

**BIRLA INSTITUTE OF TECHNOLOGY & SCIENCE, PILANI**

**FIRST SEMESTER 2022-23**

**BIO G512 (Molecular Mechanism of Gene Expression)**

**Mid-Semester Examination (OPEN BOOK)**

**Duration: 1.30 Hrs**

**02.11.2022**

**Maximum Marks: 30**

Q.1 In *Drosophila*, a female fly is heterozygous for three mutations, *Bar* eyes (*B*), *miniature* wings (*m*), and *ebony* body (*e*). Note that *Bar* is a dominant mutation. The fly is crossed to a male with normal eyes, miniature wings, and ebony body. The result of cross are shown below;

Wild, miniature, wild	111
Wild, wild, wild	29
Bar, wild, wild	117
Bar, miniature, wild	26

Bar, wild, ebony	101
Bar, miniature, ebony	31
Wild, wild, ebony	35
Wild, miniature, ebony	115

Interpret the result of this cross. If you conclude that linkage is involved between any of the genes, determine the map distance(s) between them. **(5 Mark)**

Q.2 The genetic code is degenerate. Amino acids are encoded by either 1,2,3,4 or 6 triplet codons. An interesting question is whether the frequency of triplet codes is in any way correlated with the frequency that amino acid appears in proteins? That is, is the genetic code optimized for its intended use? Some approximations of the frequency of appearance of nine amino acids in proteins in *E.coli* are shown in the adjacent table.

- Determine how many triplets encode each amino acid.
- Analyze your data to determine what if any, correlations can be drawn between the relative frequencies of amino acids making up proteins with the number of for each triplets.
- Write a paragraph that states your specific and general conclusions.

<u>Amino acids</u>	<u>Percentage</u>
Met	2
Cys	2
Gln	5
Pro	5
Arg	6
Ile	7
Glu	8
Ala	10
Leu	10

**(3 +4 +3 Marks)**

Q.3 (a) Give an alternative translation mechanism that would require only one transfer RNA site on the ribosome.

(b) What amino acids could replace methionine if a one-base mutation occurred?

**(5 + 5 Marks)**

**P.T.O**

Q.4. A series of overlapping deletions in phage T4 are isolated. All pairwise crosses are performed, and the progeny scored for wild-type recombinants. In the following table, + = wild-type progeny recovered; - = no wild-type progeny recovered.

	1	2	3	4	5
1	-	+	-	-	-
2		-	+	+	-
3			-	+	+
4				-	-
5					-

(a) Draw a deletion map of these mutations.

(b) A point mutation, 6, is isolated and crossed with all of the deletion strains. Wild-type recombinants are recovered only with strains 2 and 3. What is the location of the point mutation?

**(3 +2 Marks)**

=====Good Luck=====