

**STUDY GUIDE TO CHAPTER 10 : Answers to Boxed Questions**

Shown below is the snapshot of a DNA strand that is being replicated. The primers X, Y and Z are indicated as \*\*\*\*\*.

3'-----5'  
5'-----\*\*\*X\*\*\*-----\*\*\*Y\*\*\*-----\*\*\*Z\*\*\*-----3'

- (a) Which of the three RNA primers would first be incorporated as part of Okazaki fragment? Explain.  
(b) Which of the three primers will be the first to be removed, and why?

(a) The first to be incorporated would be Z, followed by Y, and finally X. [The key concepts to understand is that since new strand synthesis takes place in the 5' to 3' direction, the replication fork is moving from right to left; and what is being shown is just the replication of the lagging strand template.]

(b) The order of removal of primers is the same as the order of addition – Z, Y and X.

For the peptide *Met – Trp – Gly – Met – Ser*, what is the:

- (a) number of possible unique mRNA sequences that encode it, assuming the stop codon is the same.  
(b) sequence of any one mRNA that encodes it?  
(c) sequence of the coding strand corresponding to (b)?

(a) The number of possible combinations is obtaining by multiplying the numbers of codons representing each amino acid of the sequence. That would be  $1 \times 1 \times 4 \times 1 \times 6 = 24$ . (Note: It is a good idea to make a list of how many codons are there to represent each amino acid. E.g., Met – 1, Trp – 1, Ser – 6, and so on.)

(b) One of the 24 combinations would be: 5' - AUG UGG GGG AUG AGC UAA – 3' (assuming UAA is the stop codon). Remember to mark the polarity whenever you write a nucleic acid sequence.

(c) The coding strand is exactly similar to the mRNA, except for the U→T replacement. Hence, it would be 5' – ATG TGG GGG ATG ATC TAA – 3'.

A point mutation changes a peptide sequence from *Met – Asn – Trp – Ser – Gly* to *Met – Thr – Gly – Val*. Write out the sequence of the portion of mRNA that corresponds to the original pentapeptide.

Original pentapeptide: *Met – Asn – Trp – Ser – Gly*

Tetrapeptide resulting after a point mutation: *Met – Thr – Gly – Val*

Let us begin by writing out the possible mRNA corresponding to the tetrapeptide. Looking up the codon table, we can come up with this sequence: AUG – ACN – GGN – GUN, where 'N' stands for any of the four bases A, U, C, G.

Now, writing out the contents of the original pentapeptide, it is: AUG – AA(U/C) – UGG – AG(U/C) – GGN.

Comparing both peptides, we see that everything starting from the second amino acid has changed. So, it is easy to infer the point mutation has caused a change of reading frame (frameshift mutation), and so should be a deletion or an addition of one or two bases.

The first codon (and the amino acid) of both peptides is the same – AUG (Met). The second codon of the tetrapeptide is ACN, while for the original peptide, it is AA(U/C). So, we can guess that the second A was deleted.

If so, the modified sequence could be: AUG – ACU – GGA – GUG. Hence, the sequence coding for the original pentapeptide would be: AUG – AAC – UGG – AGU – GGN.

Tanishq Rupaal's turned in a more detailed and well-written answer that I want to share it with the class:

All possible codon sequences for met-thr-gly-val are

AUG ACU GGU GUU

ACC GGC GUC

ACA GGA GUA

ACG GGG GUG

All possible sequences for met-asn-trp-ser-gly are

AUG AAU UGG AGU GGU

AAC AGC GGC

GGA

GGG

As per question, only one point mutation has occurred.

1. Matching sequence of both sets, it can be inferred that point mutation has been carried out at second place of the second codon.
2. By hit and trial, a possible solution is the deletion of the second base of the second codon.
3. The final sequence has AC\_ as the second codon. Therefore if the second A is deleted, we get two possible codons – AUU and ACU. ACU matches the codon present in the final sequence.
4. Therefore the resulting solution is AUG AAC .... Since A is deleted the third codon will be GGA. The fourth codon will read G\_G, where the \_ can be either U or C.
5. The final sequence has only GUG that matches the conditions. Therefore, the fourth codon is AGU.

After these steps, it can be said that the sequences are

AUG AAC UGG AGU G\_\_ ----deletion of second A in second codon

AUG ACU GGA GUG

Therefore the original codon sequence is AUG AAC UGG AGU G\_\_.

Here, G\_\_ can be any one of GGU, GGC, GGA, GGG.