

Protein Modeling Answer Key

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) **Van der Waals**, 2) **Hydrogen bond**, 3) **Ionic Bond**
- 3) (2 pts) Two functional groups which exist on every amino acid are **amino group** and a **carboxyl group**
- 4) (2pts) Describe chirality

A geometric property of molecules/ions in which there exist two optically active asymmetric forms of the molecule that are the mirror images of each other.

- 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 **methionine**.
- 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 **trans (or R)** 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)?

The angle between the nitrogen and the alpha carbon of the same amino acid and left is negative while the right is positive

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

The angle between the N-C bond of that amino acid and carbonyl - N/C or one amino acid away by the right-hand rule

- 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?

Competitive inhibition is when molecules that are similar to the substrate molecules bind to the active site and the actual substrate from binding.

- b) (2 pts) What is noncompetitive inhibition?

Noncompetitive inhibition is when an inhibitor binds to the enzyme at a site that isn't the active site.

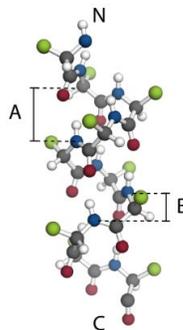
- 21) (2 pts) What is Anfinsen's Dogma and its three conditions?

The idea that if a protein is folding into its native structure it's done automatically by the protein's amino acid sequence. The three conditions would be uniqueness (or different from others), stability, and kinetical accessibility.

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

States that the possible number of conformations available for a specific protein is extremely large (or astronomically large) thus proteins must follow some ordered pathway when folding.

- 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?

Pitch of an alpha helix or the height between one turn in an α -helix

- b) The height of measurement A would be 5.4 angstroms and would contain about 3.6 amino acids.
- c) What does measurement B describe and define it?

Rise of an alpha helix or distance between two amino acids

- d) The distance of measurement B would be 1.5 angstroms.

Section II: Gene Editing Mechanisms

*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) (2 pts) What are yeast artificial chromosomes (YAC)?

Yeast artificial chromosomes are genetically engineered chromosomes from DNA of yeast. They are linear DNA and contain all that is required for replication in yeast.

- b) (2 pts) What are bacterial artificial chromosomes (BAC)?

Circular plasmids that normally replicate long regions of DNA and are maintained at a level of approximately one copy per cell and contain all that is required for replication.

- 9) What does TALENS stand for?

Transcription activator-like effector nuclease

- 10) What does CRISPR stand for?

Clustered Regularly Interspaced Short Palindromic Repeats

- 11) What are palindromic repeats?

20-40 letter repeats of DNA same left to right

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

Dead Cas9 is a protein that cannot cut DNA. However, it can be used to affect gene expression (being attached to a promoter/repressor).

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

Cas9 Nickase has 1 inactive nuclease domain to induce specific single-strand DNA nicks. The benefits are high specificity and want to minimize off-target effects.

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

(any of the options below are answers)

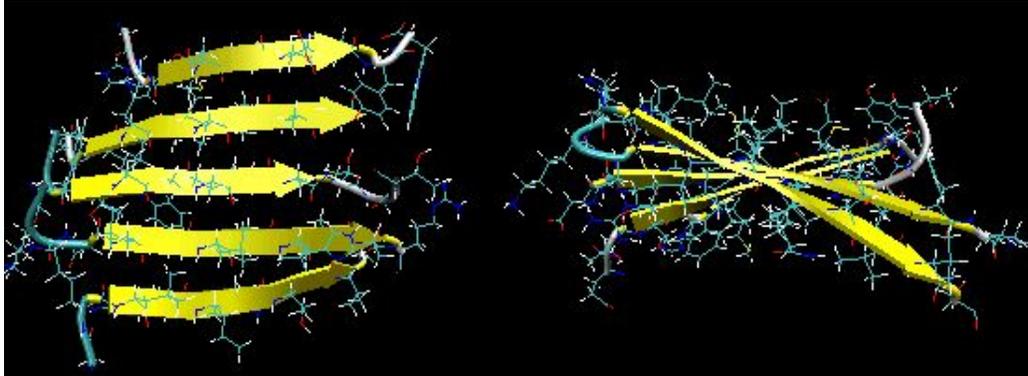
- a) Specific RNA to target a sequence (sgRNA)
- b) Can inactivate both nuclease sites
- c) Cytidine deaminase to n-terminus of cas9 (AID)

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

PAM stands for protospacer adjacent motifs and cas9 binds to: 5'-N-G-G-3' (N could be any nucleotide base)

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://qrqo.page.link/utBxW>)

- 1) What is/are the main secondary structure(s) shown?

Beta Sheets

- 2) How many beta sheets are present?

5

- 3) How many alpha helices are present?

0

- 4) (2 pts) Are the Beta sheets shown antiparallel or parallel? Also, are parallel or antiparallel beta sheets more stable?

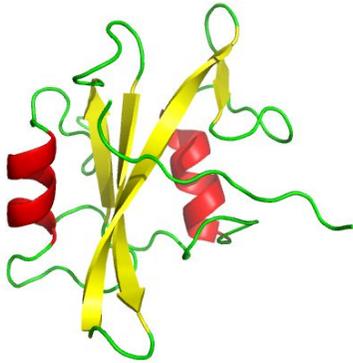
They are parallel and antiparallel beta sheets are a bit more stable than parallel β sheets since their hydrogen bonding pattern is more optimal

- 5) (2 pts) How are beta pleated sheets held together and what are the bonds holding beta sheets together formed between?

Beta sheets are held together by hydrogen bonds that form between carbonyl and amino groups of backbone, while the R groups extend above and below the plane of the sheet.

- 6) What is another name given to this specific secondary structure (ex. Beta sheets in a circular structure are known as a beta barrel)?

Twisted beta sheet or twisted beta saddle



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

7) What is the main secondary structure shown?

Beta Sheets

8) How many beta sheets are present?

3

9) How many alpha helices are present?

2

10) Are the Beta sheets shown antiparallel or parallel?

Antiparallel

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

Alpha helices are held together by hydrogen bonds between the amino and carbonyl groups of every fourth amino acid. The side chains extend outwards.

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

Proteins usually are made of right-handed alpha helices while left-handed alpha helices are more rare since right handed helices are more stable.

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

Primary