

**A template strand of a gene has this base sequence:  
3'–TACAT\*CCGATAGGGTCAT–5'. Exposure to radiation causes a  
mutation in this gene. The thymine at the site of the mutation (\*)  
is deleted. This will most likely result in:**

- A. mRNA codons preceding (towards the 3' end) the mutation to be misread
- B. mRNA codons downstream to the start codon to be misread
- C. no change of any kind
- D. no change in the polypeptide coded by this gene
- E. the AUG triplet functioning as a chain terminator

**Which of the following is analogous to a frameshift mutation?**

- A. THERATATETHECAT
- B. THETACATETHERAT
- C. THECATARETHERAT
- D. THECATATTHERAT
- E. CATATETHERAT

Assume that the following polypeptide chain is produced by a wild-type gene in an organism:

**N-met-lys-trp-leu-his-ala-glu-gly-lys-C**

Assume that a phenotypically observable mutation occurred in the coding region of the mRNA that coded for this polypeptide. Assume that a base substitution occurred in the 7<sup>th</sup> base position counting from the 5' end of that coding region. Without referring to actual codons, what is a likely sequence resulting from such an alternation?

- A. N-met-lys-arg-leu-his-ala-glu-gly-lys-C**
- B. N-met-C**
- C. N-met-lys-trp-leu-his-ala-ala-gly-lys-C**
- D. N-met-lys-trp-leu-his-ala-glu-gly-lys-C**
- E. None of the above**