Marking Scheme

Strictly Confidential

(For Internal and Restricted use only)

Senior School Certificate Examination, 2024

SUBJECT NAME BIOTECHNOLOGY .(SUBJECT CODE 045) (PAPER CODE 99)

General Instructions: -

1	You are aware that evaluation is the most important process in the actual and correct assessment of the candidates. A small mistake in evaluation may lead to serious problems which may affect the future of the candidates, education system and teaching profession. To avoid mistakes, it is requested that before starting evaluation, you must read and understand the spot evaluation guidelines carefully.
2	**"Evaluation policy is a confidential policy as it is related to the confidentiality of the examinations conducted, Evaluation done and several other aspects. Its' leakage to public in any manner could lead to derailment of the examination system and affect the life and future of millions of candidates. Sharing this policy/document to anyone, publishing in any magazine and printing in News Paper/Website etc may invite action under various rules of the Board and IPC."**
3	Evaluation is to be done as per instructions provided in the Marking Scheme. It should not be done according to one's own interpretation or any other consideration. Marking Scheme should be strictly adhered to and religiously followed. **However, while evaluating, answers which are based on latest information or knowledge and/or are innovative, they may be assessed for their correctness otherwise and due marks be awarded to them. In class-X, while evaluating two competency-based questions, please try to understand given answer and even if reply is not from marking scheme but correct competency is enumerated by the candidate, due marks should be awarded.**
4	The Marking scheme carries only suggested value points for the answers These are in the nature of Guidelines only and do not constitute the complete answer. The students can have their own expression and if the expression is correct, the due marks should be awarded accordingly.
5	The Head-Examiner must go through the first five answer books evaluated by each evaluator on the first day, to ensure that evaluation has been carried out as per the instructions given in the Marking Scheme. If there is any variation, the same should be zero after delibration and discussion. The remaining answer books meant for evaluation shall be given only after ensuring that there is no significant variation in the marking of individual

	evaluators.
6	Evaluators will mark(√) wherever answer is correct. For wrong answer CROSS 'X" be marked. Evaluators will not put right (✓)while evaluating which gives an impression that answer is correct and no marks are awarded. **This is most common mistake which evaluators are committing.**
7	If a question has parts, please award marks on the right-hand side for each part. Marks awarded for different parts of the question should then be totaled up and written in the left-hand margin and encircled. This may be followed strictly.
8	If a question does not have any parts, marks must be awarded in the left-hand margin and encircled. This may also be followed strictly.
9	If a student has attempted an extra question, answer of the question deserving more marks should be retained and the other answer scored out with a note **"Extra Question"**.
10	No marks to be deducted for the cumulative effect of an error. It should be penalized only once.
11	A full scale of marks _____(example 0 to 80/70/60/50/40/30 marks as given in Question Paper) has to be used. Please do not hesitate to award full marks if the answer deserves it.
12	Every examiner has to necessarily do evaluation work for full working hours i.e., 8 hours every day and evaluate 20 answer books per day in main subjects and 25 answer books per day in other subjects (Details are given in Spot Guidelines).This is in view of the reduced syllabus and number of questions in question paper.
13	Ensure that you do not make the following common types of errors committed by the Examiner in the past:- ● Leaving answer or part thereof unassessed in an answer book. ● Giving more marks for an answer than assigned to it. ● Wrong totaling of marks awarded on an answer. ● Wrong transfer of marks from the inside pages of the answer book to the title page. ● Wrong question wise totaling on the title page. ● Wrong totaling of marks of the two columns on the title page. ● Wrong grand total. ● Marks in words and figures not tallying/not same. ● Wrong transfer of marks from the answer book to online award list. ● Answers marked as correct, but marks not awarded. (Ensure that the right tick mark is correctly and clearly indicated. It should merely be a line. Same is with the X for incorrect answer.) ● Half or a part of answer marked correct and the rest as wrong, but no marks awarded.
14	While evaluating the answer books if the answer is found to be totally incorrect, it should be marked as cross (X) and awarded zero (0)Marks.
15	Any un assessed portion, non-carrying over of marks to the title page, or totaling error

	detected by the candidate shall damage the prestige of all the personnel engaged in the evaluation work as also of the Board. Hence, in order to uphold the prestige of all concerned, it is again reiterated that the instructions be followed meticulously and judiciously.
16	The Examiners should acquaint themselves with the guidelines given in the "**Guidelines for spot Evaluation**" before starting the actual evaluation.
17	Every Examiner shall also ensure that all the answers are evaluated, marks carried over to the title page, correctly totaled and written in figures and words.
18	The candidates are entitled to obtain photocopy of the Answer Book on request on payment of the prescribed processing fee. All Examiners/Additional Head Examiners/Head Examiners are once again reminded that they must ensure that evaluation is carried out strictly as per value points for each answer as given in the Marking Scheme.

MARKING SCHEME

SUBJECT : BIOTECHNOLOGY THEORY (045)

AISSCE 2024

SET 4 QP. CODE 99

SESSION: 2023-24

GENERAL INSTRUCTIONS :

a. The Marking Scheme carries suggested value points for the answers.
b. These are guidelines which constitute the complete answer.
c. The students can have their own expression and if the expression is correct the marks can be awarded accordingly.

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

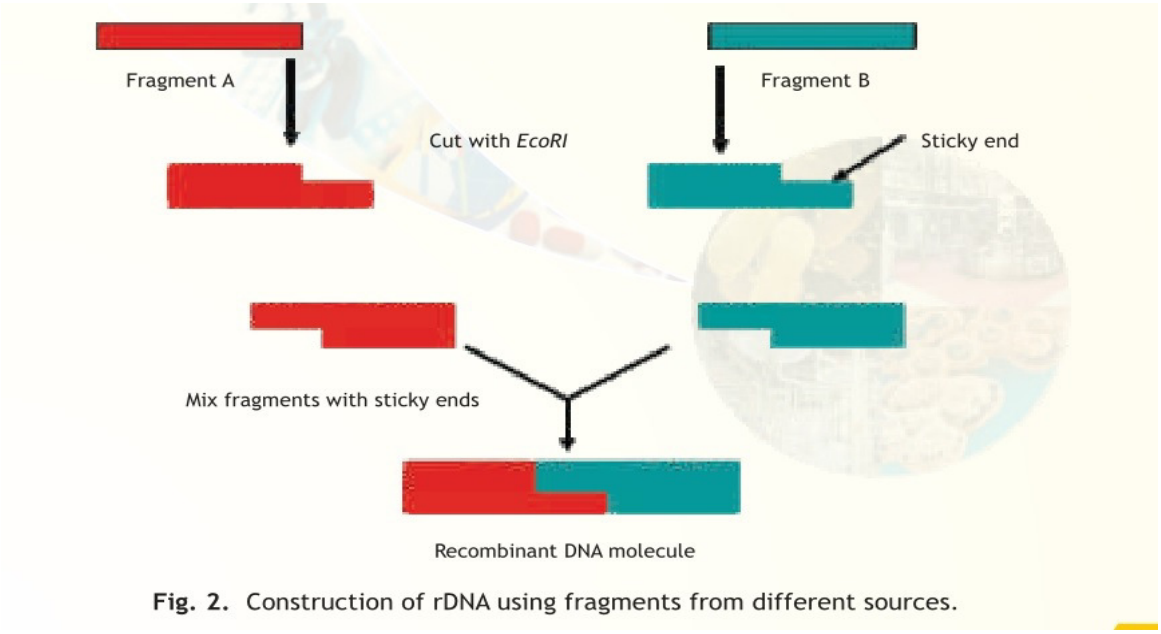

Fig. 2. Construction of rDNA using fragments from different sources.

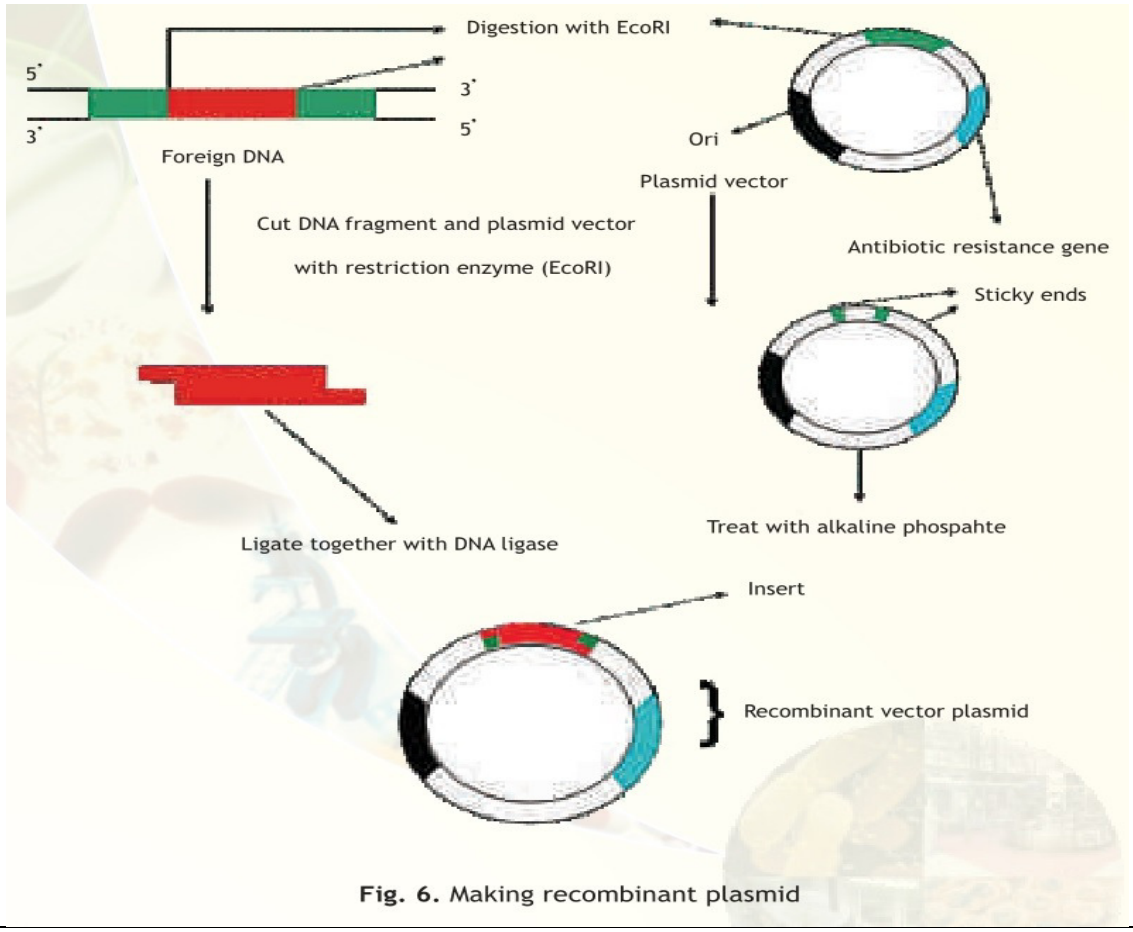

Fig. 6. Making recombinant plasmid

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

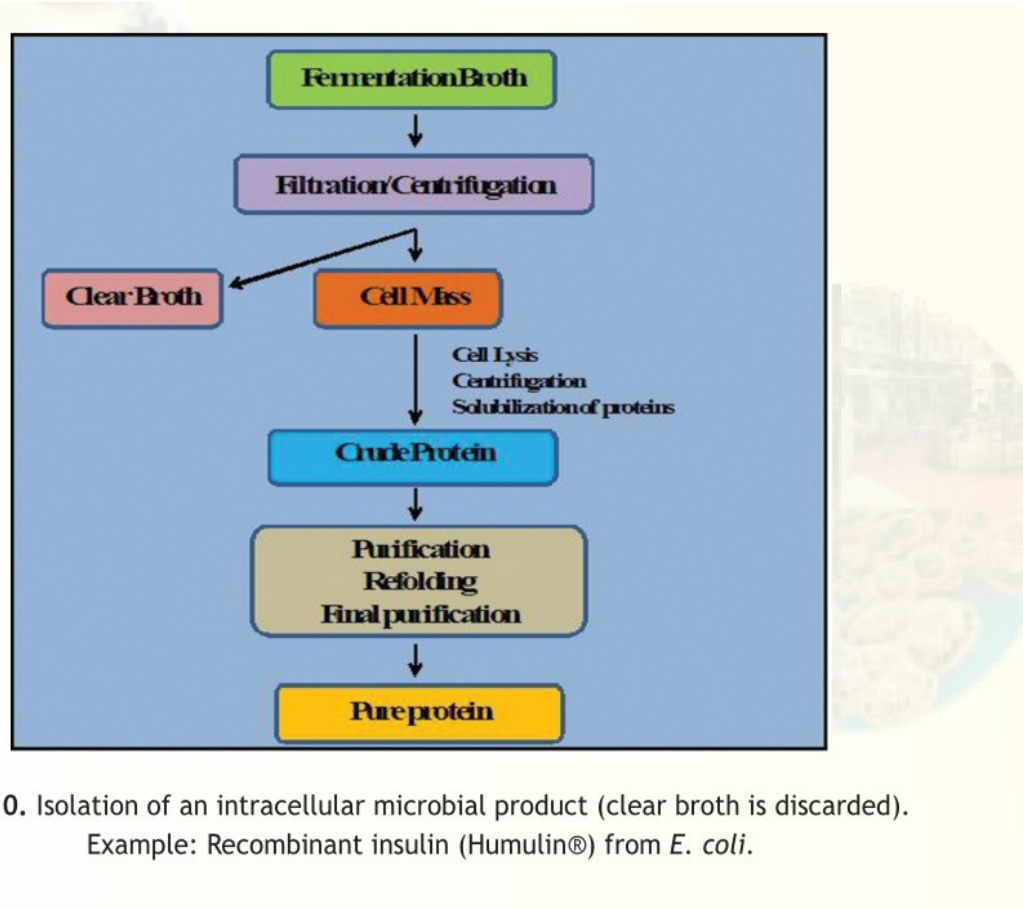
Any Three

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