

Protein Modeling Test

Section I: General Biochemistry

*All questions are worth 1 point unless noted differently next to the question

- 1) What type of bond is formed when amino acids polymerize?
 - a) Phosphodiester bond
 - b) Hydrogen bond
 - c) Peptide bond
 - d) Metallic bond

- 2) (3 pts) Rate the following intramolecular forces/interactions from least to greatest strength: hydrogen bonds, Van der Waals forces, ionic bond (3pts)
 - a) 1) _____, 2) _____, 3) _____

- 3) (2 pts) Two functional groups which exist on every amino acid are _____ and _____

- 4) (2pts) Describe chirality

- 5) All amino acids are chiral *except* for?
 - a) Glycine
 - b) Alanine
 - c) Phenylalanine
 - d) Histidine

- 6) The start codon for translation is?
 - a) UAA
 - b) AUG
 - c) UGA
 - d) UUU
 - e) GUA

- 7) (2 pts) The amino acid that is coded for by the start codon is _____.

- 8) Which of the following amino acids can form disulfide bonds?
 - a) Tyrosine

- b) Asparagine
 - c) Glutamic Acid
 - d) Cysteine
- 9) What level of protein structure is characterized by hydrogen bonding between Beta sheets?
- a) Primary
 - b) Secondary
 - c) Tertiary
 - d) Quaternary
- 10) What intermolecular force contributes most strongly to the folding of tertiary structures (ex. packing of α -helices against one another into a four-helix bundle)?
- a) Electrostatic interactions
 - b) Van der Waals Force
 - c) Hydrogen Bond
 - d) Hydrophobic interactions
- 11) If protein folding forces the formation of intramolecular disulfide bonds when in the folding process would the disulfide bonds actually form?
- a) After tertiary structure
 - b) Between secondary and tertiary structure
 - c) Between primary and secondary structure
 - d) In the primary structure
- 12) (2 pts) Most proteins are in the _____ configuration where r-groups extend in opposite sides of the peptide bond plane.
- 13) Which of the following is a function of proteins?
- a) Catalysis as enzymes
 - b) Structural support
 - c) Transport
 - d) Signal transduction
 - e) All of the above
- 14) Which of the following methods would allow a scientist to identify the primary structure of a protein without any prior knowledge of the protein of interest?
- a) Edman degradation
 - b) Tandem mass spectrometry (MS/MS)

- c) Matrix-assisted laser desorption ionization-time of flight (MALDI-TOF)
- d) Enzyme digestion

15) A protein solution has a low salt concentration and then salt is added, at first the solubility of proteins increases since the salt ions shield charged regions of proteins from each other. What happens at a high salt concentration to the solubility of proteins?

- a) Decrease, salt ions disrupt hydrophobic interactions
- b) Decrease, salt ions compete with proteins for water molecule interactions
- c) Increase, there are more electrostatic interactions since salt ions deprotonate ionizable side groups
- d) Increase, salt ions continue to shield charged regions of the proteins

16) What proteins would migrate through native gel electrophoresis towards the positively charged end faster than the other proteins described in the options below?

- a) Negatively charged, globular
- b) Negatively charged, fibrous
- c) Positively charged, globular
- d) Positively charged, fibrous

17) How many possible proteins 300 amino acids in length could exist?

- a) 10^{290}
- b) 20^{300}
- c) 20^{290}
- d) 10^{300}

18)

- a) (2 pts) What does the dihedral angle Φ (phi) measure and when is it positive or negative (view down from N-C alpha bond)?

- b) (2pts) What does the dihedral bond ψ (psi) measure?

19) A protein that is composed of mainly α -helices is plotted on the Ramachandran plot. Which statement best describes the Ramachandran plot of amino acids in the protein that you would expect based on its structure?

- a) Most data points in the two left quadrants
- b) Most data points in the top left quadrant
- c) Most data points in the top right quadrant
- d) Most data points in the bottom left quadrant

20)

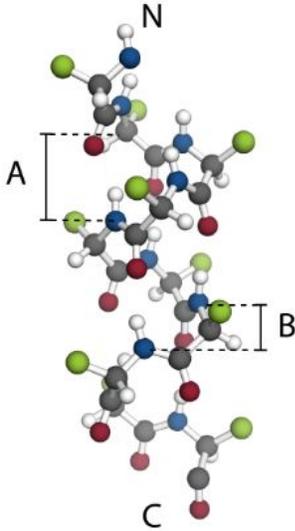
a) (2 pts) What is competitive inhibition?

b) (2 pts) What is noncompetitive inhibition?

21) (2 pts) What is Anfinsen's Dogma and its three conditions?

22) (2 pts) What is Levinthal's paradox?

23) (5 pts) Below is a diagram (credit to <https://qrqo.page.link/CQULU>) of an alpha helix and answer the next 4 questions based on this diagram:



- a) What does measurement A describe and define it?

- b) The height of measurement A would be _____ angstroms and would contain about _____ amino acids.

- c) What does measurement B describe and define it?

- d) The distance of measurement B would be _____ angstroms.

Section II: Gene Editing Techniques

**All questions are worth 1 point unless noted differently next to the question*

- 1) In which bacteria was the CRISPR structure first discovered (1978)?
 - a) E. Coli
 - b) Campylobacter
 - c) Norovirus
 - d) Salmonella

- 2) Which gene-editing mechanism has nucleases that recognize one long, specific sequence?
 - a) Zinc finger nucleases (ZNFs)
 - b) TALENS
 - c) Meganucleases
 - d) CRISPR

- 3) Which gene-editing mechanism uses DNA binding motifs to direct non-specific nuclease to cleave the genome?
 - a) Zinc finger nucleases (ZNFs)
 - b) TALENS
 - c) Meganucleases
 - d) CRISPR

- 4) Which gene-editing mechanism recognizes all of the 64 possible trinucleotide combinations?
 - a) Zinc finger nucleases (ZNFs)
 - b) TALENS
 - c) Meganucleases
 - d) CRISPR

- 5) Which gene-editing mechanism is made up of a transcription activator-like protein?
 - a) Zinc finger nucleases (ZNFs)
 - b) TALENS
 - c) Meganucleases
 - d) CRISPR

- 6) Which gene-editing mechanism has about 70% efficiency?
 - a) Zinc finger nucleases (ZNFs)
 - b) TALENS
 - c) Meganucleases
 - d) CRISPR

- 7) How many base pairs long is the region targeted by Cas9?
 - a) 10 base pairs
 - b) 20 base pairs
 - c) 30 base pairs
 - d) 40 base pairs

8)

a) What are yeast artificial chromosomes (YAC)?

b) What are bacterial artificial chromosomes (BAC)?

9) What does TALENS stand for?

10) What does CRISPR stand for?

11) What are palindromic repeats?

12) (2 pts) What is a "dead" Cas9 (dCas9) and what are they used for?

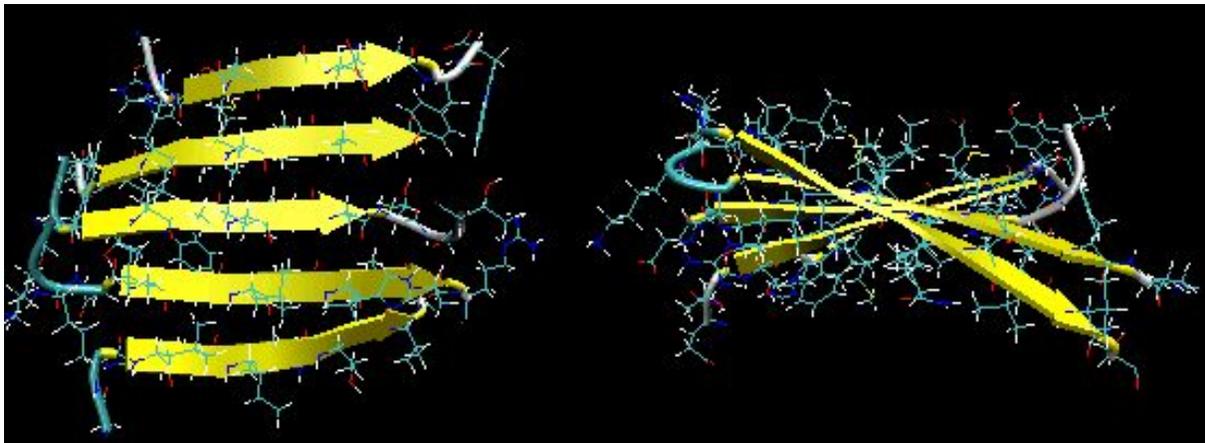
13) (2pts) How many inactive domains are/is there in a Cas9 nickase and what are the benefits of using a Cas9 nickase?

14) (2 pts) How is the original CRISPR structure in bacteria different from CRISPR Cas9 structures researchers use (please state at least one difference)?

15) (2 pts) What does the abbreviation PAM stand for and what PAM sequence does Cas9 recognize?

Section III: Jmol Exploration

*All questions are worth 1 point unless noted differently next to the question

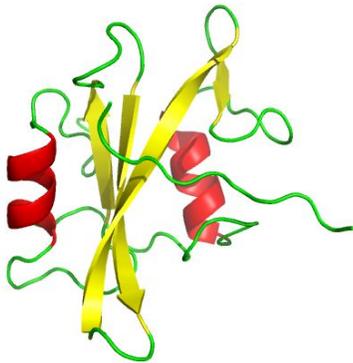


Answer the following 5 questions based on the image shown above from Jmol (picture based on (credit to) <https://qr.go.page.link/utBxW>)

- 1) What is/are the main secondary structure(s) shown?
- 2) How many beta sheets are present?
- 3) How many alpha helices are present?
- 4) (2 pts) Are the Beta sheets shown antiparallel or parallel? Also, are parallel or antiparallel beta sheets more stable?

- 5) (2 pts) How are beta pleated sheets held together and what are the bonds holding beta sheets together formed between?
- 6) What is another name given to this specific secondary structure (ex. Beta sheets in a circular structure are known as a beta barrel)?

Answer the following 5 questions based on the image shown below from Jmol (picture based from (credit to) <https://qrqo.page.link/ygD2j>)



- 7) What is the main secondary structure shown?
- 8) How many beta sheets are present?
- 9) How many alpha helices are present?
- 10) Are the Beta sheets shown antiparallel or parallel?

11) (2 pts) How are alpha helices (right handed) held together and what are the bonds holding them together formed between?

12) (2 pts) Are right handed or left handed alpha helices more commonly found in nature and why?

13) Assuming this protein is made from one polypeptide chain, what is the lowest level of structure it has (primary, secondary, etc.)?