

Additional sample exam questions:

1. Dot plots are fast and efficient when examining very large sequences

True False

2. RNA-Seq measures *relative* RNA abundance

True False

3. The first free living organism to have their genome sequenced was an isolate of *Escherichia coli*

True False

4. Multiple sequence alignments

- a) are the basis for phylogenetic analyses
- b) can aid identification of domains of a protein
- c) cannot aid the identification of secondary or tertiary protein structure
- d) two of the above are correct
- e) three of the above are correct

5. Define: BLASTP

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6. Define: Paired-end sequencing

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7. What are the benefits of RNA-seq over Microarray-based technologies for transcriptome analysis?

8. What are two pitfalls of the RMSD measure for protein structure comparison?

9. a) Describe the how Amplicon sequencing differs from Metagenomics sequencing.

b) Which method would you use if studying a whole viral community? Why?