

Question 23 (Answer: **B**)

- Purines (adenine and guanine) have two rings; pyrimidines (thymine and cytosine) have one.
- Count the rings drawn for each labelled base to sort purine from pyrimidine.
- Then use the hydrogen bonds: A–T has two and G–C has three.

Question 24 (Answer: **A**)

- DNA polymerase can only add nucleotides to a free 3' end, so it works 5' to 3'.
- That forces the lagging strand to be made in short Okazaki fragments.
- DNA ligase then joins those fragments together.

Question 24 (Answer: **D**)

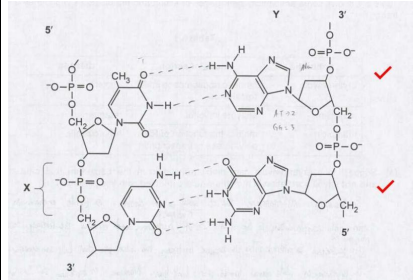
- DNA ligase joins fragments together, so it acts last on the lagging strand.
- The fragments are made first, each 5' to 3'.
- Ligase then seals the gaps between them into a continuous strand.

Question 25 (Answer: **B**)

- Complementary base pairing happens in transcription and translation, so statement 1 is right.
- A purine is larger than a pyrimidine, so statement 2 is wrong.
- Every pair is one purine with one pyrimidine, which is why all base pairs are the same length – statement 3 is right.

Question 22 (Answer: **D**)

- DNA polymerase can only add nucleotides to a free 3' end.
- So it always moves along the template in the 3' to 5' direction, building the new strand 5' to 3'.
- The two template strands are antiparallel, so the enzyme moves in opposite directions along them.

4(a)(i)	repeating , units / sub-units / molecules / nucleotides (used to make a, polymer / polynucleotide / strand (of DNA)) ;
4(a)(ii)	any one from: (pentose / sugar is) ribose (not deoxyribose) ; C2 on the, pentose / sugar, is -OH not -H ;
4(a)(iii)	respiration ;
4(b)(i)	two hydrogen bonds drawn correctly between A and T ; three hydrogen bonds drawn correctly between C and G ; <i>for positioning of H bonds on C-G, A from either H on amine group on C to link with oxygen on G</i>  <i>if no marks gained but A-T has two lines and C-G has three lines between bases award 1 mark</i>
4(b)(ii)	phosphodiester ;

3(a)(i)	<i>if DNA or thymine stated within response, allow <u>only</u> H-bond mark (ecf)</i> any two from: (paired section) contains, complementary nucleotides / complementary bases / base pairs ; adenine-uracil <u>and</u> guanine/cytosine ; A A/U and G/C (paired by) hydrogen / H, bonds ; I strong (bonds) ecf from mp1 R if another bond also named I phosphodiester bonds between, adjacent / AW, nucleotides
3(a)(ii)	any two from: (enzyme / Drosha / Dicer) active site is specific (to site on dsRNA) ; <i>can apply in context of specific shaped active site or active site specific to a particular location</i> detail of different active sites of Drosha and Dicer ; site to be cleaved / AW, (only), fits into / can bind with / is complementary to (the specific) active site forms enzyme-substrate complex at a particular site Drosha and Dicer require different, conditions / cell locations, to function ; AVP ; e.g. <i>suggestion that</i> Dicer too large to enter nucleus Drosha exposed to degradation in cytoplasm

3(b)	<i>any two from:</i> mRNA is single-stranded and siRNA is double-stranded ; A polynucleotide / chain, for strand siRNA has paired and unpaired nucleotides or mRNA has, only unpaired nucleotides / no base pairing ; mRNA codes for a, sequence of amino acids / protein ; ora for siRNA mRNA has a longer sequence of nucleotides ; A mRNA, is longer / has more nucleotides AVP ; e.g. <i>ref. to</i> siRNA antiparallel / mRNA only 5' to 3' mRNA has no H bonds
3(c)(i)	<i>any one from:</i> RISC must, align with / attach to / form H bonds with, (target) mRNA ; (passenger strand needs to be, separated / released) to allow guide strand to, be exposed / bind to mRNA ; AW ora e.g. (otherwise) guide strand cannot bind to mRNA passenger strand prevents guide strand binding guide strand has complementary sequence to target sequence of mRNA ; ora passenger strand does not

3(c)(ii)	<i>allow protein for polypeptide</i> <i>points need the correct context of cleaved mRNA</i> <i>any three from:</i> <i>no protein formed</i> 1 <i>idea that</i> mRNA may be degraded in cell before attaching to ribosome ; 2 mRNA may not (be able to) attach to ribosome so no, polypeptide formed / translation ; 3 cleaved mRNA results in loss of start, sequence / codon ; <i>abnormal polypeptide formed</i> 4 polypeptide chain is not released from ribosome ; A cleaved mRNA results in loss of stop codon 5 polypeptide chain degraded within cytoplasm / AW ; 6 cleaved mRNA results in short(er) (polypeptide) chain being produced ; 7 polypeptide does not, fold up / form correct tertiary structure / form correct 3D shape ; I tertiary structure changes 8,9 AVP ; e.g. (results in) different R-group interactions / change in number of bonds that can form active site / site of activity, changed / lost
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