Enrollment No._____

NAVRACHANA UNIVERSITY
a UGC recognized University

School: School of Science
Program/s: BMS
Year: 3rd **Semester:** 9th
Examination: End Semester Examination
Examination year: December - 2021

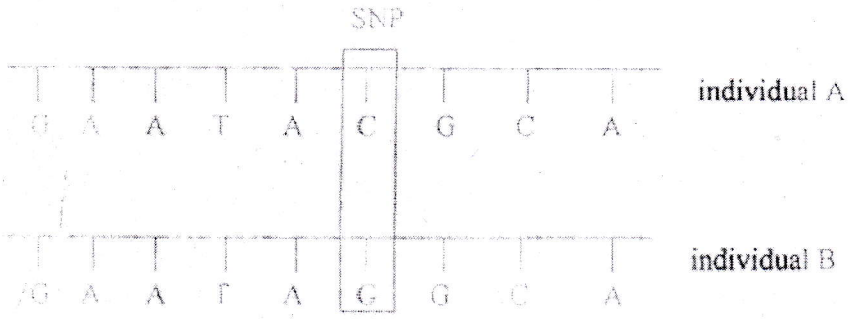
Course Code: BM508 **Course Name:** Molecular Medicine IV
Date: 07/12/2021
Time: 8.30 am to 10.30 am

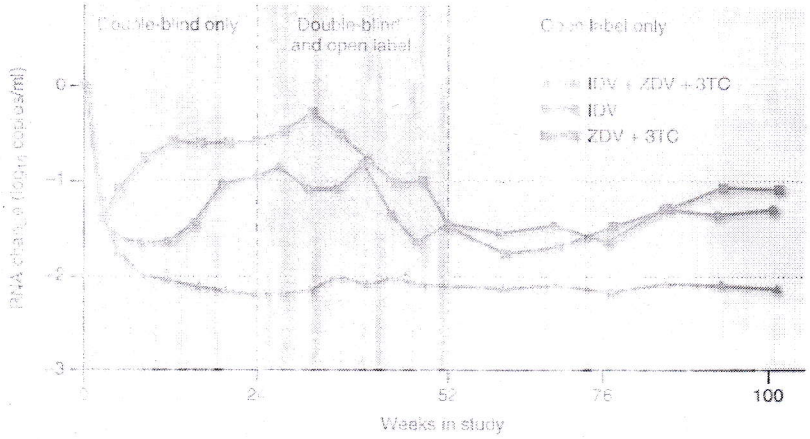
Total Marks: 40
Total Pages: 04

Instructions:

- *Write each answer on a new page.*
- *Draw the diagram wherever necessary*
- *Stick to the Word Limit given in the Questions.*

Q. No	Details	Marks	CO	BTL
Q.1	**Do as directed** 1. In the human genome project, the total number of chromosomes size which was sequenced was estimated to be 3.286 however, the number of contigs obtained was_____. 2. While performing and analyzing the human genome, scientists came to a consensus that _____ and _____ was a major point for the consideration for resolving and deciphering the genome. 3. A long stretch of DNA (e.g., 100000 bases) with a distinctive pattern of SNPs at a given location of a chromosome can be reffered to as _____. 4. What will be the condition of the progeny if the father is normal, while the mother has one gene for hemophilia and one gene for color blindness on one of the X chromosomes? a. Only daughters are hemophilic and color blind b. Both sons and daughters will be hemophilic and color blind c. 50 % hemophilic and colour blind sons and 50% normal sons d. 50 % hemophilic colour blind daughters and 50% colour blind daughters 5. In RNAi mechanism, RNA-induced silencing complex (RISC) loading complex (RLC). Shorter siRNAs and analogues can bypass Dicer cleavage and enter the RISC by a crosstalk mediated by _____. 6. In 1940, Chemotherapeutics were developed for clearing off the cancer cells. The main focus of these drugs was to target _____ and _____ tumors.	1x8=8	CO 1 CO2 CO3 CO4	BTL 1 BTL2 BTL3 BTL4
Q.2	**Answer the following (20-30 words only per answer)** 1. The bone marrow toxicity of the nitrogen mustard is due to its alkylating activity toward DNA occurring in two major steps. Name the two steps with their significance.	2x4=8	CO 1 CO2	BTL 1 BTL2

	2. Draw the structure of secondary structure motifs of N-acetylgalactosamine (GalNAc) of synthetic RNAi. 3.Several serious viral infections of humans produce disease via an excessive or imbalanced host response, leading to intense dysregulation of proinflammatory cytokines and chemokines. This cytokine storm can cause a range of serious disease manifestations. What can be done to solve this problem using anti-viral therapy? 4.A young boy was showing phenotypic characteristics of elongated ears, a palette which was arched and long-distance forehead and was assumed to be in depression due to inferiority complex. What could be deciphered with this? Justify your answer.		CO3 CO4	BTL3 BTL4
Q.3	**Answer the following-*any three* (max 300-350 words per answer)** 1. A researcher was analyzing different cells in rats, and found that blood vessel together with heart and eyes was severely damaged. Astonishingly, while visualizing the nervous system, the neurons were found to be having retarded growth. Going through all the changes observed which disease(s) is likely be occur. Design a strategy using RNAi to combat it. 2. Consider the following diagram  A drug was tested on these two individuals having a transition mutation which was found in the DNA sequence at a stretch of ~1500 sequences. What will happen: a. When a drug will be tested on both of the individuals. b. What happens when the SNP is found in the promoter region, exon, or intronic portion. 3. Taking the human genome project as an example, how will you decipher the genome of *Drosophila* (The genome size of Drosophila is 180 Mb).	**4x3=12**	CO 1 CO2 CO3 CO4	BTL 1 BTL2 BTL3 BTL4



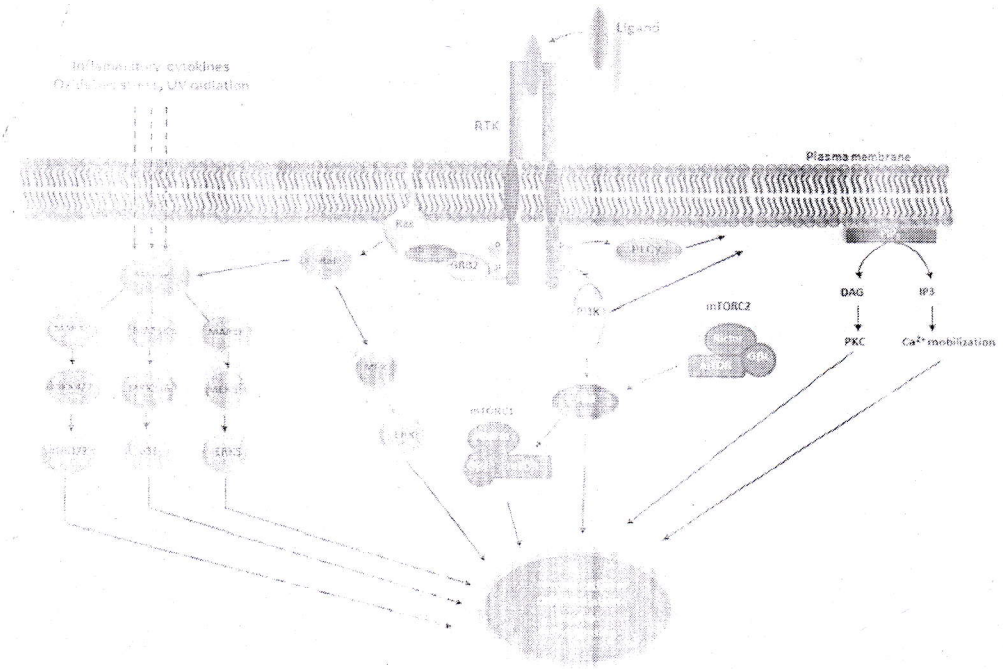
4. The above graph shows drug effects on HIV mRNA. Virus mutants may escape a single or even two drugs but are much less likely to escape from three or more drugs administered simultaneously. HIV-infected treatment-naïve patients were started in regimens of two nucleosides (azidothymidine (ZDV) and lamivudine (3TC)), the protease inhibitors indinavir (IDV), or the combination of all three drugs. The decrease in the level of blood HIV RNA from baseline is shown.

a. What is the mechanism of action of ZDV and 3TC in regards to weeks

b. The rise in plasma HIV RNA after several months in the nucleoside and protease-only arms indicates a type of adaptation. Which type of adaptation here it is referring to? Formulate the strategy to address this.

Q.4	**Answer the following (max 500 words per answer).**	**6x2=12**	CO1 CO2 CO3 CO4	BTL 1 BTL2 BTL3 BTL4

1. Consider the following diagram:



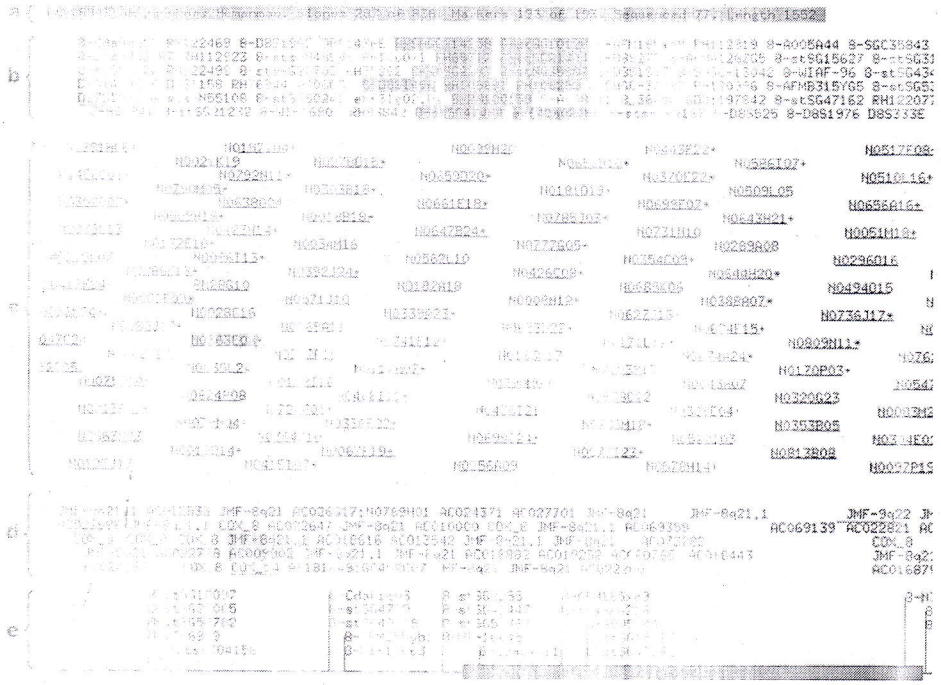
The above diagram shows the RTK signaling in normal cells. It has been estimated that the cancerous cells are having around 30-35% mutations in this pathway. So majorly the anti-

cancerous drugs are targeted against this. Using the known candidate targets given in the diagram, how a combinational therapy can be developed using a multiple target approach. If the targets possess SNPs in their promoter/exons, will your combinational therapy work? If yes Justify your answer and if no suggest alternative strategies.

OR.

1. Using the multidrug approach, design/draw a combinational therapy for breast cancer with the mechanism of action of each drug. Discuss the thermodynamic properties of the cancerous cell and how are the drugs can be used against it. Using RNAi synthetic analogs, make a drug-RNAi therapy to combat the different targets of this cancer.

2. Consider the Example contig from the whole-genome BAC map of Human Genome Project:



A portion of the contig shown is localized to chromosomal region 8q21, composed of 836 sequences ordered by restriction fingerprint mapping. GenBank accession numbers are indicated as given in a,b,c,d,e. Answer the following questions:

a. What are the sequences called which are described in the above diagram? How is it obtained?

b. Why the scientist has done multiple alignments? What does it will help for? Elucidate the description of the labeled portion of certain sequences.

c. Does this map denote the whole genome of Humans? Justify your answer in regards to a,b,c,d,e mentioned in the diagram.

**********All the Very Best*********