OXFORD
INTERNATIONAL
AQA EXAMINATIONS

INTERNATIONAL AS
BIOLOGY
BL01 (9610)

Unit 1 The Diversity of Living Organisms

Mark scheme

January 2020

Version: 1.0 Final

Mark schemes are prepared by the Lead Assessment Writer and considered, together with the relevant questions, by a panel of subject teachers. This mark scheme includes any amendments made at the standardisation events which all associates participate in and is the scheme which was used by them in this examination. The standardisation process ensures that the mark scheme covers the students' responses to questions and that every associate understands and applies it in the same correct way. As preparation for standardisation each associate analyses a number of students' scripts. Alternative answers not already covered by the mark scheme are discussed and legislated for. If, after the standardisation process, associates encounter unusual answers which have not been raised they are required to refer these to the Lead Examiner.

It must be stressed that a mark scheme is a working document, in many cases further developed and expanded on the basis of students' reactions to a particular paper. Assumptions about future mark schemes on the basis of one year's document should be avoided; whilst the guiding principles of assessment remain constant, details will change, depending on the content of a particular examination paper.

Further copies of this mark scheme are available from oxfordaqaexams.org.uk

Question	Marking guidance	Mark	Comments
01.1	20 000;	1	Allow answers in range 20 000 – 20 250 Reject if units given on answer line e.g. µm
01.2	**Cell wall** contains glycoprotein/peptidoglycan/murein/no cellulose; **Ribosomes** are smaller/70S/not 80S/not attached to ER/free in the cytoplasm;	2	1. Ignore reference to capsule 1. Reject 'chitin'
01.3	1. Ribosomes identified as site of protein synthesis; 2. tRNA not able to bind (to ribosomes) **so** prevents translation/production of proteins; 3. No/less enzymes **so** unable to catalyse reactions for synthesis of materials needed for division; **OR** No/less (structural) proteins **so** prevents formation of new cell membrane/wall;	3	1. Can be implied by descriptions in MP2 or MP3 1. Reject other molecules e.g. lipids are produced at ribosomes 2. Accept mRNA not able to bind 3. Need idea of how it stops cell division. Examples: Cells cannot produce enzymes needed for: • DNA replication **so** cells cannot complete division • Respiration **so** no/less ATP for division

Question	Marking guidance	Mark	Comments
02.1	Any **two** from the following: 1. Concentration of lipid (in the milk); 2. Concentration of enzyme/lipase; 3. Concentration of sodium carbonate; 4. Speed of stirring e.g. always slow or fast (continuously); 5. Same person to judge when the solution loses pink colour/compare to a colour standard;	2 max	1. Allow same fat content of the milk/same type/source of milk 3. Allow starting pH Ignore temperature / volumes/amounts as given in the question.
02.2	To allow the solution/milk/contents of the test tube to reach the correct temperature; **OR** To allow the solution/milk to reach the same temperature as the water bath/30^{o}C;	1	Allow to 'maintain' temperature / to have 'constant' temperature
02.3	(Buffer solution maintains a constant pH and) students were measuring change in pH;	1	Ignore 'not trying to keep pH constant' Allow idea that if a buffer solution was used then there would be no colour change / solution would remain pink Allow the idea that no buffer solution was used so that phenolphthalein would show a change in colour
02.4	1. Large intervals/10^{o}C intervals; 2. Optimum temperature could be between 30^{o}C – 40^{o}C / 40^{o}C – 50^{o}C / 30^{o}C – 50^{o}C;	2	1. Allow the idea that smaller intervals are needed Allow reference to only a single investigation / need to repeat to verify

02.5	1. (As temperature increases) increase in kinetic energy of enzymes/substrates; 2. More (successful) collisions between enzymes and substrates/more E-S complexes form; 3. High temperature/50°C/temperatures above 40°C (slows reaction as) denatures the <u>active site</u> / causes <u>active site</u> to change shape; 4. Reference to breaking hydrogen/ionic/disulfide bonds (within tertiary structure);	3 max	1. & 2. Allow converse answer for low temperatures 1. Accept enzymes/substrates move faster 2. & 4. Allow lipid/fat/triglyceride as alternatives to substrate 4. Ignore 'bonds' unqualified 4. Reject peptide bonds broken

02.6	1. Correct tangent drawn; 2. (−)0.04 (pH units s^{-1});	2	Allow one mark calculation without the use of a tangent e.g. $\frac{(8.5 - 5.2)}{60}$ = 0.055/0.06 2. Allow answers in range 0.03 – 0.07

02.7	1. (Decrease in pH as) as <u>fatty acids</u> are produced (from the hydrolysis of lipids); 2. High initial rate of reaction as large amount of substrate; 3. Curve plateaus as less/no substrate to be hydrolysed / no more fatty acids produced / substrate concentration becomes limiting factor **OR** Lipase would be denatured as pH decreases;	3	2. Allow lipid/fat/triglyceride as alternatives to substrate 3. Allow all the substrate has been used up

Question	Marking guidance	Mark	Comments
03.1	1. Bilayer; 2. (Hydrophobic) fatty acids/lipids (tails) to the inside; **OR** (Hydrophilic) phosphate group (head) to the outside;	2	1. Accept double layer 1. Accept drawing which shows bilayer Allow a fully labelled diagram for 2 marks
03.2	Diffusion;	1	Reject facilitated diffusion
03.3	1. (Many narrow tubes gives a) large surface area; 2. (So) high(er) rate of diffusion/exchange of substances; **OR** 3. (Artificial) thin membranes; 4. Short(er) distance for diffusion / for faster rate of diffusion / easier for substances to pass through; **OR** 5. Blood and dialysis fluid flow in opposite directions / dialysis fluid in continuous circulation; 6. Maintains concentration gradient so higher rate of diffusion / diffusion along the full length of the surface;	2	Mark in pairs e.g. either 1. + 2. or 3. + 4. 2. and 4. For substances allow exchange of materials/urea 6. Allow so equilibrium not reached 6. Allow blood always flows past dialysis fluid with a lower concentration of urea

03.4	52.8;	1	

03.5	(No) dialysis adequacy = 1.1;;	2	Allow ecf from 03.4 If no / incorrect answer, then allow for 1 mark: 52.8 or answer from 03.4 0.6 × 80 If the answer from this calculation using the ecf from 03.4 is: <1.2 = 2 marks ≥1.2 = 1 mark (as this would suggest adequate dialysis)

Question	Marking guidance	Mark	Comments
04.1	**A** = Trachea **B** = Bronchus/bronchi;	1	Both correct answers needed for one mark Allow incorrect spelling of structures but must be correct phonetically. Ignore windpipe Ignore left/right Reject 'Bronchiole' / 'Tracheole' / 'Trachae'
04.2	1. Contraction of diaphragm (muscles) **and** flattens the diaphragm; 2. Contraction of (external) intercostal muscles **and** raises ribcage; 3. Volume of the lungs/thoracic cavity increases **and** the pressure decreases;	3	1. Allow diaphragm moves downwards 2. Reject contraction of the internal intercostal muscles Two aspects needed for each marking point
04.3	1. Method to determine level of fitness (of participants/volunteers); 2. Large number of participants required (for each group) **OR** Large number of repeat measurements per person; 3. Matching a named factor e.g. ages/sex/ethnicity/smoking or non-smoking; 4. Method of measuring their resting breathing rate; 5. Calculate mean (and standard deviation) of each group **OR** Calculate mean for each individual (after several repeats); 6. Statistical test is t-test / standard error and 95% confidence limits (to see if there is a significant difference between means);	5 max	1. Allow idea e.g. measure resting heart rate / completion of a (standard) exercise test 2. If a number is given then must be at least 10 people per group 6. Allow reference to Spearman rank in the correct context Only allow max marks if point 6 has been covered

<table>
<tr><th>Question</th><th>Marking guidance</th><th>Mark</th><th>Comments</th></tr>
<tr><td>05.1</td><td>1. A section of DNA that codes for a polypeptide/protein/enzyme;
2. The complete set of genes in a cell/organism/population/species;</td><td>2</td><td>Also accept the genome is all of the DNA in an organism including in eukaryotes the non-coding DNA and DNA in mitochondria/chloroplasts
2. Instead of ‘complete set of genes’ allow all the genetic material / the genetic constitution</td></tr>
<tr><td>05.2</td><td><table>
<tr><th></th><th>Prokaryotic cell</th><th>Eukaryotic cell</th><th>Mitochondrial DNA</th></tr>
<tr><td>Genetic material held in a nucleus</td><td></td><td>✓</td><td></td></tr>
<tr><td>Histones present</td><td></td><td>✓</td><td></td></tr>
<tr><td>DNA in the form of linear molecules</td><td></td><td>✓</td><td></td></tr>
<tr><td>DNA found as a double helix structure</td><td>✓</td><td>✓</td><td>✓</td></tr>
</table></td><td>3</td><td>Need whole column to be correct to get the mark
Assume unfilled boxes are false</td></tr>
</table>

Question	Marking guidance	Mark	Comments
06.1	(Further) folding/coiling of a (secondary structure) protein/polypeptide due to interactions between R-groups;	1	For 'interactions between R-groups' allow examples e.g. ionic/disulfide bonds / hydrophobic/Van Der Waals interactions
06.2	R group/side chain;	1	Allow sulfhydryl group
06.3	1. Hydrogen/H-(bonds); 2. Ionic (bonds);	1	Allow hydrophobic (bonds) / non-polar interactions Reject peptide bonds
06.4	1. Disulfide bonds too strong (to break with this method); 2. (Titin molecules) not fully stretched to (primary/secondary structure) / disulfide bonds hold molecule together / prevents/reduces stretching;	2	2. Accept that the structure has greater rigidity due to (strong) disulfide bonds
06.5	1. Use a large number of samples/titin molecules for each group; 2. Keep pH constant/use a buffer; 3. Keep temperature constant/use a water bath; 4. Apply the same force/apply force for same length of time; 5. Same number of disulfide bonds; 6. Measure results to **same** level of precision; 7. Use titin molecules from same source/same species/same section of the heart; 8. Same size/thickness of titin;	4 max	1. Allow large sample size 1. Accept many/multiple repeats taken. Ignore 'several' 6. Allow measure lengths with the same microscope 8. Ignore 'amount'

06.6	1. Shape of curve described e.g. no/slow rise initially/with a low number of amino acids **and** then rapid/exponential rise (with higher number of amino acids); 2. Use of data – e.g. little effect up to 30 or 40 amino acids then exponential rise above this **OR** Takes up to 1 second with up to 60 amino acids but 6-fold increase between 60 and 100 amino acids;	2	1. Ignore reference to positive correlation alone 2. Accept below around 60 amino acids there is very little change in folding time/converse 2. Allow other suitable use(s) of data

06.7	Chaperone (proteins);	1	Allow incorrect spelling but must be correct phonetically.

06.8	2.3 x 150 = 345;;	2	2 marks for correct answer within the range 345 - 360 1 mark for correct working or incorrect figure from the graph but answer correct for this figure e.g. 2.6 x 150 = 390

06.9	1. Disulfide bonds reduce amount of unfolding of the protein; 2. Disulfide bonds hold adjacent parts of polypeptide chain in place for re-forming (R-R) bonds;	2	1. No/few disulfide bonds (in the original tertiary structure) are broken

Question	Marking guidance	Mark	Comments
07.1	1. First division separates homologous chromosomes **so** each daughter cell receives one chromosome from each pair; 2. Second division separates chromatids **so** produces haploid (daughter) cells; 3. At fertilisation the diploid number is restored / a constant number of chromosomes is maintained across generations;	3	2. Allow cells with half the number of chromosomes for haploid
07.2	Random fertilisation (of gametes);	1	Allow random fusion of gametes Allow random mating
07.3	1,941	1	Ignore 1940.6
07.4	1. Homologous pairs of chromosomes associate / form a bivalent; 2. Chiasma(ta) form; 3. (Equal) lengths of (non-sister) chromatids / alleles are exchanged; 4. Producing new combinations of alleles;	4	1. Accept descriptions of homologous pairs 2. Accept descriptions of chiasma(ta) e.g. chromatids / chromosomes entangle / twist 2. Neutral 'crossing over / cross over' 3. Ignore genes are exchanged 3. Accept lengths of DNA are exchanged 4. Do not allow reference to 'new combinations of genes' unless qualified by alleles Allow a series of annotated diagrams
07.5	C	1	

Question	Marking guidance	Mark	Comments
08.1	21	1	
08.2	1. Humans most closely related to chimpanzees **as** the amino acid sequence is the same/no differences; 2. Humans least related to gorillas **as** there are two differences (in the amino acid sequence); 3. Humans more related to orangutans than gorillas **as** there is only one difference (in the amino acid sequence between the human and the orangutan);	3	Accept correct reference to recency of common ancestor If no conclusion given, allow one mark for the correct order e.g. chimpanzee – 0 differences, orangutan 1 difference and gorilla – two differences
08.3	1. The code is degenerate/more than one triplet for each amino; 2. Data only shows part of the amino acid sequence **OR** There may be more/less differences in other parts of the sequence (that are not shown); 3. Data only shows the amino acid sequence for one protein **OR** Other proteins may show more/less differences in the amino acid sequence; 4. Differences may be found within introns/non coding regions;	3 max	1. Allow reference to codon instead of triplet