

YILDIZ TECHNICAL UNIVERSITY FACULTY OF ELECTRICAL AND ELECTRONICS ENGINEERING DEPARTMENT OF BIOMEDICAL ENGINEERING



BME 2901 – BIOCHEMISTRY 2020 – FALL

MIDTERM I

Student Name:				
ID	:			
1.	Aspartame, a dipeptide composed of Asp-Phe, is used as an artificial sweetener. It is 180-200 times sweeter than sucrose so that the quantity of aspartame needed to produce a sweet taste is so small that its caloric contribution is negligible. Thus, it is used by people who are on calorie restricted diets as well as diabetic patients. However, it is widely used in beverage industry to increase the sweetness of the beverages without increasing the calorie intake. Based on these information about aspartame:			
	a) Draw the structure of aspartame. (5 points)			
	b) Name the dipeptide using dipeptide nomenclature rules. (3 points)			
	c) Indicate N and C terminal aminoacids in the structure. (2 points)			
	 d) Calculate the theoretical pI of aspartame using the pKa values in the following table. (10 points) 			

Aminoacid	pK ₁ (-COOH)	pK ₂ (-NH ₃ +)	pKR
Alanine	2,34	9,69	
Arginine	2,17	9,04	12,48
Asparagine	2,02	8,80	
Aspartic Acid	2,09	9,82	3,86
Cysteine	1,71	10,78	8,33
Glutamic Acid	2,19	9,67	4,25
Glutamine	2,17	9,13	
Glycine	2,34	9,60	
Histidine	1,82	9,17	6,00
Isoleucine	2,36	9,60	
Leucine	2,36	9,60	
Lysine	2,18	8,95	10,53
Methionine	2,28	9,21	
Phenylalanine	1,83	9,13	
Proline	1,99	10,60	
Serine	2,21	9,15	
Threonine	2,63	10,43	
Tryptophan	2,83	9,39	
Tyrosine	2,20	9,11	10,07
Valine	2,32	9,62	

2. Answer the following questions.

a. The nucleotide sequence of one DNA strand of a DNA double helix is:

5'-GGATTTTTGTCCACAATCA-3'.

What is the sequence of the complementary strand? (2 points) Please show Watson-Crick base pairing and indicate 5' and 3' ends of the complementary strand. (2 points) What does 5' and 3' refer to? (3 points) Comment on the antiparallelity of the strands. (3 points)

b. In the DNA of certain bacterial cells, 13% of the nucleotides are adenine. What are the percentages of the other nucleotides? (5 points)

3. Our growing understanding of how proteins fold allows researchers to make predictions about protein structure based on primary amino acid sequence data. Given that below peptide sequence:

- a) Indicate N- and C-terminus of the above peptide (3 pts).
- b) In the amino acid sequence below, where would you predict that bends or β turns would occur? Why? (5 pts)
- c) Where intrachain disulfide cross-linkages might be formed? Explain briefly. (5 pts)
- d) Assuming that this sequence is part of a larger globular protein, indicate the probable location (the external surface or interior of the protein) of the following amino acid residues: Asp, Phe, Lys. Explain your reasoning briefly. (5 pts)
- e) Which weak interactions might play roles in folding of this peptide? (5 pts)
- 4. In sickle cell anemia a change in a single nucleotide in hemoglobin gene causes a change in single aminoacid in the protein to turn from glutamic acid to valine.
 - a) Why do you think a change from Glu to Val affects the function of the protein that much so that it causes patients to suffer from anemia, weakness and even organ failure? (5 pts)
 - b) What does it tell you about the relationship between the primary sequence and the protein's native conformation? (5 pts)
- 5. Scurvy is a disease resulting from a lack of vitamin C (ascorbic acid). People with scurvy suffer from loose teeth, delayed wound healing, sore arms and legs which are found to be associated with defects in collagen structure.
 - a) Why vitamin C is required for the correct conformation of collagen? (5 pts)
 - b) What are the contributions of hydroxyprolines and hydroxylysines to the native conformation of collagen? (5 pts)

6.	Suppose that you are given a project in Biochemistry Laboratory to isolate mRNA from a cell lysate. Propose a chromatographic method to effectively isolate mRNA without protein or DNA contamination. (5 pts)
	Hint: Mature mRNA has a poly-A tail.

- 7. Suppose that you are given a project in Biochemistry Laboratory to purify an enzyme.
 - a) You are also told that iron is a ligand of this enzyme. Which chromatographic method would you choose to purify this protein effectively? Explain briefly. (3 pts)
 - b) You are also given aminoacid sequence of the enzyme in which you noticed that enzyme is very small and mostly consist of negatively charged aminoacids. Which chromatographic methods would you choose to purify this protein effectively? Explain briefly. (3 pts)
 - c) At the end of purification steps how can you be sure that you actually purified the correct enzyme and that the enzyme you think you purified is actually pure? (3 pts)

8. As a biomedical engineer owning a firm suppose that in sectoral conversations you heard that protein X has a wide industrial use and a huge economical value. You thought that you could obtain protein X and earn lots of money by selling it. What are your choices to obtain protein X in large amounts? Which of those methods you would choose and why? (8 pts)

GOOD LUCK 29.11.2020