

**F212: Module 1: Nucleic Acids**  
**From June 2009-January 2013**  
**Mark schemes**

- |   |
|---|
| (a) state that deoxyribonucleic acid (DNA) is a polynucleotide, usually double stranded, made up of nucleotides containing the bases adenine (A), thymine (T), cytosine (C) and guanine (G);  |
| (b) state that ribonucleic acid (RNA) is a polynucleotide, usually single stranded, made up of nucleotides containing the bases adenine (A), uracil (U), cytosine (C) and guanine (G);  |
| (c) describe, with the aid of diagrams, how hydrogen bonding between complementary base pairs (A to T, G to C) on two antiparallel DNA polynucleotides leads to the formation of a DNA molecule, and how the twisting of DNA produces its 'doublehelix' shape |
| (d) outline, with the aid of diagrams, how DNA replicates semi-conservatively, with reference to the role of DNA polymerase;  |
| (e) state that a gene is a sequence of DNA nucleotides that codes for a polypeptide   |
| (f) outline the roles of DNA and RNA in living organisms (the concept of protein synthesis must be considered in outline only).   |

F212

Mark Scheme

June 2011

Question	Expected Answers	Mark	Additional Guidance
7 (a)	<p>X phosphate ;</p> <p>Y <u>d</u>eoxyribose ;</p> <p>Z <u>t</u>hymine ;</p>	3	<p><b>Mark the first answer for each letter.</b> If the answer is correct and an additional answer is given that is incorrect or contradicts the correct answer then = 0 marks</p> <p><b>DO NOT CREDIT</b> PO<sub>4</sub> or 'phosphate , molecule / backbone' <b>IGNORE</b> group</p> <p><b>DO NOT CREDIT</b> deoxyribulose</p> <p><b>IGNORE</b> (pentose) sugar</p> <p><b>DO NOT CREDIT</b> incorrect spelling</p> <p><b>IGNORE</b> (nitrogenous) base / T</p>

F212

Mark Scheme

June 2011

Question	Expected Answers	Mark	Additional Guidance
7 (b)	<p>1 <u>semi-conservative</u> (replication) ;</p> <p>2 (double) <u>helix</u>, untwists / uncoils / unwinds / unravels ;</p> <p>3 hydrogen bonds (between bases) break ;</p> <p>4 each strand acts as the <u>template</u> (for the formation of a new molecule) ;</p> <p>5 free (DNA) nucleotides (align with exposed bases) ;</p> <p>6 complementary base pairing / purine to pyrimidine ;</p> <p>7 hydrogen bonds (re)form ;</p> <p>8 sugar-phosphate backbone forms / adjacent nucleotides join ;</p> <p>9 <u>DNA</u> polymerase joins , backbone / strands ;</p> <p>10 each new molecule has 1 old and 1 new strand ;</p> <p>11 AVP ;</p> <p><b>QWC</b> ~ events in correct sequence so long as no ref to transcription / translation , seen ;</p>	<p>6 max</p> <p>1</p>	<p><b>CREDIT</b> answers from clearly labelled diagram <b>IGNORE</b> anything after it becomes clear that a candidate is <b>describing</b> transcription</p> <p>2 <b>IGNORE</b> straightens <b>DO NOT CREDIT</b> <math>\alpha</math>-helix</p> <p>3 <b>IGNORE</b> unzips</p> <p>5 <b>IGNORE</b> in cytoplasm</p> <p>6 <b>IGNORE</b> A to T / C to G (as given in Q) <b>ACCEPT</b> base pair rule</p> <p>8 <b>CREDIT</b> formation of phosphodiester bond</p> <p>9 <b>ACCEPT</b> in context of H bonds forming</p> <p>10 <b>DO NOT CREDIT</b> half old and half new strand</p> <p>11 e.g. correct ref to , (DNA) helicase (in context of unwinding or unzipping) / (DNA) ligase ( in context of joining Okazaki fragments or role in backbone formation) / leading or lagging strand / 3' / 5' / antiparallel / activation of free nucleotides / 3 H bonds between C and G / 2 H bonds between A and T / Okazaki fragments / proof reading</p> <p>1 mark from mps 2 to 4 <b>then</b> 1 mark from mps 5 to 7 <b>then</b> mp 8 or 9</p>
	<b>Total</b>	<b>[10]</b>	

Question	Expected Answer	Mark	Additional Guidance
4 (a) (i)	1 (m)RNA is single stranded / DNA is double stranded ; 2 (m)RNA is non helical / DNA is helical ;	1	Mark the first response but do not award the mark if a further answer is incorrect or contradictory <b>DO NOT CREDIT</b> refs to length as given in stem 1 <b>ACCEPT</b> DNA is a double helix (as stranded is implied) <b>for this mp</b> <b>DO NOT CREDIT</b> DNA is a double <i>molecule</i> 2 <b>ACCEPT</b> (mRNA) not twisted / not coiled / not spiral / straight / ora
4 (a) (ii)	1 RNA contains ribose <b>and</b> DNA contains deoxyribose ; 2 RNA contains, uracil / U, <b>and</b> DNA contains, thymine / T ; 3 / more than 1, forms of RNA ; 4 RNA is, single stranded / non helical, <b>and</b> DNA is, double stranded / helical ; <i>if not already awarded as answer in (i)</i>	1	Mark the first response to (a)(ii) – but but do not award the mark if a further answer is incorrect or contradictory 2 <b>DO NOT CREDIT</b> th <u>y</u> amine 3 <b>ACCEPT</b> 'one form of DNA'
4 (a) (iii)	gene ;	1	<b>IGNORE</b> allele / operon
4 (a) (iv)	too big to / does not, fit through pore (in nuclear envelope) ;	1	<b>ACCEPT</b> 'too long to fit ... pore'
4 (a) (v)	<i>idea that only copies one, gene / section / part / AW, (of DNA) ; idea that DNA comprises many, genes / alleles ;</i>	2	e.g. mRNA only codes for 1 protein <b>DO NOT CREDIT</b> '1 DNA molecule contains <u>all</u> the genes' 'mRNA only codes for 1 protein but DNA codes for many proteins' = 2 marks

Question	Expected Answers	Marks	Additional Guidance
6 (a) (i)	<p>deoxyribose (sugar) ; phosphate (group) ;  (nitrogenous / purine or pyrimidine) base / one correctly named base ;</p>	3	<p><b>DO NOT CREDIT</b> dioxynribose <b>DO NOT CREDIT</b> phosphate head or phosphate backbone  <b>DO NOT CREDIT</b> letter instead of named base <b>DO NOT CREDIT</b> uracil <b>DO NOT CREDIT</b> incorrect spelling of thymine with 'a'</p>
6 (a) (ii)	<p>has ribose ; uracil / U, instead of, thymine / T ; single stranded ; 3 forms / AW ;</p>	2 max	<p>assume answer refers to RNA unless otherwise stated  <b>DO NOT CREDIT</b> incorrect spelling of thymine with 'a'</p>

Question	Expected Answers	Marks	Additional Guidance
6			
(b)			
1	untwist / unwind ;		<b>1 DO NOT CREDIT</b> unravel
2	unzip / described ;		
3	H bond breaks ;		<b>2 DO NOT CREDIT</b> strands separating without qualification
4	both strands act as template ;		
5	(aligning of) free (DNA) nucleotides ;		<b>5 DO NOT CREDIT</b> bases
6	<u>complementary</u> , base / nucleotide, pairing ;		<b>6 &amp; 7</b> Do not consider for <b>QWC</b> if mark awarded in the context of breaking apart or DNA structure only, rather than forming new double helix
7	C to G <b>and</b> T to A / purine to pyrimidine ;		
8	hydrogen bonds reform ;		
9	sugar-phosphate back bone forms ;		
10	(using) covalent / phosphodiester, bond ;		
11	<u>semi-conservative</u> replication ;		
12	DNA polymerase ;		<b>12 CREDIT</b> at any stage in the process
13	AVP ;		<b>13 e.g.</b> ligase / helicase / gyrase used in correct context C – G 3 H bonds / T – A 2 H bonds activation of free nucleotides (with 2 phosphates) synthesis in the 5' to 3' direction Okazaki fragments on lagging strand
		<b>6 max</b>	
	<b>QWC</b> - correct sequence – 1 <b>S</b> mark, then 1 <b>N</b> mark, then 1 <b>R</b> mark ;	<b>1</b>	It should be clear that candidate realises that the sequence is <b>S</b> , then <b>N</b> then <b>R</b> – even if not written in that order <b>DO NOT CREDIT</b> if any ref to transcription / translation

Question	Expected Answers	Marks	Additional Guidance
6 (c) (i)	polypeptide / protein / primary structure / a sequence of amino acids ;	1	<b>DO NOT CREDIT</b> 'codes for an amino acid' <b>IGNORE</b> enzyme / named protein
6 (c) (ii)	different, sequence of amino acids / primary structure / AW ; different protein / protein folds up differently / different tertiary structure ; (product) no longer functions / different function ;	2 max	<b>DO NOT CREDIT</b> 'product' or incorrect biochemical (e.g. carbohydrate) <b>ACCEPT</b> suitable example, e.g. active site of enzyme no longer complimentary to substrate
<b>Total</b>		<b>15</b>	

## F212 Molecules, Biodiversity, Food and Health

Question	Expected Answers	Marks	Additional Guidance
1 (a)	double helix ; anti-parallel ; sugar-phosphate ; hydrogen ;	4	
1 (b)	percentages / amount , C & G similar (in all organisms) ; percentages / amount , A & T similar (in all organisms) ; <u>different / named</u> , <u>organisms</u> have different proportions of , bases / named base / AW ; greatest similarity between human and grasshopper ; least similarity between <i>E coli</i> and the other three ; <i>E. coli</i> has similar proportions of all bases / <i>E.coli</i> has <u>slightly</u> more CG than AT / (named) eukaryote has more AT than CG ; comparative figs with units to support any statement ;	3 max	mp 1 & 2 <b>DO NOT CREDIT</b> ref to a single organism mp 1 & 2 <b>IGNORE</b> ref to complementary <b>DO NOT CREDIT</b> statements in context of organism size e.g. statement that human has more A than <i>E. coli</i> / human has the most AT / <i>E. coli</i> has the most CG This mark is for a general statement  e.g. human C = 19.8% <u>and</u> G = 19.9% human A = 30.9% <u>and</u> <i>E. coli</i> A = 24.7% 'human has more A (30.9%) than wheat (27.3%)' = 2 (mp 3 & 7)



Question	Expected Answers	Marks	Additional Guidance
1 (b)	(suggests) A, bonds / pairs / links / connects / joins, to T ; (suggests) C, bonds / pairs / links / connects / joins, to G ; (suggests) purine bonds to pyrimidine ; (evidence for) complementary base pairing / which bases pair with each other / base pairing rules ; suggests bases point 'inwards' rather than 'outwards' ;	2 max	IGNORE A – T or A = T unqualified IGNORE C – G or C = G unqualified  ACCEPT 'bond' instead of 'pair'

Question	Expected Answers	Marks	Additional Guidance												
1 (c)	<p><b>Award 1 mark per correct row</b></p> <table border="1" data-bbox="352 1032 852 1778"> <thead> <tr> <th data-bbox="352 1608 427 1778">feature</th> <th data-bbox="352 1308 427 1608">DNA</th> <th data-bbox="352 1032 427 1308">RNA</th> </tr> </thead> <tbody> <tr> <td data-bbox="427 1608 533 1778">number of strands</td> <td data-bbox="427 1308 533 1608">two / double</td> <td data-bbox="427 1032 533 1308">one / single</td> </tr> <tr> <td data-bbox="533 1608 746 1778">bases present</td> <td data-bbox="533 1308 746 1608">thymine / T (+ adenine + cytosine + guanine)</td> <td data-bbox="533 1032 746 1308">uracil / U (+ adenine + cytosine + guanine)</td> </tr> <tr> <td data-bbox="746 1608 852 1778">sugar present</td> <td data-bbox="746 1308 852 1608">deoxyribose</td> <td data-bbox="746 1032 852 1308">ribose</td> </tr> </tbody> </table>	feature	DNA	RNA	number of strands	two / double	one / single	bases present	thymine / T (+ adenine + cytosine + guanine)	uracil / U (+ adenine + cytosine + guanine)	sugar present	deoxyribose	ribose	3	<p>If a choice of answers is given, do not credit unless both answers are valid (e.g. two and double strands for DNA / ribose and pentose sugar)</p> <hr/> <p><b>ACCEPT</b> letters instead of names of bases Names of bases must be unambiguous, so <b>DO NOT CREDIT</b> adenosine / thiamine / cysteine / etc. If more bases mentioned than T and U, then all bases must be included</p> <hr/> <p><b>DO NOT CREDIT</b> dioxiribose / oxyribose/ hexose / sugar <b>IGNORE</b> pentose</p>
feature	DNA	RNA													
number of strands	two / double	one / single													
bases present	thymine / T (+ adenine + cytosine + guanine)	uracil / U (+ adenine + cytosine + guanine)													
sugar present	deoxyribose	ribose													
1 (d)	<p>carries / transfers, the (complementary DNA), code / genetic information / copy of gene ; out of the nucleus ; (transfers it) to the, ribosome / RER / site of translation ; for, protein / polypeptide, synthesis ;</p>	2 max	<p><b>IGNORE</b> transcription <b>DO NOT CREDIT</b> ref to the <u>whole</u> DNA code / molecule</p> <p><b>ACCEPT</b> 'to make protein'</p>												
<b>Total</b>		14													