Quiz 3

Due Mar 30 at 11:20am   **Points** 5   **Questions** 5

Available Mar 30 at 11am - Mar 30 at 11:20am 20 minutes   **Time Limit** 20 Minutes

Attempt History

	Attempt	Time	Score
LATEST	**Attempt 1**	15 minutes	5 out of 5

⊙ Correct answers are hidden.

Score for this quiz: **5** out of 5

Submitted Mar 30 at 11:15am

This attempt took 15 minutes.

Question 1	1 / 1 pts

It is possible to overlay proteomics data on top of a pathology slide.

⦿ True

◯ False

Question 2	1 / 1 pts

Sequence alignment algorithms such as Needleman-Wunsch and Smith-Waterman draw inspiration from algorithms originally designed to process text strings.

⦿ True

○ False

Question 3   1 / 1 pts

Select the most efficient sequence alignment algorithm:

○ Brute Force

◉ BLAST

○ Smith Waterman

○ Needleman Wunsch

Question 4   1 / 1 pts

Efficient sequence alignment algorithms are based on dynamic programming.

◉ True

○ False

Question 5   1 / 1 pts

Dynamic Programming algorithms work by breaking down a problem into subproblems that can be solved in a recursive fashion.

⦿ True

○ False

Quiz Score: **5** out of 5