SBL201 (High Dimensional Biology) - Minor II

March 20, 2015
Total: 25 marks
Time: 1 hour

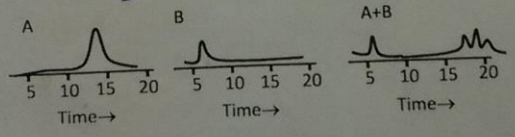
Part I: Answer ANY TEN of the following questions (1.5 x10 =15 Marks)

1. What do you understand by programmed self assembly?
2. What are biomedical applications of nanorobots ?
3. Give three applications of the field of nanomedicine.
4. What is the medical application of nanoscale cantilever?
5. Mention three types of naturally occurring molecular motors.
6. Explain intelligent design with a suitable example.
7. How does a virus work as a nanobiomachine?
8. Give three main features of cell cytoskeleton?
9. What is the difference between kinesin, dyenein and myosin?
10. What do you understand by minimal genome?
11. Give advantages and disadvantages of designer biology.
12. What is Cynthia?
13. Describe three important applications of synthetic biology.

Part II: Answer all questions (1+1+3 =5 marks)

1. Detection of protein-protein interaction can generally be correlated with genetic makeup and is directly proportional to (1 mark)
   a) Proximity of the protein coding genes in the genome, proteins belonging to an operon are likely to interact.
   b) Distance of protein coding genes in the genome, larger is the distance higher is the probability of interaction
   c) Sequence similarity of the genes coding for the proteins in question.
   d) The expression level of the proteins in question and does not depend on distance

2. Figures below are the gel filtration profiles of proteins A, B and a mixture of A+B where B is a non-specific protease. From comparison of the profiles we can say that (1 mark)



   a) A interacts with B transiently
   b) A interacts with B permanently
   c) A and B do not interact
   d) information is insufficient to conclude anything

3. What is a metabolome and why is it important to study human metabolome? (3 marks)

OR

Explain with diagram the two basic routes adopted to get the biomarker information through metabolomics.

Part III: Answer all questions (1+1+1+2 = 5 marks)

1. Which of the following is **unlikely** to be a co-factor or an underlying causal mechanism in carcinogenesis?

a) Formation of DNA adducts
b) Over expression of miRNA targeting oncogenes
c) Insertional mutagenesis by integration of virus DNA
d) Major changes in DNA methylation
e) None of the above

2. Which of the following statements is NOT true about heterochromatin?
a) It is NOT transcriptionally active
b) The DNA in heterochromatin is often methylated
c) The histone tails in the heterochromatin are often acetylated
d) It has a highly compacted or closed structure
e) None of the above

3. Tissue microarrays are used to
a) Detect mutations /SNPs
b) Detect differences in DNA methylation in the promoter regions
c) Detect gross chromosomal rearrangements in the genome
d) Detect changes in protein expression
e) None of the above

4. **Case study:** You are a cancer biologist studying mechanisms leading to pancreatic cancer. You have access to a tissue bank with a large number of pancreatic cancer tissues as well as normal pancreatic tissues. You screened 100 pancreatic cancer and 100 normal pancreatic tissue for mutations and found no interesting leads. List 4 other parameters you will screen to understand changes common in pancreatic cancer; also mention a method that you would use for each of these parameters (2 marks)