# DEPARTMENT OF BIOCHEMICAL ENGINEERING AND BIOTECHNOLOGY

## Major Examination

## BEL 311: Physical and Chemical Properties of Biomolecules

**Max. Marks: 45** **Time: 2 hour**

*Brevity is the soul of communication. Extraneous information will be penalized!*

1. Show that the wavelength of the emitted photons cannot be ~~longer~~ smaller than the wavelength of the excitation photons for a fluorophore.

(4)

2. Given a microbial cell, provide a protocol (in form of a flow diagram/table) to purify intracellular proteins. What would be the major difference in the methodology for purifying membrane proteins? Clearly mark the steps in the flow diagram/table for answering the latter.

(4 + 2 = 6)

3. What is the fluid-mosaic model for biological membranes? What are membrane rafts? What biochemical and biophysical experimental evidence demonstrates the presence of membrane rafts.

(2 + 2 + 4 = 8)

4. Biomolecular asymmetry is an inherent feature of biological membranes, when they are a part of a living system. List the asymmetries. Why are these asymmetries absent in synthetic systems (e.g. liposomes)?

(4 + 2 = 6)

5. Name the weak and strong interactions of biomolecules. Why is it important that weak interactions, not strong ones, mediate biomolecular interactions including recognition?

(4 + 2 = 6)

6. What are the limitations of SDS-PAGE? Why does one require a crosslinker to identify protein complexes by SDS-PAGE?

(2 + 2 = 4)

7. A microbe having biological membranes of thickness of 1 nm has been discovered. Total protein analyses from that microbe reveal the same components for protein formation as discovered in general till date. It is hypothesized that protein folding in the microbe follows the same general principles that are well accepted so far. Analysis of the whole cell lysate resulted in a large amount of a low molecular weight (8.5 KDa) protein. Sequencing could reveal only a portion of the protein as: KKKYSTDWGILMAIGREKGVFLLAIWQRKA. Answer the following questions regarding the protein (use the hydrophobicity scale provided below):
   (a) How many amino acid residues would be expected in the full protein?
   (b) How many transmembrane domains does the protein have?
   (c) Assuming that the values provided in the hydrophobicity scale below represent change in free energy, what can be said about the experimental system used for generating the scale?

(2 + 7 + 2 = 11)

The hydrophobicity scale given by Eisenberg et al., J. Mol. Biol. (1984):

| A | R | N | D | C | E | Q | G | H | I | L | K | M | F | P | S | T | W | Y | V |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 0.62 | -2.53 | -0.78 | -0.9 | 0.29 | -0.85 | -0.74 | 0.48 | -0.4 | 1.38 | 1.06 | -1.5 | 0.64 | 1.19 | 0.12 | -0.18 | -0.05 | 0.81 | 0.26 | 1.08 |