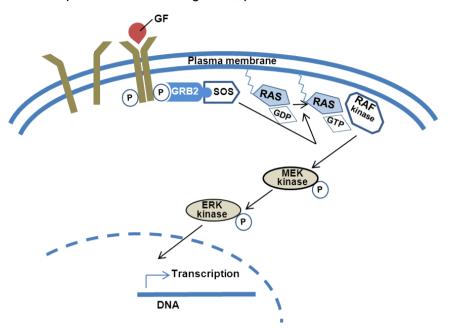
glucose concentration is lowered from <u>7.4 to 5.5mmol/dm³</u> between <u>60 to 120min</u> via <u>negative feedback</u>*.
 Or

Decreased blood glucose levels serves as **negative feedback**^{*} (of a diminished stimulus) to the β -cells which <u>decreased the secretion of insulin</u>, lowering insulin levels from <u>55 to 15 arbitrary units</u> from <u>60 to 120mins</u>

A: Norm/set point in place of 5.5 mmol/dm³

(b) The signal transduction pathway in **Fig. 7.2** is initiated by the binding of the growth factor (GF) to the receptor tyrosine kinase (RTK). This pathway controls the fundamental cellular processes such as growth, proliferation and differentiation.

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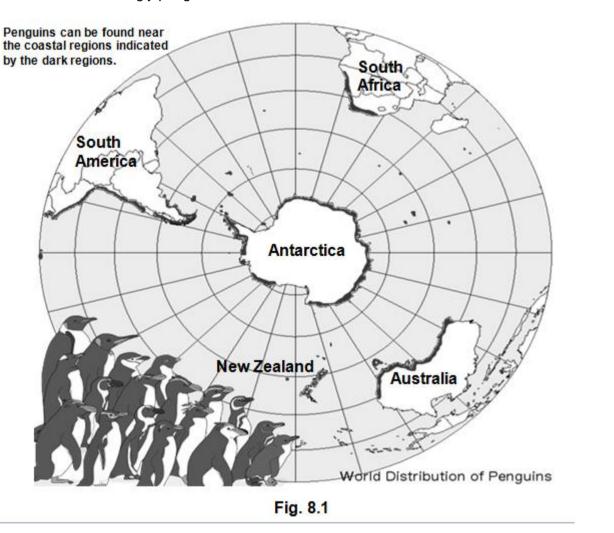


- (i) With reference to Fig. 7.2 describe how Ras, a G protein, is activated; [4]
 - 1. <u>GF</u> binds to extracellular ligand-binding site of specific transmembrane <u>receptor</u> which causes the <u>dimerization</u> of <u>two receptor subunits</u>
 - 2. <u>Conformational change</u> in the <u>intracellular</u> domain of receptor results in <u>activation</u> of intrinsic tyrosine <u>kinase</u>
 - 3. Intrinsic kinase activity of each subunit in the intracellular domain <u>cross-phosphorylates</u> /autophosphorylates the **tyrosine*** residues
 - Grb2 binds to the phosphorylated tyrosine residues which in turn binds to the SOS protein OR
 - Grb2-Sos complex is activated and
 - 5. in turn activates Ras when GDP is displaced with GTP
- (ii) explain one significance of the series of events that occurs after the activation of Ras protein. [2]
 - 1. allows <u>signal transduction</u> when activated <u>ras</u> protein triggers a <u>phosphorylation cascade</u> via <u>kinases</u> or allows signal transduction where Ras activates Raf which in turn phosphorylates

allows signal transduction where Ras activates Raf which in turn phosphorylates Mek and then phosphorylates Erk

- 2. <u>ERK</u> relays the signal to the nucleus, where it induces the <u>expression of gene/s</u> leading to cell proliferation/growth/differentiation.
- <u>signal amplification</u> occurs where <u>one activated protein activates several</u> others resulting in a <u>large number</u> of <u>activated molecule</u>, <u>an example required</u> such as ERK (ref to diagram, accept example)
- <u>large cellular response</u> it induces the <u>expression of gene/s</u> leading to cell proliferation/growth/differentiation. (1+2 or 3+4)

8 Penguins are a group of aquatic, flightless birds living almost exclusively in the Southern Hemisphere. There are 17 species of penguins and they are all found in the South Pole including the continents indicated in **Fig. 8.1** below. Penguins are well adapted to the cold polar climate and feed on fish, krill, squid and any other forms of sea-life that they can catch underwater. Interestingly penguins do not exist in the North Pole.



The oldest known fossil penguin species lived some 62 million years ago in the region of the supercontinent that eventually formed New Zealand. The map of that time is shown in **Fig. 8.2**. The shapes of the modern continents and their names are superimposed over the supercontinent of that time.

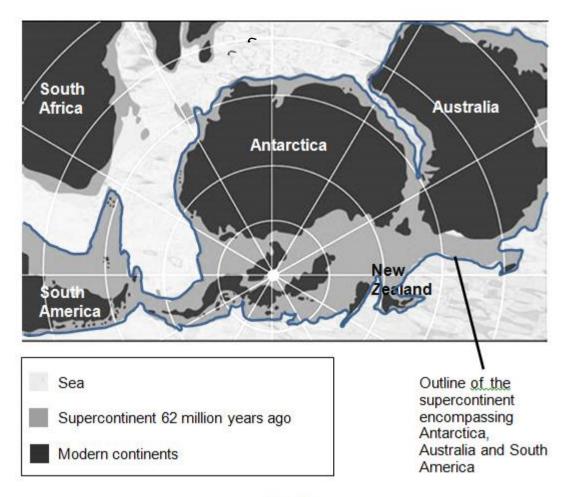


Fig. 8.2

(a) (i) Using all the information provided, explain how the biogeography of 17 existing penguin species supports Darwin's theory of evolution. [4]

Explain descent from a common ancestor:

- <u>All species of penguins</u> descended from a <u>common ancestor</u>*; (has to be explicitly stated no mark for implied statements)
- 2. Which originated in the <u>supercontinent/Paleocene epoch/62 million years ago</u>; (The center of origin being where NZ will form in the future);

Explain disparate distribution across continents even though oceans pose a barrier to migration: (this is an anomaly in biogeography that you need to explain since the species are no longer in close proximity to each other and are in different continents)

- 62mya they could <u>disperse</u> across the continents with <u>reason</u>* i.e. continents were close together/continents not separated by large oceans/single continuous land mass;
- 4. <u>Continental drift followed/continents eventually separated</u>, with <u>penguin populations</u> being <u>distributed/isolated in all the 4 continents</u>;

Explain how they were modified from the common ancestor:

- 5. The oceans separating the continents were barriers, that disrupted gene flow;
- 6. There existed <u>different selection pressures</u> on different continents that led to natural selection acting on the subpopulations resulting in phenotypic differences in size, colour patterns and head crests of the different species/over time resulted in <u>speciation</u>; (quoting evidence)

- (ii) Suggest why there are no penguins in the North pole? [1]
 - 1. Penguins from the South Pole cannot pass through the hot equatorial region to get to the North Pole;
 - 2. The distance from South Pole is too far to the North Pole;
 - 3. The ability for flightless birds to disperse from the centre of origin is limited;
 - 4. There are predators in the North Pole not found in the South that preyed on flightless birds;
 - There may be more established competitor species that fed on the same food/occupied the same niche as the penguins; AVP

When Darwin proposed his theory of evolution by natural selection, one of the most important types of evidence he used to support the idea was fossil records.

One important evolutionary change is from fish to amphibians, the first air breathing, fourlegged animals. Until 20 years ago almost no fossils had been found that were intermediate between the two. Critics of evolution referred to a 'missing link'. However scientists predicted that such intermediates would eventually be found.

Several such fossils have now been found, exactly as predicted. **Fig. 8.3** shows some of these intermediate forms in order of age, with the oldest at the bottom.

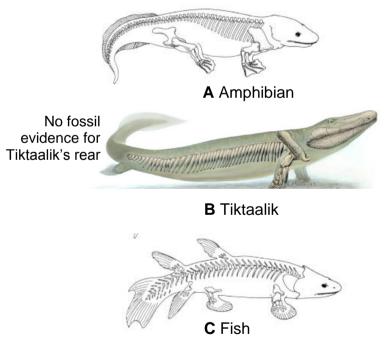


Fig. 8.3

- (b) (i) Use Darwin's theory of natural selection to explain the process by which the four-legged amphibian, A, may have evolved, over about 20 million years, from the fish-like creature, C, in the swampy conditions of that time. [4]
 - 1. There was <u>variation*</u> in the population of C e.g. some had the <u>ability to breathe air</u> <u>better/stronger fins/different shaped fins/different fin mobility/sturdier fins</u>;
 - 2. Strong <u>selection pressure to move to land</u> e.g. Predators at sea, competition for food in sea, many new niches on land, no predators on land (<u>name at least one factor</u>);
 - 3. Such fish had the ability to <u>survive</u>, <u>reproduce and pass on advantageous alleles to</u> <u>the next generation</u>; Reject: if no mention of beneficial/advantageous
 - 4. And over time a new species, the Tiktaalik evolved;
 - 5. Terrestrial environment is very different from sea, with <u>further selection pressure</u> selecting for ability to move quickly on land and breathe air resulting in the emergence of amphibian, A; selection against aquatic environment (<u>idea of continued selection especially for well developed legs</u>)
 - (ii) Tiktaalik was only found in 2004 and aroused great interest. Explain the significance of this 'missing link'. [2]
 - 1. It was a *transitional fossil** that that fits the 'gap' in the fossil record;
 - 2. It further supports Darwin's theory of evolution by illustrating <u>descent</u> from a common ancestor <u>with</u> (incremental) <u>modification;</u>
 - 3. They demonstrate a significant <u>evolutionary transition from sea to land;</u> OR

They have features of both C and A.

[Total : 11]

Section B Answer EITHER 9 OR 10.

Write your answers on the separate answer paper provided.

Your answers should be illustrated by large, clearly labeled diagrams, where appropriate. Your answers must be in continuous prose, where appropriate.

Your answers must be set out in sections (a), (b) etc., as indicated in the question.

9 (a) Explain why the population is the smallest unit that can evolve.

[5]

For Examiner's Use

- 1. (defn) A <u>population</u> is a group of <u>interbreeding</u> individuals belonging to a particular <u>species</u> and sharing a <u>common geographic area/common</u> <u>habitat.</u>
- 2. (defn) <u>Evolution</u> is the <u>change in allelic frequency</u> in a <u>population</u> over the <u>generations/time</u>.
- 3. A population needs to have <u>variation/different phenotypes</u> among individuals before selection can take place.
- 4. An individual cannot evolve/ Individuals don't change in their lifetimes.
- 5. <u>Individuals</u> are <u>selected for or against</u> by <u>natural selection</u>/ Some <u>individuals succumb</u> to <u>selection pressure</u> while others thrive.
- 6. Those individuals that <u>survive</u> can <u>pass</u> favourable <u>alleles</u> to the next generation
- 7. Individuals can only introduce <u>new allele</u> to the <u>next generation</u> through <u>mutation</u> during the <u>formation of gametes</u>

(b) Explain the ways in which islands favour the formation of new species. [7]

- 1. Islands are <u>geographically isolated</u>* as they are surrounded by water that acts as a physical barrier preventing interbreeding.
- 2. This results in the *disruption of gene flow**;
- 3. The different islands due to their <u>differing habitats / environments</u>, present <u>many niches</u> for the species to fill (idea of adaptive radiation);
- 4. Differences in environment can be due to differences in availability of water, availability of shade, plant types, food types, predators (any one)
- Thus the (common) ancestral species on different islands were exposed to <u>different selection pressures</u>* and natural selection act will on them;
- 6. There exist <u>variation</u> in the population and those with <u>advantageous</u> <u>characteristics</u>/best adapted to the local conditions are more likely to <u>survive</u>, <u>reproduce</u> and <u>pass on their alleles</u> to the next generation;
- 7. As the different populations <u>evolve/change independently</u> from each other, their <u>allele frequencies change</u> and they accumulate <u>different</u> genetic <u>mutations</u> over time;
- <u>Allele frequencies also change</u> due to <u>natural selection</u> and <u>genetic</u> <u>drift/founders effect</u> (which are random events that are due to chance);
- Over <u>hundreds and thousands of generations/ long</u> periods of <u>time</u>, accumulation of many genetic differences led to each population on different islands (to become so different that they) to become <u>reproductively isolated</u>*;
- 10. Eventually they can <u>no longer</u> *interbreed** to produce *viable, fertile** <u>offspring</u>
- 11. hence islands cause new species to form through allopatric speciation;

[8]

(c) Describe and explain how genetic variation may be preserved in a population.

Heterozygote protection/Diploidy

- 1. <u>Heterozygote protection*/diploidy*</u> occurs in diploid organism with <u>2 copies</u> of <u>each gene</u>
- 2. <u>2 different alleles at 1 gene</u> locus where <u>dominant allele</u> determines the <u>organism's phenotype/recessive allele</u> remains <u>hidden/masked</u>
- 3. <u>Recessive homozygote</u> with unfavourable phenotype <u>selected</u> <u>against/dominant phenotype selected for + heterozygotes survive</u>
- 4. thus heterozygotes pass on <u>recessive allele</u> to <u>offspring</u> when heterozygotes <u>propagate/interbreed</u> maintaining recessive allele in population
- e.g. Heterozygous condition hides recessive Hb^S allele that is less favourable from natural selection which only acts on sickle cell anaemia phenotypes any relevant example with details

[cap at 4m for heterozygote protection]

Balancing selection

6. <u>balancing selection</u>* where natural selection <u>maintains</u> <u>two or more</u> <u>alleles</u> at <u>a gene locus</u> (such as in heterozygote advantage and frequency dependent selection)

Heterozygote advantage

- <u>heterozygote advantage</u>* when individuals who are <u>heterozygous</u> at a particular locus have <u>greater fitness</u> than / <u>selective advantage</u> over / can survive and reproduce better than <u>both kinds of homozygotes</u>
- 8. <u>Heterozygote</u> is <u>selected for</u> with <u>named e.g.</u> in <u>malaria prone</u> <u>regions</u>, Hb^AHb^S do not suffer from negative effects/do not die of sickle cell anemia or more resistant to malaria
- thus heterozygotes pass on <u>recessive allele</u> (Hb^S) to <u>offspring</u> when heterozygotes <u>propagate/interbreed</u> maintaining recessive allele in population
- 10. <u>Both homozygotes</u> are <u>selected against</u> with <u>named e.g.</u> Hb^SHb^S individuals will be disadvantaged due to serious effect of sickle-cell anaemia and Hb^A Hb^A will be susceptible to malaria. any relevant example with details

Frequency-dependent selection

- 11. <u>frequency dependent selection</u>* is where the <u>fitness/selective</u> <u>advantage</u> of the <u>phenotype</u> <u>depends on how common it is</u>
- 12. the <u>frequency</u> of <u>each phenotype</u> <u>oscillates over time</u> but is kept <u>close</u> <u>to 50%</u>, thus <u>maintaining both alleles</u>
- 13. e.g. in Lake Tanganyika in Africa, there are two forms of the scaleeating fish i.e. left-mouthed and right-mouthed. The prey of the scaleeating fish guards itself against attack from whatever phenotype of scale-eating fish is most common in the lake. So from year to year, selection favours whichever mouth phenotype is least common.

Neutral mutations

14. <u>Neutral mutations*</u> are those that do not undergo natural selection because when they are expressed, they do not confer <u>a selective</u> disadvantage or advantage to the individual/do not affect

[5]

fitness/selectively neutral

- 15. They can occur as a result of: (any 1)
 - <u>Silent mutations</u>* where despite a mutation, the same amino acid is coded for, so <u>no change in protein</u> structure and <u>function</u>
 - <u>Conservative substitution*</u> where mutation codes for another chemically similar amino acid resulting in <u>no change in protein</u> structure and <u>function</u>
 - Mutations in non-regulatory sequences in non-coding regions/mutations that do not fall within regulatory sequences resulting in no change in protein function and quantity of protein produced
- **10 (a)** Compare glycosidic bonds in carbohydrates with peptide bonds in protein. Similarities
 - 1) Both glycosidic bonds and peptide bonds are *covalent bonds**
 - 2) In the formation of both glycosidic bond and peptide bond, condensation reaction occurs / water is formed
 - R: Both the bonds join monomers of biological molecules to form polymers

Differences

	Differences							
	Point of Comparison	Glycosidic bonds	Peptide bonds					
4	Monomer OR	glycosidic bonds are formed <u>between</u> <u>monosaccharides</u>	peptide bonds are formed <u>between amino</u> <u>acids</u>					
	Product	Many glycosidic bonds in carbohydrates linked monosaccharides to form <u>polysaccaharides</u>	many peptide bonds in protein linked amino acids to form polypeptides					
5	Bonds formation between functional groups	formed between <u>hydroxyl</u> groups of two different monosaccharides	formed between the amino group of an amino acid and the <u>carboxyl group</u> of another amino acid					
6	Types of bonds	Several / different types of glycosidic bonds can be formed e.g. α (1,4) or (1,6) glycosidic bond	<u>One</u> type of peptide bond is always formed between 2 amino acids					
7	Branched vs linear	Could result in the formation of <u>branched</u> α (1,6) or <u>linear</u> α (1,4) polymer.	Results only in <u>linear</u> polymer.					

NB: at least 1 similarity and 1 difference to get full marks

- 1) An example of a fibrous protein is collagen*
- 2) Collagen is a structural protein that <u>provides support</u> e.g. collagen is found in skin, bones, blood vessels etc
- A <u>tropocollagen</u>* molecule consists of <u>three</u>* helical <u>polypeptide</u>* chains wound around each other like a rope
- Repeating tripeptide unit: <u>Glycine-X-Y</u> in each polypeptide chain, where X is usually <u>proline</u>* and Y is usually <u>hydroxyproline</u>*.
- 5) <u>Glycine</u>*, the smallest amino acid results in a <u>compact coil / tight</u> <u>triple helix.</u>
- <u>Bulky</u> and relatively inflexible <u>proline</u>* and <u>hydroxyproline</u>* residues confer <u>rigidity</u> of the molecule.
- <u>Hydrogen bonds</u>* are formed <u>within each helical polypeptide</u> chain and this <u>stabilise each polypeptide chain</u> which helps with providing support
- <u>Hydrogen bonds</u>* are also formed <u>between adjacent polypeptide</u> <u>chains</u> and this increases <u>tensile strength</u>* which provides it with the ability to resist snapping due to stretching
- 9) <u>Insoluble</u> due to: <u>large molecular size</u> of tropocollagen molecule OR

*hydrogen bonds** formed between adjacent polypeptide chains make collagen

which contributes to the function of providing structural support.

- 10) <u>Cross-linking</u>* involving <u>lysine</u>* residues of <u>adjacent tropocollagen</u> molecules
- 11) results in the formation of <u>fibrils / parallel bundles / idea of fibres</u> which greatly increases <u>tensile strength</u>*.
- 12) <u>Staggered/overlapping arrangement</u> of tropocollagen <u>minimizes</u> <u>points of weaknesses</u> along the length of the fibrils contributes to structural support
- (c) Explain how primary, secondary and tertiary structures of a protein affect the [8] functions of a proteinaceous enzyme.

Structure

- 1. Primary structure refers to the unique <u>sequence and number of</u> <u>amino acids</u> in a polypeptide linked by peptide bonds.
- Secondary structure refers to the <u>regular</u> coiling and folding/pleating of the polypeptide held by <u>hydrogen bonds</u>* between <u>CO and NH</u> <u>groups</u> of the <u>polypeptide backbone</u>;
- In <u>alpha helix</u>*, <u>hydrogen bonds</u>* form between CO and NH groups <u>4 a.a. apart</u>, forming a 3D <u>helical</u> structure OR

In **beta pleated sheet***, **hydrogen bonds*** form between CO (or NH) group of one region/segment and NH (or CO) group of an adjacent region/segment of a single polypeptide chain, forming a flat/pleated sheet;

 Tertiary structure refers to the folding of polypeptide into a specific conformation, held by <u>bonds between *R-groups*</u>* of structural amino acids <u>within same polypeptide</u>

- 5. Tertiary structure is maintained by <u>hydrophobic interaction</u>, <u>hydrogen bonds, ionic bonds, disulfide bridges</u>
- 6. To give rise to **globular proteins*** like enzymes.
- 7. Whereby R groups of <u>catalytic amino acids</u> and <u>contact amino acids</u> are brought close together in the active site
- 8. <u>R groups</u> of <u>contact/binding residues bind</u> reversibly with <u>substrate</u> to position it in the <u>correct orientation</u> for catalysis to occur.
- 9. <u>R groups</u> of <u>catalytic residues</u> present within active site <u>catalyze</u> <u>conversion of substrate to product</u>.
- 10. Enzymes have <u>specific</u> <u>active site</u> that is <u>complementary in shape</u> <u>and charge</u> to its <u>substrate</u>.
 (The <u>3D conformation</u> of the active site is dependent on the <u>primary</u>, <u>secondary and tertiary structure</u> of the protein.)

[Total: 20]