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**)

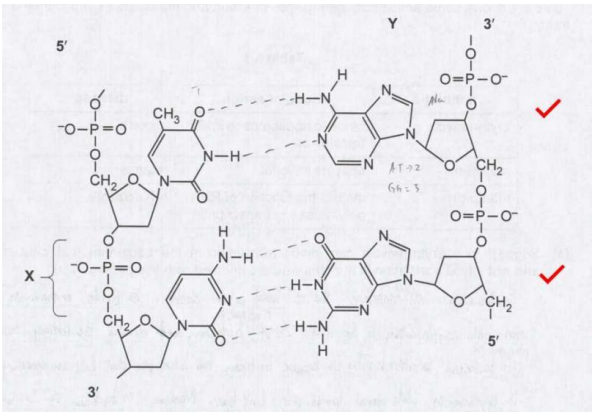
- DNA ligase joins fragments together, so it acts last on the lagging strand.
- The fragments are made first, each 5′ to 3′.
- Ligase then seals the gaps between them into a continuous strand.

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 ; *for positioning of H bonds on C-G, **A** from either H on amine group on C to link with oxygen on G*  *if no marks gained but A-T has two lines and C-G has three lines between bases award 1 mark*
4(b)(ii)	phosphodiester ;

3(a)(i)	*if DNA or thymine stated within response, allow only H-bond mark (**ecf**)* *any **two** from:* (paired section) contains, complementary nucleotides / complementary bases / base pairs ; adenine-uracil and 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) ; *can apply in context of specific shaped active site or active site specific to a particular location* 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. *suggestion that* Dicer too large to enter nucleus Drosha exposed to degradation in cytoplasm

3(b)	*any **two** from:* mRNA is single-stranded <u>and</u> 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. *ref. to* siRNA antiparallel / mRNA only 5' to 3' mRNA has no H bonds
3(c)(i)	*any **one** from:* 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)	*allow protein for polypeptide* *points need the correct context of cleaved mRNA* *any **three** from:* *no protein formed* **1** *idea that* 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 **;** *abnormal polypeptide formed* **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