MARKING SCHEME
BIOTECHNOLOGY (045)
SET-4 (Series &RQPS)
Q.P. CODE 99
(2023-24)

SECTION – A

Sl. No.	Value Points	Marks
1	(C) Bacillus amyloliquefaciens	1
2	(B) Adenosine deaminase	1
3	(B) Non-coding **/** (A) Coding (As per the prescribed text book, pg63,both options(A)and(B) are correct)	1
4	(A) Torpedo	1
5	(C) Blood serum	1
6	(D) M13	1
7	(D) Antibiotics	1
8	(B) Gene pollution	1
9	(A) 2001	1
10	(B) Pluripotent	1
11	(B) *Penicillium chrysogenum*	1
12	(C) Callus	1
13	(A) Both Assertion (A) and Reason (R) are true and Reason (R) is the correct explanation of the Assertion (A) .	1
14	(D) Assertion (A) is false, but Reason (R) is true.	1
15	(B) Both Assertion (A) and Reason (R) are true, but the Reason (R) is ***not*** the correct explanation of the Assertion (A).	1
16	(C) Assertion (A) is true, but Reason (R) is false.	1

SECTION – B

17 Fig 2, Pg 6 / Fig 6, Pg 14 (**Any One Fig**.) 2

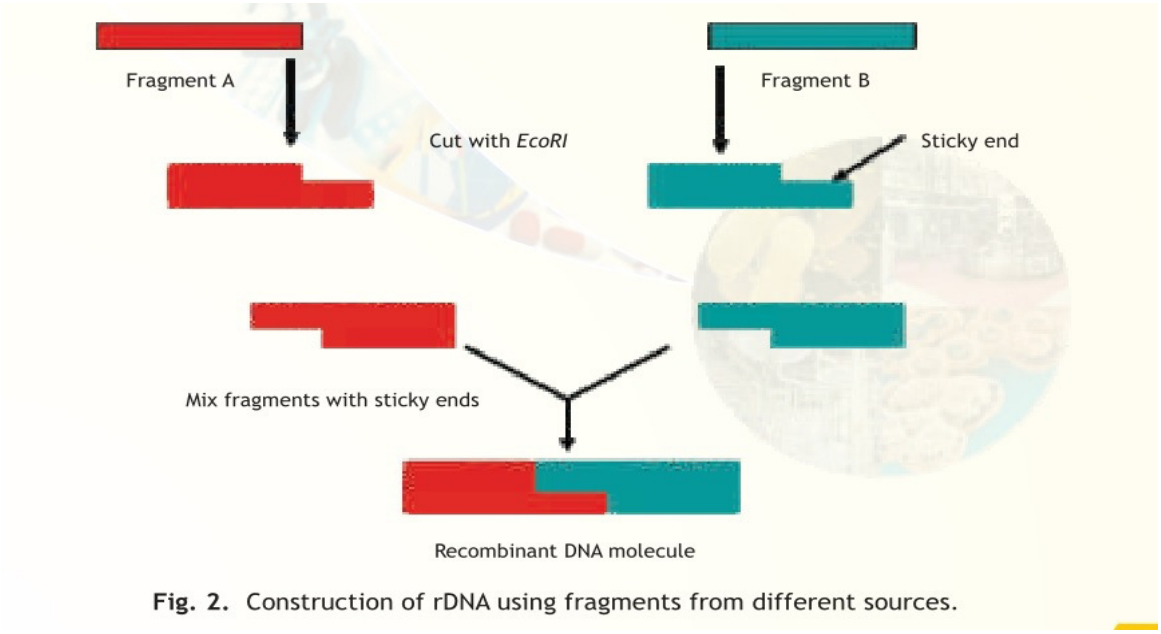

Fig. 2. Construction of rDNA using fragments from different sources.

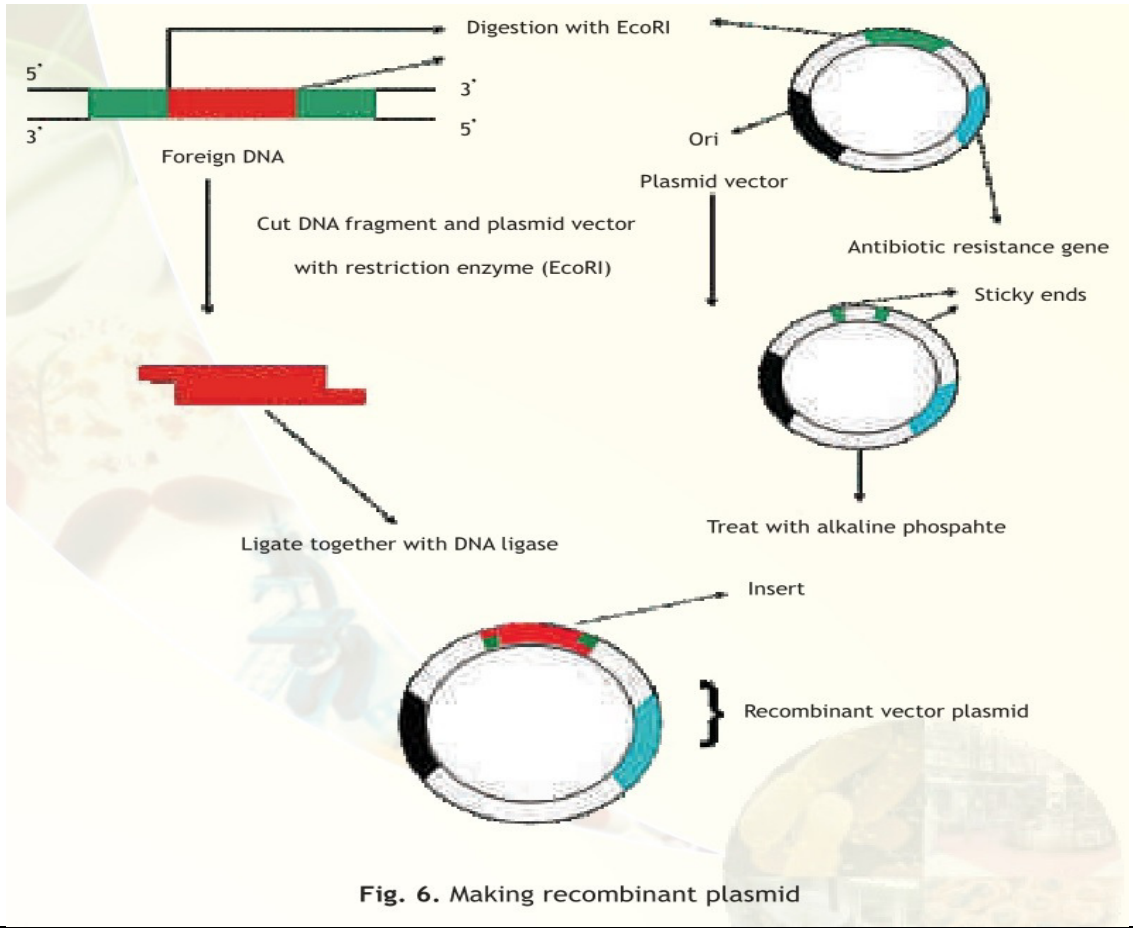

Fig. 6. Making recombinant plasmid

18	To understand the genetic basis of a disease To search for new diagnostic methods To search for new therapeutic modality or uses (Any two)	1+1= 2
19	Two dimensional Gel Electrophoresis Technique / Mass Spectrometry Technique Principle of Two dimensional Gel Electrophoresis Technique: Separation of proteins is on the basis of charge and size. First proteins get separated on the basis of isoelectric pH (pI) by IEF technique and then on the basis of molecular size by SDS PAGE technique . Principle of Mass Spectrometry Technique: It determines the molecular weight of a chemical compound or protein by separating the molecular ions according to m/z ratio. **(Any one technique with principle)**	1+1=2
20	-To overexpress a gene that encodes for the first enzyme in the biosynthetic pathway -To use Agrobacterium rhizogenes to induce excessive secondary roots (hairy roots) in plants that normally produce useful secondary metabolites in this region.	1+1= 2
21	(a) Drawbacks : Small size / Scale up is challenging / may not represent in vivo phenotype or genotype (Any two for 1 mark each) OR (b) (i) The oncologist is trying to determine whether the tumour is cancerous or not. (ii)Cell comprising tissues and organs like liver of an animal grow only to a certain size after which they cease to grow / Infant animal grow only to adulthood and not any further.	1+1= 2 1+1= 2
	SECTION C	
22	(a) The principle involved in FISH technique is hybridization of DNA of metaphase chromosomes affixed to a microscopic slide with a fluorescent DNA probe. The principle of Microarray is that complementary sequences will bind to each other by base pairing or hybridisation. Fluorescently labelled single stranded probe binds with single stranded DNA molecule spotted on the microarray plate. Applications of FISH are : Diagnosis of genetic diseases Locating specific DNA sequences	1 1

Identification of presence or absence of a gene

To study translocation of genes on chromosomes. (Any 1 point) ½

Applications of Microarray are :

To monitor the whole genome on a single chip for interactions among thousands of genes simultaneously. ½

To compare the amounts of many different mRNA in two cell populations in tissue specific genes to study the regulatory gene defects, cellular response to environment, cell cycle variations. (Any 1 point)

OR

(b)

	Expression Proteomics	Functional Proteomics
1	Study of qualitative and quantitative expression of proteins in different environment or disease.	Identification and analysis of protein networks involved in a living cell/ nuclear pore complex/ study of protein functions and interactions/ molecular mechanisms and biological roles.
2	Used to identify disease specific proteins	To analyse the properties of molecular networks involved in a living cell.
3	To provide understanding of the basis of tumour development.	Identification of novel proteins which are important for translocating important molecules from cytoplasm of a cell to nucleus and vice versa.

½ x 6 =3

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23

S. No.	Protein Pharmaceutical	Therapeutic Use	Animal Cell Line
(A)	Erythropoietin	Anaemia	CHO cell line
(B)	Herceptin	Breast cancer therapy	CHO cell line
(C)	Interleukin 2	Cancer therapy	CHO cell line
(D)	Tissue plasminogen activator	Stroke	CHO cell line

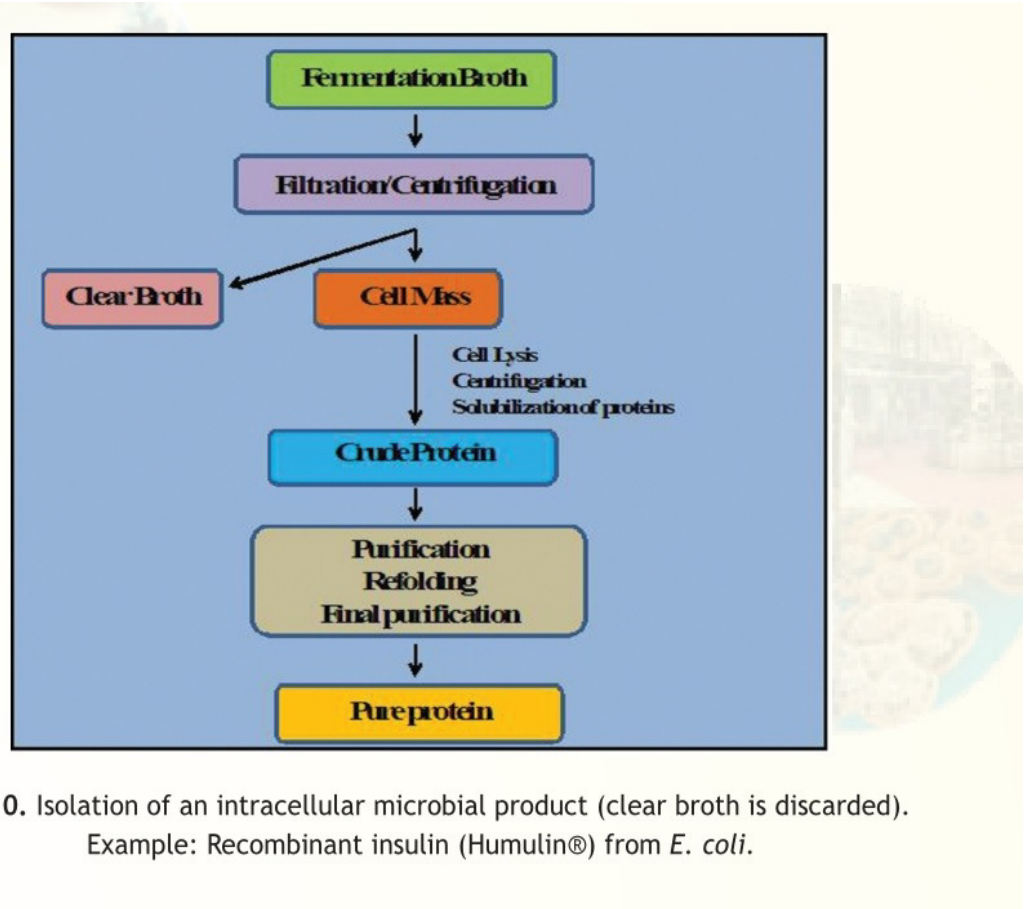
Any Three

½ x 6 =3

<table>
<tr><td>24</td><td>Step 1 –
Denaturation : The DNA duplex gets separated at temperature above 80°C to form two single stranded DNA templates.
Step 2 –
Annealing : Two primers bind to the 3’ end of DNA templates at temperature between 50 - 60°C
Step 3 –
Extension : Each primer is extended by Taq DNA polymerase in 5’► 3’ direction using dNTPs and the DNA strand as template at 70°C</td><td>½ x 6= 3</td></tr>
<tr><td>25</td><td>A – Trypsin
B – Paper Electrophoresis
C – Sequencing</td><td>1 x 3 = 3</td></tr>
<tr><td>26</td><td>Viable plate count method [colony forming units(CFU)]– counting the number of live cells
Turbidity measurement – Absorbance at a particular wavelength is proportional to cell concentration
Coulter counter – Direct counting of cells in suspension as they pass through electrical field in a single file.
Dry weight – to measure constant weight of fixed volume of culture after drying.
Wet weight- to measure weight of fixed volume of culture. ATP measurement- to measure ATP in the beginning end at the end of the culture.
[Any Three ways with explanation]</td><td>½ x 6 =3</td></tr>
<tr><td>27</td><td>Inactive, harmless precursors of proteolytic enzymes are called zymogens.

<table><tr><td>Sl. No.</td><td>Chymotrypsinogen</td><td>Chymotrypsin</td></tr><tr><td>1</td><td>It is inactive precursor of chymotrypsin enzyme.</td><td>It is fully active enzyme.</td></tr><tr><td>2</td><td>The substrate-binding pocket is blocked/ not exposed.</td><td>The substrate-binding pocket is not blocked and is exposed.</td></tr><tr><td>3</td><td>Serine 195 is not acidic.</td><td>Serine 195 is acidic.</td></tr><tr><td>4</td><td>Charge relay doesn’t operate</td><td>Charge relay operates</td></tr></table>
Any two points</td><td>1

1+1 = 2</td></tr>
</table>

28	Ampicillin resistance gene -- provides ampicillin resistance Lac Z gene -- produces β galactosidase enzyme GFP gene – Produces Green Fluorescent Protein Tetracycline resistance gene -----provides tetracycline resistance Leu 2 gene -- codes for an enzyme needed for synthesis of amino acid leucine Any three	½ x 6 =3
	SECTION D	
29	(a) Protein A is extracellular (b) Solvent extraction / Chromatography (c) Fig 10, Pg. 100  **Fig. 10.** Isolation of an intracellular microbial product (clear broth is discarded). Example: Recombinant insulin (Humulin®) from *E. coli*. OR (c) Lesser number of steps for downstream processing are advisable for : - Less cost - High yield	1 1 2 1+1 = 2

30	(a) Sucrose (b) Inositol (c) Auxins and Cytokinins **OR** (b) - Autoclaving: Sterilisation is performed at 15 pounds per square inch pressure for 20 minutes in an autoclave - Membrane filter sterilisation- Culture medium is forced through a membrane of very fine pore size.	1 1 2 1+1 = 2
	SECTION E	
31	(a) (i) Elevation of glutathione (a reducing compound) in cells that detoxifies xenobiotics. Protects cellular components from oxygen intermediates and free radicals. (ii) Jaundice / Infected skin lesions / genito urinary tract infections / Intestinal infections. (iii) Curd is used as a probiotic as it is a source of beneficial bacteria which can colonise the intestinal tract. **OR** *(b)* (i) Recombinant vaccine based on selected epitope: Synthetic gene for an epitope of a virus is assembled and introduced into host cells which are grown on large scale . The epitope protein is isolated, purified and used as recombinant or subunit vaccine. (ii) Thermal stability / pH stability / Solvent tolerance / Solubility / Catalytic potency/ Biological adaptation to environmental stresses such as high salinity, drought , cold, etc. Any two	1+1=2 1+1=2 1 3 1+1= 2
32	(a) (i) ddNTPs lack 3′Hydroxyl group so the phosphodiester bond between 3' hydroxyl group of the previous nucleotide cannot be formed with the 5' phosphate group of the incoming nucleotide and hence the growing DNA chain cannot be further extended and the chain gets terminated. (ii) The sequencing technique is carried out in four test tubes, each carrying single stranded DNA template, deoxy nucleotide tri phosphates, primer and DNA polymerase. A small amount of four dideoxy nucleotide triphosphates i.e. ddATP, ddTTP, ddGTP and ddCTP are added separately into the four test tubes and the reaction is allowed to proceed. Prematurely terminated strands in a given tube are separated on special gels by electrophoresis wherein the bands can be resolved even if they differ by one nucleotide . The shorter fragments move faster towards the anode. The radioactive primers help in easy visualisation using autoradiography. The gel is read from bottom to top to arrive at 5′ to 3′ original DNA sequence.	2 3

	OR (b) (i) - The fastest moving shortest DNA fragment is obtained at 5' position (towards anode). - Since DNA synthesis occurs in 5' to 3' direction, the gel is read from 5' end (anode) (ii) Single tube DNA sequencing uses fluorescent colours rather than radioactive isotopes so is **safer.** It is **better** as it is automated /faster /uses a single lane gel for electrophoresis/ result is directly displayed on a computer screen and data can be stored in a computer. (iii) M13-based vector	2 1+1=2 1
33	(a) (i)**Entrez** allows us to access literature in the form of abstracts , sequences and structures. Entrez provides comprehensive information on a given biological question. **Taxonomy browser** provides information on taxonomic classification of various species. **Locus link** provides information on official gene names, descriptive information about genes and on homologous genes (ii) **UniProtKB** gives information about annotated protein sequences. **PDB** (Protein Database) contains information about three dimensional structure of proteins. **OR** (b) (i)In BLAST: - A given sequence is compared with the database sequences using matrices which give scores. They either reward a match or penalise a mismatch. - Top scoring matches are ranked based on whether the match was due to ancestral relationship or just a random chance. - True matches are examined through ENTREZ (ii) GeneMark for bacterial genomes and GENSCAN for eukaryotic genomes.	½ x 6= 3 1+1 =2 1 x 3 = 3 1+1= 2