

If a strand of DNA reads 5' : T C G G A C G A A : 3' then the sequence opposite this strand will read \_\_\_\_\_

Mutating a *single* nucleotide in a gene will always / sometimes / never alter the resulting protein (circle the correct answer).

When considering a scoring function with *general* gap penalties between two strings  $x$  and  $y$  of length  $n$ , the running time of the dynamic programming algorithm for global pairwise alignment runs in  $O(\text{_____})$  time.