X



# Unit 8 - Week 7

Register for Certification exam

Course outline

How to access the portal

Week 1

Week 2

Week 3

Week 4

Week 5

Week 6

Week 7

- Lecture 31 : Use of SPR in unravelling domain motif interactions of proteasomal assembly chaperones
- Lecture 32 : Next-Generation Sequencing Technology- Ion Torrent™
- Lecture 33 : NGS Technology- Bioinformatics and data

## Assignment 7

**The due date for submitting this assignment has passed.**
**As per our records you have not submitted this assignment.** **Due on 2019-04-17, 23:59 IST.**

1) Why is protein-protein interaction thought to be NOT druggable? ***1 point***

i) Protein-protein interactions are high affinity interactions
ii) The interaction bury a large surface area and the small molecule cannot reach there
iii) Proteins are large biomolecules and small drug molecules cannot inhibit their activity
iv) The structure of protein-protein interaction is not clear and hence it is difficult to target these protein-protein interactions

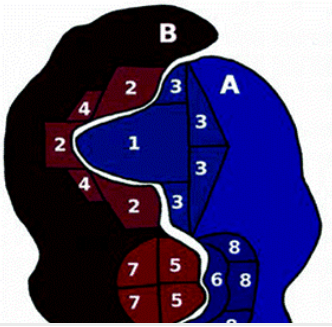
- i
- i & ii
- i, ii & iii
- i, ii, iii & iv

**No, the answer is incorrect.**
**Score: 0**

**Accepted Answers:**
*i & ii*

2) **Answer question 2 to 4 based on the paragraph given below:** ***1 point***

The image given below is an illustration of domain-motif interaction. Suppose A and B are the proteins that are interacting with each other, and 1-8 are the small segments of peptides that are involved in these interactions. Carefully study the image given below and answer question 2 to 4.



- Replace the amino acids present at either of the locations 1, 2, 5 or 6
- Replace the amino acids at the either of the locations 3, 4, 7 or 8
- Replace all the amino acid residues (1-8) that are depicted in the image
- These interactions cannot be made druggable

**No, the answer is incorrect.**
**Score: 0**

**Accepted Answers:**
*Replace the amino acids present at either of the locations 1, 2, 5 or 6*

3) Ajay has mutated the gene encoding for protein A, to replace a key interacting amino acid (Aspartate) with Lysine. He wishes to check if the site-specific mutation has happened properly or not. What should be Ajay's next step? ***1 point***

- Next generation sequencing to analyse the sequence of the mutated gene encoding for protein A
- Targeted sequencing, to analyse the sequence of the mutated gene encoding for protein A
- SPR to check if the interaction is happening
- Site-specific mutation kit is very efficient; hence, there is no need to check if the mutation has happened

**No, the answer is incorrect.**
**Score: 0**

**Accepted Answers:**
*Targeted sequencing, to analyse the sequence of the mutated gene encoding for protein A*

4) Suppose that the mutation has worked well, Ajay now want to study the interaction kinetics of the protein A and B, and to check if that mutation has affected the interaction of Protein A and B. What all strategies should Ajay apply? ***1 point***

i) Isothermal Titration Calorimetric analysis to measure the stoichiometry and Kd of only the mutated protein

ii) Isothermal Titration Calorimetric analysis to measure the stoichiometry and Kd of both mutated and native protein with protein B, separately

iii) Surface Plasmon Resonance to measure the kinetics of the interaction of only mutated protein with protein B

iv) Surface Plasmon Resonance to measure the kinetics of the interaction of both mutated and native protein with protein B, separately

- i & iii
- ii & iv
- iii
- None of the above

**No, the answer is incorrect.**
**Score: 0**

**Accepted Answers:**
*ii & iv*

5) **Answer Question 5 to 8 using the information given below.** ***1 point***
Eric has recently been appointed as a technician in a company that specializes in next generation sequencing. The first project that he received was to sequence a particular panel of genes for 15 individuals, of whom 10 were cancer patients and 5 healthy individual. Using this information answer questions 5 to 8.

5) What strategy should Eric apply sequence the gene of these 15 individuals?

- Sequence the DNA of all the 15 individuals separately, as the genetic composition of all the individual is different

- He should pool the DNA from all the 15 individual, so that he can sequence all the genes from the all the individual at once, saving time and reagents
- The DNA sequences should be tagged with adapters before pooling all the samples and then the pool can be sequenced
- DNA sequences from all the individuals should be pooled and then adapter sequence should be attached as these adapter sequences acts primer

**No, the answer is incorrect.**
**Score: 0**

**Accepted Answers:**
*The DNA sequences should be tagged with adapters before pooling all the samples and then the pool ca be sequenced*

6) Eric has heard about library preparation in NGS platform but he is not sure about it. Can you help him understand the meaning of library preparation? ***1 point***

- To prepare a collection of DNA fragments that can be cloned into the vectors
- To collect all the books available on NGS platform and create a library
- To sheer the DNA into similar sized fragments and attach a known adapter sequence at both 5' and 3' ends
- To collect all the novel sequences from the species

**No, the answer is incorrect.**
**Score: 0**

**Accepted Answers:**
*To sheer the DNA into similar sized fragments and attach a known adapter sequence at both 5' and 3' en*

7) After the completion of sequencing of all 15 patients, Eric now has to analyse the results obtained. His team has software named as Ion ReporterTM software for data analysis, which among the following functions this software CANNOT perform? ***1 point***

- Integration of the data
- Annotation of the SNPs
- Interpretation of the variants
- Analysis of the ionogram

**No, the answer is incorrect.**
**Score: 0**

**Accepted Answers:**
*Analysis of the ionogram*

8) In the next project Eric has to classify an unknown bacterium, which has been isolated from a pond. Which is the best suited strategy that Eric should follow? ***1 point***

- Sequencing the entire genome of the bacteria
- Sequencing the 16S rRNA of the bacteria
- Sequencing the plasmids of the bacteria
- Sequencing the all the RNA and DNA (including plasmids) of the bacteria

**No, the answer is incorrect.**
**Score: 0**

**Accepted Answers:**
*Sequencing the 16S rRNA of the bacteria*

9) In Illumina platform, why is a separate read needed for sequencing the indexes attached to the DNA fragment? ***1 point***

- Indexes are small fragments and do not need much time to get sequenced

Indexes are attached at the end, and as the read length increases the quality of sequencing may drop

Indexes are the sequences that are complimentary to the oligos that are attached to the low cell, hence their sequence is important

Sequencing of indexes is performed separately to ensure that the flow cell does not have any free nucleotide present, otherwise it may lead to erroneous results

**No, the answer is incorrect.**
**Score: 0**

**Accepted Answers:**
*Indexes are attached at the end, and as the read length increases the quality of sequencing may drop*

10) Why is paired end sequencing better? ***1 point***

i) It sequences both forward and reverse stand in a single set of experiment

ii) The sequence of forward and reverse strand obtained can help in cross-verification of the sequencing result

iii) It sequences the entire genome end to end

iv) The quality of the reads at the end of the sequence may drop, sequencing the complimentary strand increases the confidence in the data

i, ii & iv

i & ii

i, iii & iv

i, ii & iii

**No, the answer is incorrect.**
**Score: 0**

**Accepted Answers:**
*i, ii & iv*

Previous Page End