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

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

Question			Expected Answers	Marks	Additional Guidance
1	(c)	(i)	polypeptide / protein / primary structure / a sequence of amino acids ;	1	**DO NOT CREDIT** 'codes for an amino acid' **IGNORE** enzyme / named protein
1	(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	**DO NOT CREDIT** 'product' or incorrect biochemical (e.g. carbohydrate) **ACCEPT** suitable example, e.g. active site of enzyme no longer complimentary to substrate
			Total	15	

Question			Answer	Mark	Guidance
2	(a)		characteristics / features / AW , are passed on to / inherited (by the next generation) **;**	1	**IGNORE** genes / alleles / DNA as question asks about Darwin's conclusion **ACCEPT** 'appearance' for features **DO NOT CREDIT** answers that only refer to beneficial characteristics (as Darwin's other observations would need to be considered to arrive at this conclusion)
2	(b)		**1** B **and** C **and** D are more closely related (to each other than to A) **; ora** **2** *idea that* A is in different (taxonomic) group (from other 3) **; ora** **3** B **and** C **and** D , share more , recent common ancestor **;** **4** phylogeny / evolution , of B **and** C **and** D diverged at same point **; ora**	2 max	**IGNORE** references to relationship with organism (1) **1 IGNORE** 'B, C and D are more similar' as this could refer to appearance rather than relationship **2 CREDIT** named taxonomic group **3 IGNORE** genes etc.
2	(c)		fits evidence **;** *idea of* more **,** evidence / research (since nineteenth century) **;**	1 max	**CREDIT** examples, e.g. DNA revolution / more fossils **ACCEPT** improved technology / molecular evidence **IGNORE** 'the theory has been proved' **IGNORE** Darwin provided more evidence **ACCEPT** changes in religious belief
2	(d)	(i)	code for (one or more) polypeptide(s) **;**	1	**ACCEPT** protein **IGNORE** amino acid sequence

Question			Answer	Mark	Guidance
2	(d)	(ii)		5 max	**AWARD** marks from clearly annotated diagram
			1 double stranded **;**		**1 ACCEPT** double helix **or** two , polynucleotides / strands / chains **or** antiparallel strands **1 IGNORE** one old and one new strand
			2 each / both (strands) act as template **;**		**2 IGNORE** either **NOTE** 'there are 2 strands which act as templates' = 2 marks (mp 1 and 2)
			3 hydrogen bonds , easily , break / form , between bases ;		**3 ACCEPT** weak H bonds between bases break **3 IGNORE** refs to H bonds , breaking / forming , without qualification that the bonds are weak or , form / break , easily
			4 complementary (specified) base , pairing / AW **;**		**4 IGNORE** complementary nucleotides unless qualified with examples of base-pairing
			5 purine (only able to) bind to pyrimidine **;** **6** (due to) different sizes of purines and pyrimidines **;**		
			7 hydrogen bonding different between A & T **and** C & G **or** 3 H bonds between C & G **and** 2 H bonds between A & T **;**		**7 ACCEPT** names of bases with phonetic spellings **7 DO NOT CREDIT** thyamine **7ACCEPT** A=T **and** C≡G without reference to hydrogen bonds

Question			Answer	Mark	Guidance
2	(e)	(i)	<u>speciation</u> **;**	1	
2	(e)	(ii)	*idea that* different islands have different **,** selection pressures / habitats / environments / vacant niches **; ora** *idea of* isolation **; ora**	1 max	**CREDIT** ' the Galapagos have a wider range of habitats' **IGNORE** islands have different habitat(s) from the mainland e.g. the islands are separated from the mainland / no gene flow / geographic barrier / reproductive barrier **ACCEPT** allopatric (speciation) **IGNORE** sympatric **IGNORE** refs to succession or human habitat destruction on the mainland as the question is about evolution
			Total	**12**	

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

Question			Expected Answers	Marks	Additional Guidance
3	(b)	(ii)	(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'

<table>
<tr><th colspan="3">Question</th><th>Expected Answers</th><th>Marks</th><th>Additional Guidance</th></tr>
<tr><td>3</td><td>(c)</td><td></td><td>Award 1 mark per correct row

<table>
<tr><th>feature</th><th>DNA</th><th>RNA</th><th></th></tr>
<tr><td>number of strands</td><td>two / double</td><td>one / single</td><td>;</td></tr>
<tr><td>bases present</td><td>thymine / T
(+ adenine
+ cytosine
+ guanine)</td><td>uracil / U
(+ adenine
+ cytosine
+ guanine)</td><td>;</td></tr>
<tr><td>sugar present</td><td>deoxyribose</td><td>ribose</td><td>;</td></tr>
</table></td><td>3</td><td>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)

ACCEPT letters instead of names of bases
Names of bases must be unambiguous, so
DO NOT CREDIT adenosine / thiamine / cysteine / etc.
If more bases mentioned than T and U, then all bases must be included

DO NOT CREDIT dioxyribose / oxyribose/ hexose / sugar
IGNORE pentose</td></tr>
<tr><td>3</td><td>(d)</td><td></td><td>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 ;</td><td>2 max</td><td>IGNORE transcription
DO NOT CREDIT ref to the whole DNA code / molecule

ACCEPT ‘to make protein’</td></tr>
<tr><td></td><td></td><td></td><td>Total</td><td>14</td><td></td></tr>
</table>