

# 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	<a href="#">Attempt 1</a>	7 minutes	4 out of 5

⚠ Correct answers are hidden.

Score for this quiz: **4** out of 5

Submitted Mar 30 at 11:07am

This attempt took 7 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

Incorrect  
Blast

### Question 3

0 / 1 pts

Select the most efficient sequence alignment algorithm:

☐ Needleman Wunsch

☐ Brute Force

☐ BLAST

☒ Smith Waterman

### 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: **4** out of 5