University of Jijel
Faculty of Nature and Life Science
Department of Applied Microbiology and Food Science
Mai, 14th 2025 (2 hours)

Model correction

SPBMM S2 Exam MI Applied Microbiology

Question 1. Choose the correct answer(s): (0.5pt x 5 pt)

- 1. In a successful
- b) specific activity increases
- 2. Protein separation
- b) protein viscosity
- 3. During a protein purification,
- b) 80%
- 4. The technique used
- c) Analytical centrifugation
- d) Continuous gradient centrifugation
- 5. Ultra..
- b) generates shock waves capable of breaking cell membranes

Question 2: Answer "True" or "False" and correct the false statements (0.5pt x 6)

- 1. False,.... is the silver binding method.
- 2. False,pH should be is alkaline.
- 3. False,...to the isoelectric point of a protei to purify it.
- 4. False,...large DNA molecules.
- 5. False at pH 8 than at pH6.
- 6. True.

Question 3

Q1) What is the pur......

Protein precipitation (0.5pt)

Q2) Briefly explain its principle.

Salting out is a technique used to <u>precipitate proteins</u> based on their solubility in water at different <u>ionic strengths</u>. When salt is added to a protein solution, it increases the ionic strength, <u>causing salt ions to compete with proteins for water molecules</u>. As water becomes less available to solvate the proteins, their <u>hydrophobic regions interact more</u>, leading to precipitation of the proteins out of the solution. (1.25pt)

Q3) In which fraction (pellet

Pellet (0.5pt)

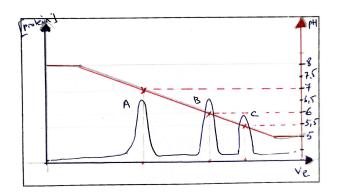
Q4) How does dialysis

Dialysis works on the principle of <u>diffusion across a semipermeable membrane</u>. <u>The membrane allows only small molecules and ions to pass through, while retaining larger molecules like proteins</u>. When the protein solution is placed inside the dialysis bag and immersed in a larger volume of buffer or water, the small molecules move out through the membrane down <u>their concentration gradient</u>, leaving the proteins behind. (1pt)

Purpose: desalting (0.5pt)

Q5) What is the basis for

Proteins bind to a <u>charged resin</u> (either positively or negatively charged) in a column, depending on <u>their own charge</u>. Cation exchange chromatography uses a negatively charged resin to bind positively charged proteins, while anion exchange uses a positively charged resin for negatively charged proteins. Bound proteins are then <u>eluted</u> by gradually <u>increasing the salt concentration or changing the pH</u>, which disrupts the electrostatic interactions and causes proteins to elute based on their charge properties. (1.25pt)



Q7) What can

pl = 6 (0.5pt)

Q8) On what protein

Size and molecular weight (0.5pt)

Q9) Why are chromato.....

To determine <u>protein concentration</u> by a non destructive method (0.5pt)

Q10) Indicate the

Peack 2 (0.5pt)

Q11) Calculate.....(0.25pt x 4 for log calculation + 0.5pt for graph + 0.5pt for MW determination)

Protein	MW (kDa)	<mark>LogMW</mark>	Ve (ml)
1	94	<mark>4.97</mark>	20
2	68	<mark>4.83</mark>	40
3	43	<mark>4.63</mark>	70
4	30	<mark>4.47</mark>	90
Fraction active (F3)	<mark>75-87</mark>	4.88-4.94	<mark>25</mark>

Q12) Can we

No (0.5pt)

Q13) How can

SDS PAGE/Native PAGE (0.5pt)

Q14) Complete the purification table for the enzyme below. $(0.5pt \times 6)$

Etape	Volume (ml)	Enz activity (U/ml)	Protein(mg/ml)	Fold purification	Yield %
Crude extract	8500	1.8	40	1	100
50% AS	530	23.3	<mark>194</mark>	2.7	<mark>81</mark>
IEC	420	25	19.5	<mark>28.4</mark>	<mark>69</mark>
GF	48	<mark>198</mark>	2.2	<mark>1964</mark>	62