



UNIVERSITY OF GHANA
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BSC ENGINEERING
DEPARTMENT OF BIOMEDICAL ENGINEERING
FIRST SEMESTER EXAMINATION: 2018/ 2019
BMEN 403: CELL AND MOLECULAR BIOLOGY (2 CREDITS)

INSTRUCTION:

ANSWER ALL QUESTIONS IN THE ANSWER BOOKLET PROVIDED.

TIME ALLOWED: 2 HOURS

1. (a) Match the following list of RNAs (left side) with their function(s) (right side).
- | | |
|------------|---|
| w. mRNA | i. block translation of elected mRNAs |
| x. rRNA | ii. modification and processing of rRNA |
| y. snoRNA | iii. modification of snoRNA and snRNA |
| z. snRNA | iv. components of ribosome |
| aa. tRNA | v. splicing of RNA transcripts |
| bb. scaRNA | vi. directs degradation of selected mRNAs |
| cc. miRNA | vii. codes for proteins |
| dd. siRNA | viii. adaptor for protein synthesis |
- (4 marks)
- (b) Use a drawing to illustrate the principle of DNA gel electrophoresis. (2 marks)
- (c) Draw roughly the comparative electrophoretic mobilities of close circular DNA, open circular DNA and super coiled DNA, all having the same molecular weight. (3 marks)
- (d) Why is the separation possible given that all the DNAs (in 1(c)) have the same molecular weight? (2 marks)
- (e) Describe the process of cloning a DNA fragment into the *EcoRI* and *AluI* sites of the vector pUC18. How would you screen for clones that contain an insert? (9 marks)
2. Briefly explain the principle behind the following techniques:
- | | |
|---|------------|
| (a) ion-exchange chromatography | (3 marks) |
| (b) gel filtration chromatography | (3 marks) |
| (c) affinity chromatography | (3 marks) |
| (d) Use three diagrams to illustrate the separation of three different proteins by these methods. | (11 marks) |

3. A protein has a stability ranging from 6 to 15 kcal/mole at 37 °C. Stability is a measure of the equilibrium between the folded and unfolded protein given by the relationship;

$$\text{folded}(F) = \text{unfolded}(U), k = [U]/[F]$$

For a protein with a stability of 10 kcal/mole, calculate the fraction of unfolded protein that would exist at equilibrium at 37 °C. Use the following equation:

$$\Delta G^0 = RT \ln k = -2.3 RT \log k,$$

where $R = 1.98 \times 10^{-3}$ kcal/mole and T is temperature in Kelvin (K) and k is the equilibrium constant. (12 marks)

4. Figure 1 represents the amino acid sequence of a G-protein coupled receptor (GPCR) as determined by mass spectrometry.

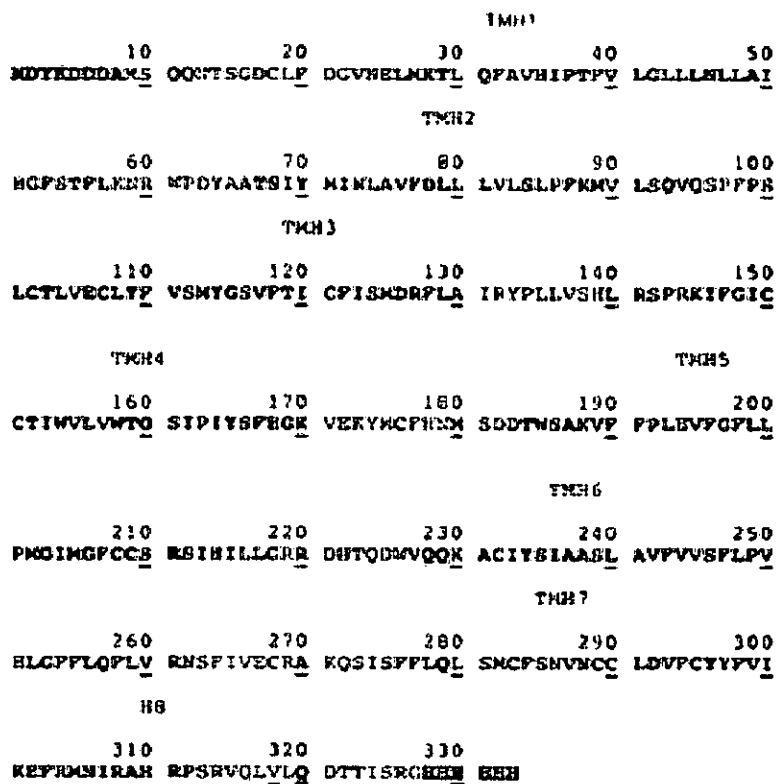


Figure 1: The amino acid sequence of a GPCR as determined by mass spectrometry

- (a) Describe the general structural features of this GPCR. (5 marks)
- (b) A ligand called **TIIF** binds to arginine-127 (R127 in transmembrane helix 3 (TMH3) to cause the activation of this GPCR. There are more than one arginine residues in this GPCR, why was the 127R selected by the ligand? (4 marks)
- (c) The binding of TIIF to **R127 in transmembrane helix 3 (TMH 3)** causes cancer, you intend to change the binding site to **R220** which is found in **TMH5** to prevent the cancer signaling pathway. Design a construct to change the site to **TMH5**. (4 marks)
- (d) Describe a spectroscopic technique that you can use to determine the structure of the GPCR apart from mass spectrometry. (6 marks)
- (e) What is the purpose of the sequence sequences “**MDYKDDDA**” and “**HHHHHH**” at the N- and C-termini respectively? (2 marks)
5. Genetic instability in the form of point mutations, chromosome rearrangements, and epigenetic changes needs to be maximal to allow the development of cancer.
- (a) With diagrams explain:
- (i) point mutations (5 marks)
 - (ii) chromosome rearrangement (5 marks)
 - (iii) epigenetic changes (5 marks)
6. Explain with a diagram how the malaria parasite is transmitted to the host by the female anopheles mosquito. (12 marks)

Question # 4: Figure 1

TMH1

10 20 30 40 50
 DDYKDDDAS QQNTSGDCLP DGVNELAKTL QFAVHIPTPV LGLLLNLLAI

TMH2

60 70 80 90 100
 HGFSTPLKNR WPDYAATSIY MINLAVFDLL LVLSLPFKIV LSQVQSPFPS

TMH3

110 120 130 140 150
 LCTLVECLYP VSMYGSVFTI CPISMDRPLA IRYPLLVSHL RSPRKIFGIC

TMH4

TMH5

160 170 180 190 200
 CTIWVLWTC SIPIYSPHOK VEKYMCFHHM SDDTWSAKVP PPLEVFGPLL

TMH6

210 220 230 240 250
 PNGIMGFCCS RSIHILLGRR DHTQDNVQQK ACIYSIAASL AVFVVSFLPV

TMH7

260 270 280 290 300
 HLGPFLOPLV RNSFIVECRA KQSI SPFLQL SKCPSNVNCC LDVPCYYFVI

H8

310 320 330
 KEPRMNIRAH RPSRVQLVLQ DTTISRGEHHH HHH