

Protein Modeling C - 2020 Rickards Protein Modeling - Rickards Invitational Div. C - 12-05-2020

Welcome to Rickards Protein Modeling!

General Biochemistry

1. (1.00 pts) What type of bond joins carbohydrate molecules to one another?

- ☐ A) Glycosydic Linkage
- ☐ B) Peptide Bond
- ☐ C) Ester linkage
- ☐ D) Ionic bond
- ☐ E) Phosphodiester bond

2. (1.00 pts) What type of bond links the pentose sugars of nucleic acids together?

- ☐ A) Ionic bond
- ☐ B) Glycosidic linkage
- ☐ C) Phosphodiester bonds
- ☐ D) Dative bond
- ☐ E) Ester linkage

3. (1.00 pts) What type of bond links amino acids together to form proteins?

- ☐ A) Coordinate covalent bond
- ☐ B) Ester linkage
- ☐ C) Peptide bonds
- ☐ D) Glycosidic linkage
- ☐ E) Ionic bond

4. (1.00 pts) Which of the following bonds would you find in a lipid?

- ☐ A) Ionic bond
- ☐ B) Coordinate covalent bond
- ☐ C) Dative bond
- ☐ D) Ester linkage
- ☐ E) Phosphodiester bond

5. (1.00 pts) Select all of the following levels of protein structure that are incorrectly matched with its description.

(Mark **ALL** correct answers)

- ☐ A) Primary Structure: Sequence of amino acids
- ☐ B) Secondary Structure: Hydrogen bonding of backbone
- ☐ C) Tertiary Structure: Formation of alpha helices and beta sheets
- ☐ D) Quaternary Structure: 3-D folding due to side chain interactions
- ☐ E) All of the above are correctly matched

6. (1.00 pts) Sickle cell anemia is caused by a point mutation that leads to the replacement of a _____ residue with a _____ residue.

7. (1.00 pts) Which of the following best explains why the peptide bond is relatively inflexible?

- ☐ A) Peptide bonds have partial double bond character
- ☐ B) Steric hindrance due to bulky substituents on either side of the bond
- ☐ C) The carbon-nitrogen bond is a polar covalent bond
- ☐ D) Peptide bonds do not exhibit abnormal inflexibility

8. (1.00 pts) The increased favorability of which of the following interactions accounts for the stability of antiparallel beta sheets relative to parallel beta sheets?

- ☐ A) Geometry
- ☐ B) Ionic bonds
- ☐ C) Hydrogen bonds
- ☐ D) Steric interactions
- ☐ E) Pi stacking interactions

9. (3.00 pts)

Disulfide bonds are generally formed [intracellularly/extracellularly] because the extracellular environment is [oxidizing/reducing] while the intracellular environment is [oxidizing/reducing].

10. (2.00 pts)

On a Ramachandran plot, left-handed alpha helices would be found in the [top left/top right/bottom left/ bottom right] while right-handed alpha helices would be found in the [top left/top right/bottom left/ bottom right].

11. (1.00 pts) The final shape of a folded protein sequence is called its _____.

- ☐ A) Transition state
- ☐ B) Molten globule
- ☐ C) Activated complex
- ☐ D) Parent conformation

☐ E) Native conformation

12. (1.00 pts) Which of the following best describes the structure of collagen?

- ☐ A) Alpha helix
- ☐ B) Double helix
- ☐ C) Triple helix
- ☐ D) Amorphous
- ☐ E) Globular

13. (1.00 pts) What set of rules accounts for the 1:1 ratio of purines to pyrimidines?

14. (2.00 pts) What two radioisotopes were used in the Hershey-Chase experiment?

15. (3.00 pts) What experiment demonstrated that, in bacteria, genetic mutations arise in the absence of selection, rather than being a response to selection?

Amino Acids

For questions 16-25, name the amino acid(s) that matches the given description.

16. (1.00 pts) The two amino acids that are almost never found in alpha helices.

17. (1.00 pts) The only achiral amino acid.

18. (1.00 pts) The two amino acids that contain sulfur.

19. (1.00 pts) Coded for by the UAG codon.

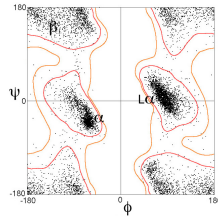
20. (1.00 pts) Coded for by the UGA codon.

21. (1.00 pts) Forms disulfide bridges.

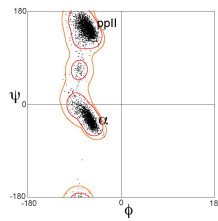
22. (1.00 pts) Most acidic amino acid.

23. (1.00 pts) Most basic amino acid

24. (1.00 pts) The one with this Ramachandran plot:



25. (1.00 pts) The one with this Ramachandran plot:



Structural Motifs

For questions 26-35, name the structural motifs that matches the given description.

26. (1.00 pts) Connecting these motifs laterally makes a beta sheet.

27. (1.00 pts) DNA binding motif that binds to the major groove of DNA.

28. (1.00 pts) Also called a 3.6₁₃-helix.

29. (1.00 pts) Can be identified as a ~7 residue "bulge" within an alpha helix.

30. (1.00 pts) 4th most common secondary structural motif. Each residue corresponds to a 120 degree turn.

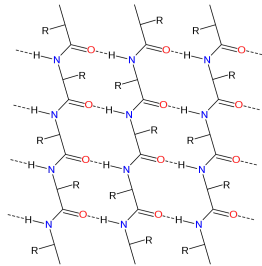
31. (1.00 pts) HLH domain found in Ca-binding proteins.

32. (1.00 pts) Highly conserved motif found in aquaporins.

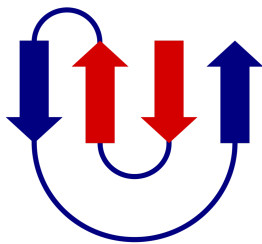
33. (1.00 pts) The one in this picture:



34. (1.00 pts) The one in this picture:



35. (2.00 pts) The one in this picture:



Protein Folding

Questions 36-40 are about protein folding.

36. (4.00 pts) Explain how hydrophobic interactions help drive protein folding.

37. (4.00 pts) Explain the function of chaperonins in protein folding and how they aid in protein folding.

38. (4.00 pts) State what Anfinsen's dogma is and the three conditions it uses to define the native structure.

39. (10.00 pts)

Outline the experimental procedure Anfinsen used to investigate his theory. What protein did he use? What parts of this protein did he target and what reagents did he use to target them? How did this support his theory?

40. (4.00 pts) State what Levinthal's paradox is and explain how it relates to Anfinsen's dogma. Provide an explanation that resolves this paradox.

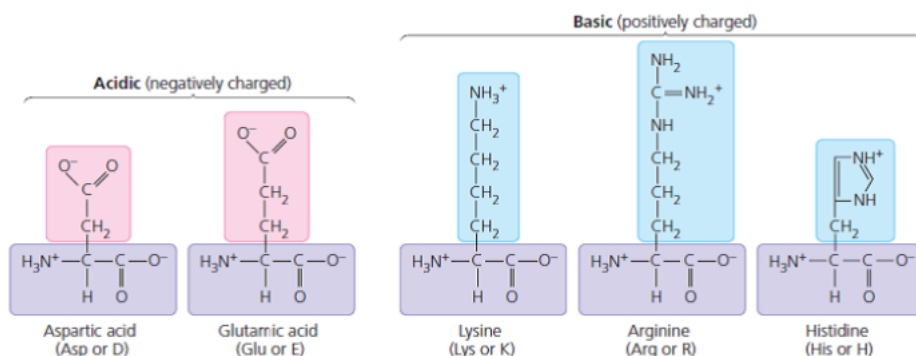
Acid-Base Chemistry of Amino Acids

41. (2.00 pts)

Because all amino acids have amine and carboxylic acid groups, they can act as both an acid and a base. What is the chemical term for molecules that can act as both acids and bases?

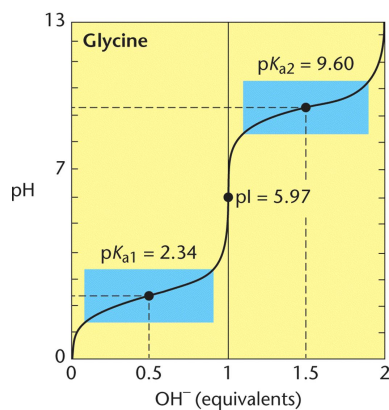
42. (2.00 pts)

The amine and carboxyl groups of amino acids also mean they simultaneously have a negative and positive charge. What is the chemical term for molecules that simultaneously have both ionic states?

43. (8.00 pts)

The amino acids shown above have side chains with acidic or basic properties. Which of these amino acids has the most acidic side chain? Why? Which has the most basic side chain? Why? [Hint: Compare the relative stability of their conjugate acids/bases in your argument.]

Questions 44-46 refer to the following titration curve:



44. (1.00 pts) Above is the titration curve for glycine. What is the net charge on glycine at pKa1, pI, and pKa2?

45. (1.00 pts) True or False: Glycine acts as a good buffer at the pH of blood.

☐ True ☐ False

46. (1.00 pts) The pI of glycine is equal to the arithmetic mean of its pKa1 and pKa2. Is this true for all amino acids?

☐ A) Yes
☐ B) No

Laboratory Methods

47. (2.00 pts)

The Edman degradation is a method for _____ polypeptides by removing residues one at a time from the _____ and identifying each residue as it is removed.

48. (2.00 pts) Outline the procedure for performing an Edman degradation. Make sure you name the specific reagents you would use at each step.

49. (2.00 pts) The Bergmann degradation is the predecessor of the Edman degradation. Briefly explain how the Edman degradation improved on the Bergmann degradation.

50. (2.00 pts) Gel electrophoresis may be used in the separation and characterization of proteins. Briefly describe the working principle behind gel electrophoresis.

51. (2.00 pts)

Sodium dodecyl sulfate or SDS is a reagent commonly used to measure the atomic mass of protein samples in gel electrophoresis. Give a reason why SDS is used in gel electrophoresis.

52. (2.00 pts) Name four variants of chromatography used in biochemistry and/or biology.

53. (2.00 pts) What two properties does 2D gel electrophoresis separate molecules by?

(Mark **ALL** correct answers)

- ☐ A) Molecular mass
- ☐ B) Molecular size
- ☐ C) Isoelectric point
- ☐ D) Ionic radius
- ☐ E) Charge density

Questions 54-56 require you to give your answer as a list of amino acids. The common name, chemical name, three letter abbreviation and one letter abbreviation are all acceptable. (These will be manually graded).

54. (2.00 pts) Trypsin cleaves on the carbonyl side of which amino acids?

55. (2.00 pts) Chymotrypsin cleaves at the carbonyl side of what residues?

56. (2.00 pts) Cyanogen bromide cleaves at the carbonyl side of what residues?

CRISPR

For questions 57-61, state what the given acronym stands for.

57. (1.00 pts) CRISPR

58. (1.00 pts) NHEJ

59. (1.00 pts) SSB

60. (1.00 pts) BER

61. (1.00 pts) HDR

62. (9.00 pts) Name the three stages of the CRISPR-Cas9 immunity pathway and briefly describe what happens during each stage.

63. (8.00 pts) Name the two nuclear domains of Cas9 along with their function, then describe the mechanism of operation for each domain.

Exploration

Questions 64-83 require you to investigate the protein at the following link: <https://www.rcsb.org/3d-view/jsmol/4ia4> (<https://www.rcsb.org/3d-view/jsmol/4ia4>) (<https://www.rcsb.org/3d-view/4IA4>)

You're free to click around the various tabs for this protein as you'd like, but you should refrain from visiting any other pages or websites.

Note: There's a lot of background questions. If you want to skip to the actual JSmol part go to question 74.

64. (1.00 pts) In what organism was this protein isolated? Give the species name.

65. (1.00 pts) What is the weight of this protein, in kilodaltons?

66. (1.00 pts) How many mutations does this sample have?

67. (8.00 pts) This experiment used X-ray diffraction to elucidate the structure of the protein. Outline the procedure for XRD.

68. (1.00 pts) At what resolution was the XRD procedure conducted?

69. (1.00 pts) What ligand species, if any, were observed in this sample?

70. (2.00 pts) What method was used to crystallize this sample?

71. (10.00 pts) Select ANY of the terms from the list below and define it as well as you can.

- Hanging drop vapor diffusion
- Matthew coefficient
- Solvent content
- Space group
- Molecular replacement

72. (10.00 pts) Using as many terms from the list below as you can, outline the computational/data science aspect of this experiment.

- Data refinement
- Data reduction
- Data scaling
- Data phasing

73. (10.00 pts) Using as many of the terms from the list below as you can in your response, describe the experimental procedure of this diffraction experiment.

- Synchrotron
- Monochromator
- CCD
- Beamline

74. (1.00 pts) How many ligands are there in each bioassembly?

75. (1.00 pts) What amino acid is at residue 39 of this protein?

76. (1.00 pts) What amino acid is at residue 264?

77. (1.00 pts) How many hydrophobic atoms are in this structure?

78. (1.00 pts) How many hydrophilic atoms are in this structure?

79. (1.00 pts) How many charged atoms are in this structure?

80. (1.00 pts) How many atoms are in sheets?

81. (1.00 pts) How many hydrogen bonds are in the entire protein?

82. (1.00 pts) How many hydrogen bonds are there from residues 59-172?

83. (1.00 pts) When the structure is restricted to water molecules, how many atoms are listed in the jsmol console?

END OF EXAM