

C - Protein Modeling - Pearl City Invitational - 12-12-2020

Pearl City Invitational Division C Protein Modeling

**Please read all directions before starting**

1. This is only the written version of the test, however, 3D structures have been included. There are multiple choice, fill in the blank, and short answer questions. Answer the prompts to best of your ability. There is **no computer exploration** for this test. You will have 50 minutes to complete this test.

2. If there are any mistakes in the exam please let me know, krussell@pchigh.k12.hi.us (<http://krussell@pchigh.k12.hi.us>)

3. Images are not owned by the test author. I apologize for strange formatting, questions did not transfer over from my original document very well.

****SOME IMAGES MAY NOT LOAD--please let me know.

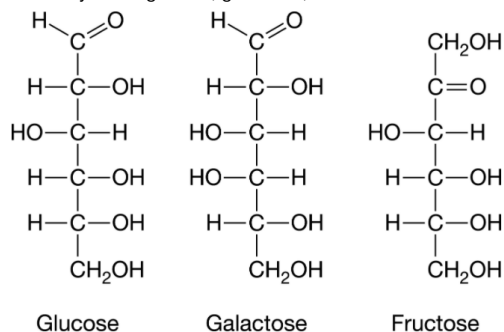
1. (1.00 pts)

The CFTR protein is made up of 1,480 amino acids linked together in a chain. Some humans produce a version of the CFTR protein in which phenylalanine (an amino acid) has been deleted from position 508 of the amino acid chain. Which of the following best predicts how the amino acid deletion will affect the structure of the CFTR protein?

- ☐ A) It will have no observable effect on the structure of the CFTR protein.
- ☐ B) It will affect the primary structure of the CFTR protein, but the other levels of protein structure will not be affected.
- ☐ C) It will affect the secondary and tertiary structures of the CFTR protein, but the primary structure will not be affected.
- ☒ D) It will affect the primary, secondary, and tertiary structures of the CFTR protein.

2. (1.00 pts)

The carbohydrates glucose, galactose, and fructose have the same chemical formula ($C_6H_{12}O_6$) but different structural formulas, as represented in the figure. Which of the following statements about glucose, galactose, and fructose is most likely true?



- ☐ A) The carbohydrates have the same properties because they have the same number of carbon, hydrogen, and oxygen atoms.
- ☐ B) The carbohydrates have the same properties because they each have a single carbon-oxygen double bond.
- ☒ C) The carbohydrates have different properties because they have different arrangements of carbon, hydrogen, and oxygen atoms.
- ☐ D) The carbohydrates have different properties because they have different numbers of carbon-carbon bonds.

3. (1.00 pts)

Which of the following best describes the effect of a greater number of cysteine amino acids on the stability of the proteins?

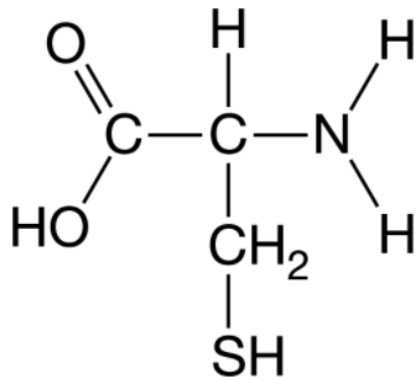


Figure 1. Chemical structure of cysteine

- ☐ A) The change has no effect on the stability of the protein because only one type of amino acid is involved
- ☒ B) The change leads to increased protein stability because of an increased number of S-S bonds in the tertiary structure of the proteins.
- ☐ C) The change leads to decreased protein stability because of an increased number of S-S bonds in the tertiary structure of the proteins
- ☐ D) The change leads to increased protein stability only when the added cysteine amino acids are next to other cysteine amino acids in the primary structure.

4. (1.00 pts)

A researcher proposes a model of an enzyme-catalyzed reaction in which a reactant is converted to a product. The model is based on the idea that the reactant passes through a transition state within the enzyme-substrate complex before the reactant is converted to the product. Which of the following statements best helps explain how the enzyme speeds up the reaction?

- ☐ A) The enzyme's active site binds to and stabilizes the reactant, which decreases the free-energy change of the reaction.
- ☒ B) The enzyme's active site binds to and stabilizes the transition state, which decreases the activation energy of the reaction
- ☐ C) The enzyme's active site binds to and stabilizes the product, which increases the amount of energy released by the reaction.
- ☐ D) The enzyme's active site binds to and stabilizes both the reactant and the product at the same time, which increases the reaction's equilibrium constant.

5. (1.00 pts)

Erwin Chargaff investigated the nucleotide composition of DNA. He analyzed DNA from various organisms and measured the relative amounts of adenine (A), guanine (G), cytosine (C), and thymine (T) present in the DNA of each organism. Table 1 contains a selected data set of his results. Which of the following statements best explains the data set?

Table 1. Nucleotide composition of sample DNA from selected organisms

Organism	Relative Amounts of Bases					
	%A	%G	%C	%T	%(G+C)	%(A+T)
Octopus	33.2	17.6	17.6	31.6	35.2	64.8
Chicken	28.0	22.0	21.6	28.4	43.7	56.4
Rat	28.6	21.4	20.5	28.4	42.9	56.0
Grasshopper	29.3	20.5	20.7	29.3	41.2	58.6
Wheat	27.3	22.7	22.8	27.1	45.5	54.4

- ☐ A) Since the %A and the %G add up to approximately 50 percent in each sample, adenine and guanine molecules must pair up in a double-stranded DNA molecule
- ☒ B) Since the %A and the %T are approximately the same in each sample, adenine and thymine molecules must pair up in a double-stranded DNA molecule.
- ☐ C) Since the %(A+T) is greater than the %(G+C) in each sample, DNA molecules must have a poly- A tail at one end.

- ☐ D) Since the %C and the %T add up to approximately 50 percent in each sample, cytosine and thymine molecules must both contain a single ring.

6. (1.00 pts) Which of the following best describes a characteristic of DNA that makes it useful as hereditary material?

- ☐ A) There are many different types of nucleotide bases that can be incorporated into DNA
- ☐ B) The nucleotide bases can also be used to provide the energy needed for reproduction.
- ☐ C) Nucleotide bases can be randomly replaced with different nucleotide bases to increase variation.
- ☒ D) Nucleotide bases in one strand can only be paired with specific bases in the other strand.

7. (1.00 pts)

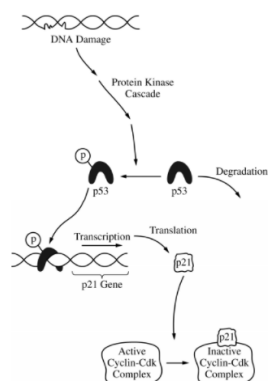
Polynucleotide Formation

Which statement best describes how the nucleotides are joined to form the polynucleotide?

- ☐ A) The phosphate group gives up an H⁺ ion and forms an ionic bond with the deoxyribose sugar.
- ☒ B) A hydrogen atom and a hydroxide group are removed from the phosphate and deoxyribose molecules, and a covalent bond is formed via dehydration synthesis.
- ☐ C) The phosphate group is strongly electronegative and forms a hydrogen bond with a positively charged region on the deoxyribose sugar.
- ☐ D) A water molecule is split via hydrolysis, and the phosphate group and the deoxyribose sugar are covalently linked

8. (1.00 pts)

The p53 protein regulates a cellular response to DNA damage. Based on the diagram above, which of the following best describes the role of p53 in the response to DNA damage?



- ☐ A) Phosphorylated p53 binds to DNA and repairs the damage.
- ☒ B) Phosphorylated p53 stimulates transcription of p21, and the resulting p21 protein suppresses cell division until the DNA damage is repaired.
- ☐ C) Phosphorylated p53 binds cyclin-Cdk complexes, and the resulting protein complex repairs the DNA damage.
- ☐ D) Phosphorylated p53 activates p21 proteins, and the p21 proteins in turn repair the DNA damage.

9. (1.00 pts) If a segment of DNA is 5'-TAC GAT TAG-3', the RNA that results from the transcription of this segment will be

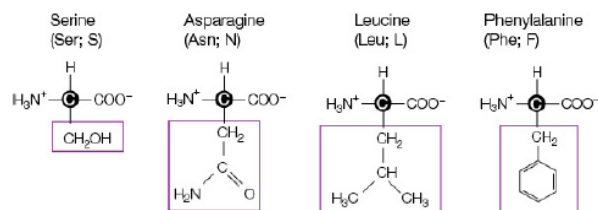
- ☐ A) 3'-TAC GAT TAU-5'
- ☐ B) 3'-ATG CTA ATA-5'
- ☒ C) 3'-AUG CUA AUC-5'
- ☐ D) 3'-UAC GAU UAG-5'

10. (1.00 pts) Which of the following statements concerning a gene is correct?

- ☒ A) A gene can code for a specific protein.
- ☐ B) A gene can exist in alternate forms called introns.
- ☐ C) A gene undergoes crossing-over during DNA replication.
- ☐ D) A gene that is very similar in sequence in a human and in a bacterium is probably a recent mutation.

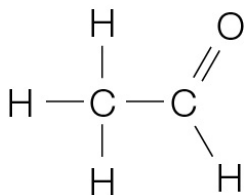
11. (1.00 pts)

The figures show structures of amino acids. Each amino acid has a unique side chain, shown in the boxed portion of each figure. Which amino acid or acids have hydrophobic side chains?



- ☐ A) Serine and asparagine
- ☐ B) Leucine only
- ☐ C) Asparagine and leucine
- ☒ D) Leucine and phenylalanine

12. (1.00 pts) The functional group shown is the _____ group.



- ☐ A) Hydroxyl
- ☒ B) Aldehyde
- ☐ C) Keto
- ☐ D) Carboxyl

13. (1.00 pts)

Pyruvate kinase, a key enzyme in the glycolysis pathway, is inhibited by the amino acid alanine. The ability of alanine to inhibit the enzyme is not affected by increasing the concentration of substrate. Which of the following best explains the mechanism by which alanine inhibits pyruvate kinase activity?

- ☒ A) Alanine binds to an allosteric site of the enzyme, changing the shape of the enzyme's active site.
- ☐ B) Alanine increases the enzyme-substrate binding until the enzyme becomes saturated.
- ☐ C) Alanine is a competitive inhibitor that reversibly binds to the active site of the enzyme.
- ☐ D) Alanine binds to the substrate, preventing the substrate from being able to bind to the active site of the enzyme.

14. (1.00 pts)

Alcohol dehydrogenase (ADH) is an enzyme that aids in the decomposition of ethyl alcohol (C_2H_5OH) into nontoxic substances. Methyl alcohol acts as a competitive inhibitor of ethyl alcohol by competing for the same active site on ADH. When attached to ADH, methyl alcohol is converted to formaldehyde, which is toxic in the body. Which of the following statements best predicts the effect of increasing the concentration of substrate (ethyl alcohol), while keeping the concentration of the inhibitor (methyl alcohol) constant?

- ☐ A) There will be an increase in formaldehyde because ADH activity increases
- ☐ B) Competitive inhibition will be terminated because ethyl alcohol will bind to methyl alcohol and decrease ADH activity.
- ☐ C) The peptide bonds in the active site of the enzyme will be denatured, inhibiting the enzyme
- ☒ D) Competitive inhibition will decrease because the proportion of the active sites occupied by substrate will increase.

15. (1.00 pts) Which of the following messenger RNA sequences could code for both of the two amino acid sequences below, simply by a shift in the reading frame?

... glutamine-glutamine-glutamine ...

... serine-serine-serine ...

<u>mRNA Codons</u>	<u>Amino Acids</u>
AGA	arginine
GGA	glycine
AGC	serine
GCA	alanine
CAG	glutamine

- ☒ A) ... AGCAGCAGCAGC ...
- ☐ B) ... AGUAGUAGUAGU ...
- ☐ C) ... CAACAACAACAA ...
- ☐ D) ... GCUGCUGCUGCU ...

16. (1.00 pts)

The figure shows a protein that contains one disulfide bridge and a covalent bond between the sulfur atoms of two amino acids. Suppose that a point mutation in the gene coding for this protein resulted in a single amino acid substitution from a hydrophilic cysteine to a hydrophobic methionine. Which of the following best explains the most likely effect of such a mutation on the structure and function of the enzyme?

- ☐ A) The structure of the mutant protein would be the same as the original protein because the substitution of only one amino acid does not change the bonding pattern.
- ☒ B) The structure of the mutant protein would change from that of the original protein, as this particular amino acid substitution will alter the tertiary structure of the amino acids
- ☐ C)
The structure of the mutant protein would change from that of the original protein, but its function would likely remain unchanged, since this was only a single amino acid substitution
- ☐ D)
The structure of the mutant protein would be the same as the original protein, but the function would change, since covalent bonds between hydrophilic and hydrophobic amino acids are not possible

17. (1.00 pts) DNA is held together by relatively weak _____ bonds between the nitrogen containing bases, which allows it to be exposed for replication and transcription.

- ☐ A) Covalent
- ☐ B) Ionic
- ☒ C) Hydrogen
- ☐ D) Phosphodiester

18. (1.00 pts) DNA replication is considered semi-conservative because _____

- ☐ A)
The strands in the original double helix are equally divided during the first replication, ensuring that genetic information is accurately transmitted by maintaining an equal split of old and new strands in each subsequent DNA molecule that is created.
- ☒ B)
One strand of the original DNA helix serves as a template for each of the new strands in the new molecule, ensuring that genetic information is accurately transmitted by pairing a new strand with an original strand which errors can be checked.

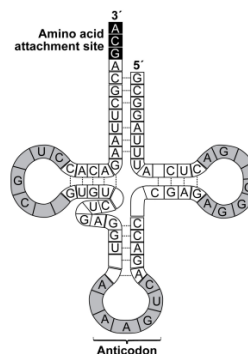
☐ C)

A hybrid double helix of old and new DNA strands is created, ensuring that genetic information is accurately transmitted by only pairing compatible DNA strands in a double helix, new with new, old with old.

☐ D) The entire double helix serves as a template for the first new strand, ensuring that genetic information is accurately transmitted by keeping the original DNA molecule intact

19. (1.00 pts)

Which statement best describes what the role of this molecule will be in protein synthesis?



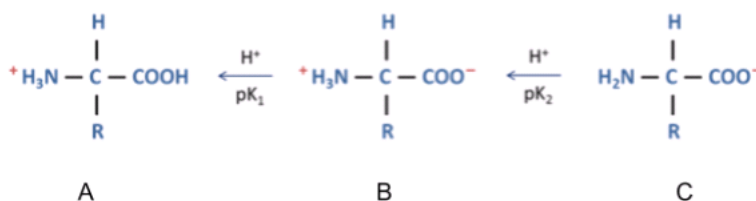
☐ A) The anticodon on the mRNA in the diagram will bind to the tRNA triplet 5'-UUC-3' in a ribosome and place a specific amino acid onto the polypeptide being assembled.

☐ B) The anticodon on the mRNA in the diagram will bind to the tRNA codon 5'-UUC-3' in a ribosome and signal to the tRNA to place the appropriate amino acid onto the polypeptide chain

☐ C) The anticodon on the tRNA in the diagram will bind to the mRNA codon 5'-UUC-3' in a ribosome and signal to the mRNA to place the appropriate amino acid onto the polypeptide chain.

☒ D) The anticodon on the tRNA in the diagram will bind to the mRNA codon 5'-UUC-3' in a ribosome and place a specific amino acid onto the polypeptide being assembled.

20. (1.00 pts) Which of the following configurations represents a zwitterion?



☐ A) A

☒ B) B

☐ C) C

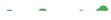
☐ D) Cannot determine

21. (2.00 pts)

If hydrogen bonding between two amino acid side chains is sufficient to maintain tertiary and quaternary protein structure, why is the presence of cysteine-cysteine disulfide bridge important?

Expected Answer: The disulfide bond is a covalent linkage and thus differs from a hydrogen bond in terms of the conditions it needs in order to be broken. Cysteine-cysteine bonds provide an added level of stability to the structure of proteins that contain them. Disulfide bridges also help determine how a protein molecule folds.

22. (2.00 pts)



The hemoglobin protein has four subunits. Explain what would happen to the structure if it were exposed to high temperatures.

Expected Answer: The protein would denature when the temperature got high enough to disrupt the hydrogen bonds maintaining secondary, tertiary, and quaternary structure. The protein would separate into its four constituent subunits, which would each lose their tertiary and secondary structure.

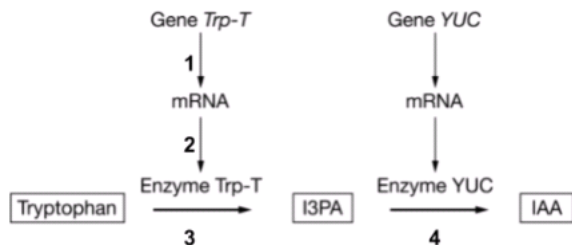
23. (2.00 pts) What would likely happen if a hemoglobin molecule exposed to high temperatures was returned to normal temperature?



Expected Answer: It would most likely refold correctly and regain its function.

24. (1.00 pts)

Auxins are plant hormones that coordinate several aspects of root growth and development. Indole-3-acetic acid (IAA) is an auxin that is usually synthesized from the amino acid tryptophan (Figure 1). Gene *Trp-T* encodes an enzyme that converts tryptophan to indole-3-pyruvic acid (I3PA), which is then converted to IAA by an enzyme encoded by the gene *YUC*. **Identify the number of the arrow in the figure that represents transcription on the template pathway.**



- ☒ A) 1
☐ B) 2
☐ C) 3
☐ D) 4

25. (1.00 pts)

Auxins are plant hormones that coordinate several aspects of root growth and development. Indole-3-acetic acid (IAA) is an auxin that is usually synthesized from the amino acid tryptophan (Figure 1). Gene *Trp-T* encodes an enzyme that converts tryptophan to indole-3-pyruvic acid (I3PA), which is then converted to IAA by an enzyme encoded by the gene *YUC*. **Identify the molecule that would be absent if enzyme *YUC* is nonfunctional.**

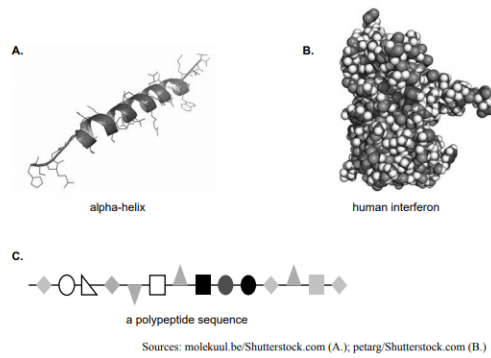
Expected Answer: IAA has been identified as the molecule that would be absent if enzyme *YUC* is nonfunctional.

26. (2.00 pts)

Auxins are plant hormones that coordinate several aspects of root growth and development. Indole-3-acetic acid (IAA) is an auxin that is usually synthesized from the amino acid tryptophan (Figure 1). Gene *Trp-T* encodes an enzyme that converts tryptophan to indole-3-pyruvic acid (I3PA), which is then converted to IAA by an enzyme encoded by the gene *YUC*. **Predict how the deletion of one base pair in the fourth codon of the coding region of gene *Trp-T* would most likely affect the production of IAA. Justify your prediction.**

Expected Answer: An acceptable prediction. Acceptable predictions include the following: A reduction in IAA production No production of IAA An acceptable justification. Acceptable justifications include the following: The mutation will result in the translation of an inactive/nonfunctional *Trp-T* enzyme. The mutation will result in no translation of the *Trp-T* enzyme. The mutation will result in no/reduced production of I3PA.

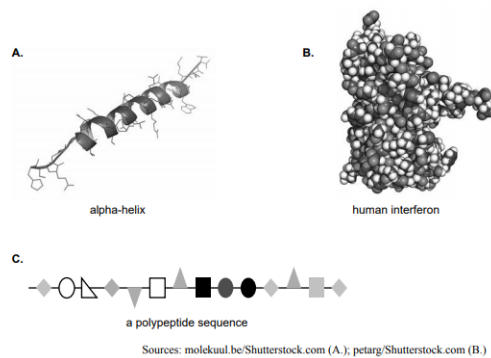
27. (1.00 pts)



Identify letter A:

Expected Answer: Alpha helix-secondary structure

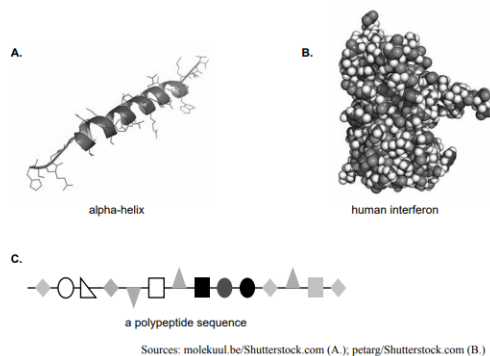
28. (1.00 pts)



Identify letter B:

Expected Answer: Tertiary structure

29. (1.00 pts)



Identify letter C:

Expected Answer: Primary structure

30. (2.00 pts) Targeting: Briefly describe and define the role PAM in targeting a DNA sequence in the CRISPR complex



Expected Answer: Cas9 recognizes and binds to PAM motifs in the cell's DNA. The motif consists of any nucleotide (designated "N") followed by two guanines, when looking at a DNA sequence in a 5' to 3' direction (5'-N-G-G-3'). This sequence motif is abundant throughout the human genome. After binding, Cas9 unwinds and pulls apart the DNA double helix upstream of PAM—in other words, closer to the 5' end of the DNA strand relative to PAM.

31. (1.00 pts) Binding: If the target DNA strand does not match the guide RNA, what happens?

Expected Answer: If the sequence of the unpaired DNA strand is not an exact match to the 20-nucleotide sequence within the guide RNA, Cas9 disengages from the DNA, which zips back up into a double helix.

32. (2.00 pts)

Cleaving: If the DNA-RNA helix forms after the binding event, describe specifically where Cas9 nuclease forms cleavage sites. What is the end result after the cleavage?

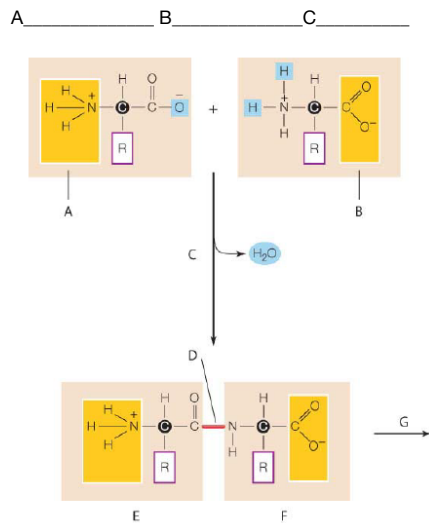
Expected Answer: This binding event activates Cas9's nuclease, or DNA-cutting, activity. It makes specific cuts in the DNA at a position three nucleotides upstream from the PAM site. Two active sites (regions where molecules bind to undergo chemical reactions) on the nuclease domain of Cas9 generate the cuts and cleave both strands of the DNA double helix, resulting in a double-stranded DNA break

33. (2.00 pts)

DNA Repair: CRISPR-induced double-stranded DNA breaks can be repaired by either nonhomologous end joining (NHEJ) or homology-directed repair (HDR). What are the pros and cons of using NHEJ for DNA repair? List at least one pro and one con.

Expected Answer: faster repair mechanism, because the cell does not use a template to join broken DNA ends together. It is, however, an error-prone process that can introduce mutations in the target sequence. Errors are rare, but when the break is repaired correctly, Cas9 will once again recognize the target sequence and cleave it. Repeated cycles of cleavage and repair eventually result in a mutation. The type of mutation is random, but it will occur precisely within the desired target sequence. If the target sequence is within a gene's coding region, the mutation will likely inactivate that gene

34. (3.00 pts) The diagram below shows the beginning formation of an oligopeptide. Fill in the three blanks with words from the list below.



Direction of polymerization
 Condensation reaction
 Amino group
 Carboxyl group
 Peptide linkage
 C terminus
 N terminus

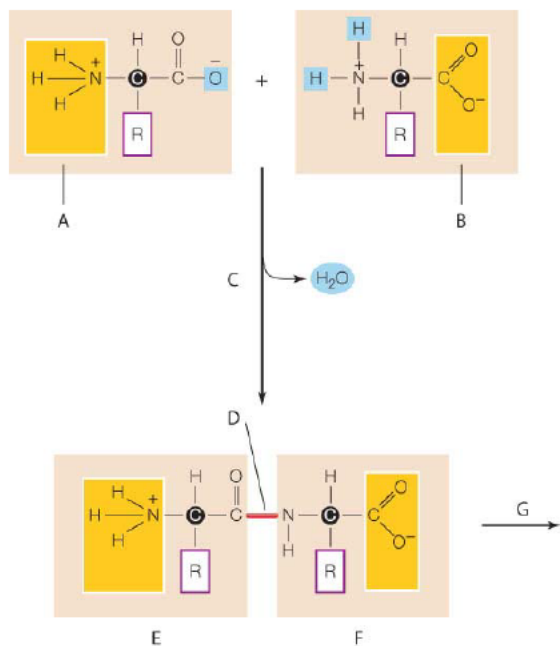
Amino group

Carboxyl group

Condensation reaction

35. (3.00 pts) The diagram below shows the beginning formation of an oligopeptide. Fill in the blanks with the words from the list at the bottom

D _____ E _____ F _____



Direction of polymerization
 Condensation reaction

Peptide linkage

Amino group

Carboxyl group

C terminus

N terminus

Peptide Linkage

N terminus

C terminus

36. (1.00 pts) PDB Molecule of the Month (December): Hepatitis C Virus Protease/Helicase

What mechanisms do RNA viruses (like Hepatitis C) use to hijack healthy cells?

NS3 helicase

Expected Answer: hijacks cellular ribosomes and forces them to make a long viral polyprotein, which must then be clipped into functional pieces by a viral protease

37. (1.00 pts) What role does the helicase complex play in this molecule?

NS3 helicase

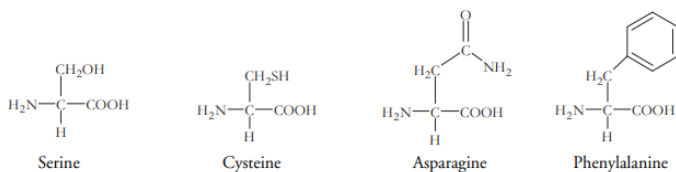
Expected Answer: What HCV protease is a serine protease similar to chymotrypsin, which is built as part of a longer protein that also includes a helicase enzyme that is involved in replication of the viral RNA genome. This composite protein is collectively called NS3 (non-structural protein 3), shown here from PDB entry 1cu1.

38. (1.00 pts) The active site of Hepatitis C virus protease does not have a deep pocket like other active sites. How did medical chemists overcome this challenge?

NS3 helicase

Expected Answer: Early breakthrough antivirals boceprevir and telaprevir (PDB entries 2oc8 and 3sv6) form a reversible covalent bond with the active site serine amino acid, helping to lock the drug to the surface of the enzyme

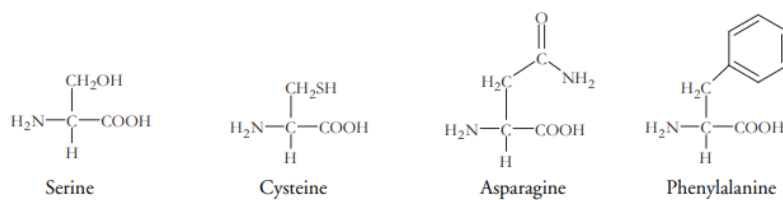
39. (1.00 pts) Imagine a protein chain that includes the following amino acids among several others.



Which of the amino acids could form a hydrogen bond with another amino acid in the chain to stabilize the secondary structure of a β -pleated sheet?

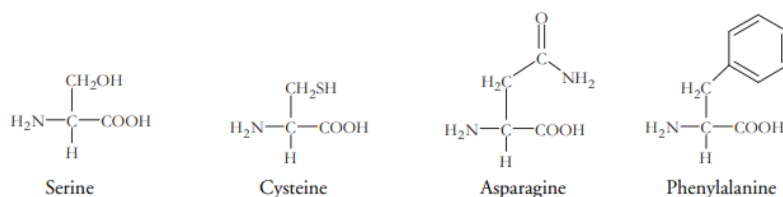
- ☒ A) Serine
☐ B) Cysteine
☐ C) Asparagine
☐ D) Phenylalanine

40. (1.00 pts) Which of the amino acids could form disulfide bonds with another amino acid in the chain to stabilize the tertiary structure of the protein?



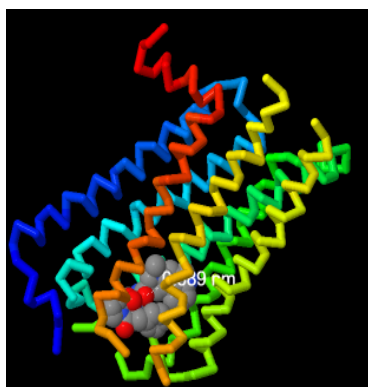
- ☐ A) Serine
- ☒ B) Cysteine
- ☐ C) Asparagine
- ☐ D) Phenylalanine

41. (1.00 pts) Which of the amino acids could participate in hydrophobic interactions with another amino acid in the chain to stabilize the tertiary structure of the protein?



- ☐ A) Serine
- ☐ B) Cysteine
- ☐ C) Asparagine
- ☒ D) Phenylalanine

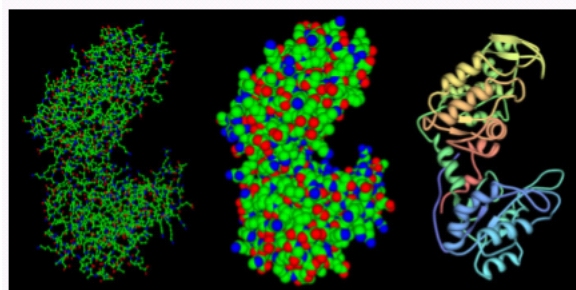
42. (1.00 pts) Pictured here is a serotonin receptor. It has seven parallel alpha helices. What common folding pattern does this molecule exhibit?



Expected Answer: G-protein coupled receptors (GPCR) /// helix bundle

43. (6.00 pts)

Below are three different representations of phosphoglycerate kinase. For each letter describe the type of structure listed and the defining feature it highlights of the protein.



A

B

C

Expected Answer: A) Wireframe Diagrams (shown at the left in the figure). For these images, a line is drawn for each of the covalent bonds formed between the atoms. In many cases, small balls and sticks are used to make the three-dimensional shape easier to understand. B) Spacefilling Diagrams (shown in the middle). For these images, a sphere is drawn around each atom, showing the relative size of the atom. C) Backbone and Ribbon Diagrams (shown on the right). These images highlight the way a protein chain folds. The simplest ones draw a tube that connects the positions of each amino acid. Ribbon diagrams add two special representations: a spring-shaped ribbon for alpha helices and a flat arrow that shows beta strands. The familiar ladder diagram is used for nucleic acids, with a smooth ribbon for the backbone and rungs for the bases.

44. (1.00 pts) RNA transcribed from the CRISPR locus and cleaved into individual targeting fragments:

- ☒ A) crRNA
- ☐ B) tracrRNA
- ☐ C) gRNA
- ☐ D) cgRNA

45. (1.00 pts) Short segments of RNA used to direct the DNA-cutting enzyme to the target location in the genome:

- ☐ A) crRNA
- ☒ B) gRNA
- ☐ C) tracrRNA
- ☐ D) tracrRNA

46. (1.00 pts)

A natural repair process used to repair broken DNA, which relies on a DNA "template" with homology to the broken stretch of DNA. This usually occurs during or after DNA synthesis, which provides this template

- ☐ A) NBS
- ☐ B) NHEJ
- ☒ C) HDR
- ☐ D) NHD

47. (1.00 pts)

A class of engineered restriction enzymes generated by the fusion of a transcription activator-like effector DNA-binding domain (that binds to a specific DNA sequence) to a DNA-cleavage domain (nuclease) to be used as a genome-editing tool

- ☒ A) TALEN
- ☐ B) ZFN
- ☐ C) EREN
- ☐ D) RNP

48. (1.00 pts) A metal-dependent DNA-specific endonuclease that produces double-stranded DNA fragments:

- ☐ A) Cas3
- ☐ B) Cas2
- ☒ C) Cas1
- ☐ D) Cas4

49. (1.00 pts) Single-stranded DNA nuclease (HD domain) and ATP- dependent helicase and required for interference.

- ☐ A) Cas2
- ☒ B) Cas3
- ☐ C) Cas4
- ☐ D) Cas1

50. (1.00 pts) What is the difference between Cas9 and dCas9?

Expected Answer: (Nuclease-deficient Cas9 or nuclease-dead Cas9)—This can still bind DNA, together with a guide RNA, but not cut it. It is often linked to a transcription factor, chromatin-modifying enzyme, or fluorescent protein to mediate alterations to gene expression or to mark specific sites. Cas9 (CRISPR Associated Protein 9)—A specialized enzyme known as a nuclease that has the ability to cut DNA sequences. Cas9 makes up part of the “toolkit” for the CRISPR/Cas9 method of genome editing.

51. (1.00 pts) Describe the role of base pairing during DNA microarray analysis, RNA sequencing, and CRISPR-Cas9 editing.

Expected Answer: Complementary base pairing is involved in cDNA synthesis, which is required for these techniques. Reverse transcriptase uses mRNA as a template to synthesize the first strand of DNA adding nucleotides complementary to those on the mRNA. The proteins must bind to a specific target sequence and this also involves using RNA to match the sequence. Additionally, in the repair of system for CRISPR also uses the complement of the bases to use as a template for repair.

52. (1.00 pts) Which chemical group is most likely to be responsible for an organic molecule behaving as a base?

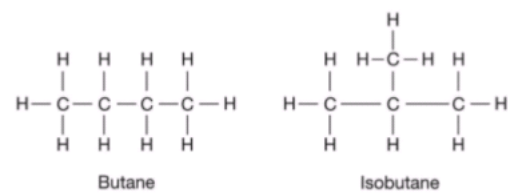
- ☐ A) hydroxyl
- ☐ B) carbonyl
- ☒ C) amino

- ☐ D) phosphate

53. (1.00 pts) Visualize the structural formula of each of the following hydrocarbons. Which hydrocarbon has a double bond in its carbon skeleton? (*should be subscripts)

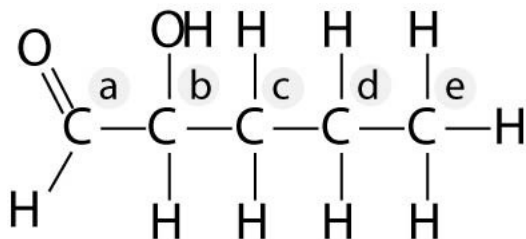
- ☐ A) C₃H₈
☐ B) C₂H₆
☒ C) C₂H₄
☐ D) C₂H₂

54. (1.00 pts) Choose the term that correctly describes the relationship between these two molecules:



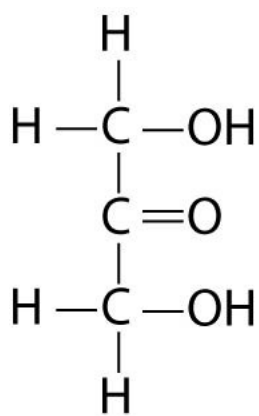
- ☒ A) structural isomers
☐ B) cis-trans isomers
☐ C) enantiomers
☐ D) isotopes

55. (1.00 pts) Identify the asymmetric carbon in this molecule:

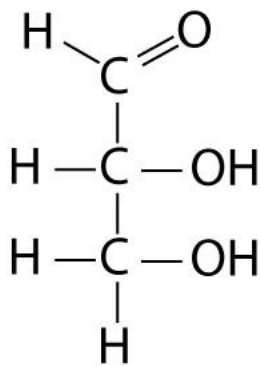


- ☐ A) A
☒ B) B
☐ C) C
☐ D) D
☐ E) E

56. (1.00 pts) Which of the molecules shown has an asymmetric carbon?



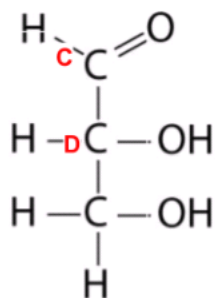
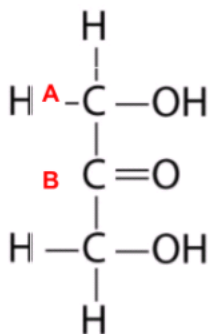
left



right

- ☐ A) Left
- ☒ B) Right

57. (1.00 pts)



Which carbon is asymmetric?

- ☐ A) A
- ☐ B) B
- ☐ C) C
- ☒ D) D

58. (1.00 pts) Where would you expect a polypeptide region rich in the amino acids valine, leucine, and isoleucine to be located in a folded polypeptide?

Expected Answer: These are all nonpolar, hydrophobic amino acids so you would expect them to be located near the interior where it would not contact the aqueous environment of the cell.

59. (1.00 pts)

A biochemist isolates, purifies, and combines in a test tube a variety of molecules needed for DNA replication. When she adds some DNA to the mixture, replication occurs, but each DNA molecule consists of a normal strand paired with numerous segments of DNA a few hundred nucleotides long. What has she probably left out of the mixture?

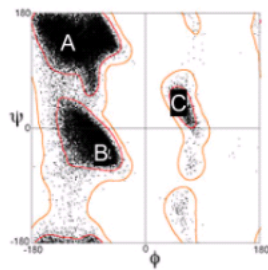
- ☐ A) DNA polymerase
- ☒ B) DNA ligase
- ☐ C) Okazaki fragments
- ☐ D) primase

60. (1.00 pts)

The spontaneous loss of amino groups from adenine in DNA results in hypoxanthine, an uncommon base, opposite thymine. What combination of proteins could repair such damage?

- ☒ A) nuclease, DNA polymerase, DNA ligase
- ☐ B) telomerase, primase, DNA polymerase
- ☐ C) telomerase, helicase, single-strand binding protein
- ☐ D) DNA ligase, replication fork proteins, adenylyl cyclase

61. (1.00 pts) Identify the structures associated with the locations on this Ramachandran plot. A _____ B _____ C _____

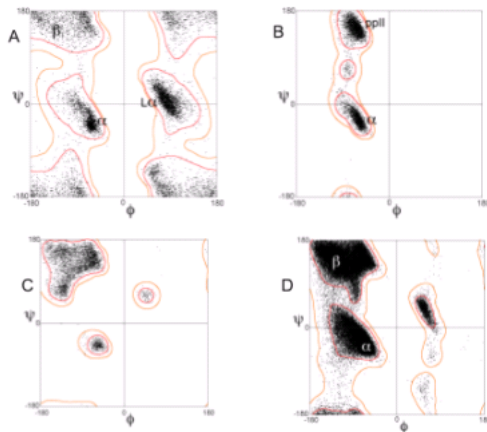


Beta-pleated sheet

Right-handed alpha hel

left-handed alpha helix

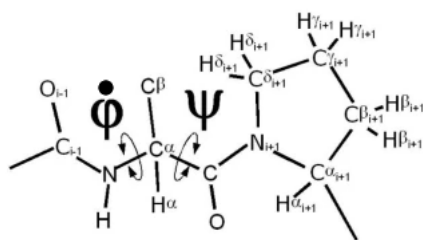
62. (1.00 pts) Which is most likely the Ramachandran plot for glycine?



- ☒ A) A
- ☐ B) B
- ☐ C) C

☐ D) D

63. (1.00 pts) What Ramachandran plot (from the figure above) best represents this molecule?



☐ A) A

☐ B) B

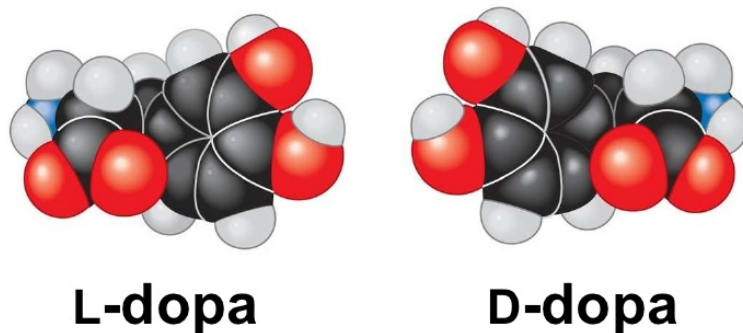
☒ C) C

☐ D) D

64. (1.00 pts)

In 1918, an epidemic of sleeping sickness caused an unusual rigid paralysis in some survivors, similar to symptoms of advanced Parkinson's disease. Years later L-dopa, a chemical used to treat Parkinson's disease, was given to some of the patients. L-dopa was remarkably effective at eliminating the paralysis, at least temporarily. However, its enantiomer, D-dopa was subsequently shown to have no effect at all, as is the case for Parkinson's disease. In a few sentences, describe how the effectiveness of one enantiomer and not the other illustrates structure guiding function.

Fig. 4-UN9



Expected Answer: Answer could include mention of chirality and is therefore able to stimulate production of dopamine in the brain due to its conformation, whereas D-dopa does not due to its shape so it doesn't fit into the receptor and form dopamine in the brain.

65. (1.00 pts) If 30% of the nucleotides in a single-stranded RNA molecule are adenine, then what percent are expected to be thymine?

- ☒ A) 0
- ☐ B) 20
- ☐ C) 30
- ☐ D) 70

66. (1.00 pts)

Antigens are foreign proteins that invade the systems of organisms. Vaccines function by stimulating an organism's immune system to develop antibodies against a particular antigen. Developing a vaccine involves producing an antigen that can be introduced into the organism being vaccinated and which will trigger an immune response without causing the disease associated with the antigen. Certain strains of bacteria can be used to produce antigens used in vaccines. Which of the following best explains how bacteria can be genetically engineered to produce a desired antigen?

- ☒ A) The gene coding for the antigen can be inserted into plasmids that can be used to transform the bacteria.
- ☐ B) The bacteria need to be exposed to the antigen so they can produce the antibodies.
- ☐ C) The DNA of the antigen has to be transcribed in order for the mRNA produced to be inserted into the bacteria.
- ☐ D) The mRNA of the antigen has to be translated in order for the protein to be inserted into the bacteria.

67. (1.00 pts)

Genetic engineering techniques can be used when analyzing and manipulating DNA and RNA. Scientists used gel electrophoresis to study transcription of gene L and discovered that mRNA strands of three different lengths are consistently produced. Which of the following explanations best accounts for this experimental result?

- ☐ A) Gel electrophoresis can only be used with DNA (not mRNA), so experimental results are not interpretable.
- ☐ B) RNA polymerase consistently makes the same errors during transcription of gene L.

- ☐ C) Gene L is mutated, so RNA polymerase does not always transcribe the correct sequence.
- ☒ D) Pre- mRNA of gene L is subject to alternative splicing, so three mRNA sequences are possible.

68. (1.00 pts) The sequences for two short fragments of DNA are shown above. Which of the following is one way in which these two segments would differ?

Segment 1:

5' - ATATGAGTAGT - 3'
3' - TATACTCATCA - 5'

Segment 2:

5' - GCGCAGACGAC - 3'
3' - CGCGTCTGCTG - 5'

- ☐ A) Segment 1 would not code for mRNA because both strands have T, a base not found in RNA.
- ☐ B) Segment 1 would be more soluble in water than segment 2 because it has more phosphate groups.
- ☒ C) Segment 1 would become denatured at a lower temperature than would segment 2 because A-T base pairs have two hydrogen bonds whereas G-C base pairs have three.
- ☐ D) Segment 1 must be from a prokaryote because it has predominantly A-T base pairs.

69. (1.00 pts) A student analyzed a viral genome and found that the genome had the following nucleotide composition.

• 28% adenine

• 20% thymine

• 35% cytosine

• 17% guanine

Which of the following best describes the structure of the viral genome?

- ☐ A) Double-stranded DNA
- ☐ B) Single-stranded RNA
- ☐ C) Double-stranded RNA
- ☒ D) Single-stranded DNA

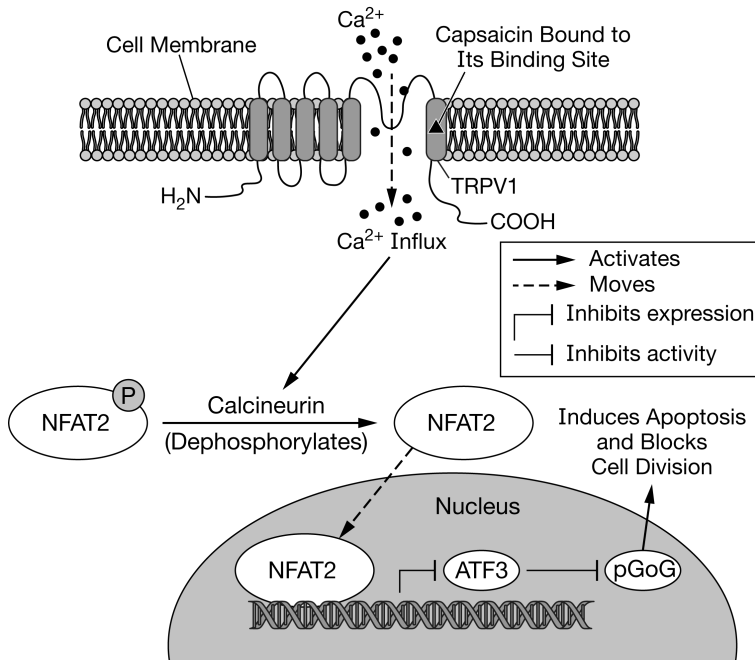
70. (1.00 pts) Which of the following best illustrates the flow of information required for the synthesis of proteins encoded in the genome of a retrovirus?

- ☐ A) DNA > RNA > Protein
- ☐ B) RNA > DNA > Protein
- ☒ C) RNA > DNA > RNA > Protein
- ☐ D) DNA > RNA > DNA > Protein

The next few questions will relate to this passage and figure.

The structure of the TRPV1 protein consists of several transmembrane domains that are embedded in the membrane as well as a carboxy-terminus and an amino-terminus that are located inside the cell. TRPV1 is activated by several stimuli, including the binding of capsaicin, a chemical found in chili peppers. Capsaicin enters the cell by simple diffusion and then binds to one of the transmembrane domains of TRPV1, which opens the ion channel. The opening of the TRPV1 channel allows Ca^{2+} ions to enter the cell, leading to the

activation of the enzyme calcineurin. Calcineurin removes phosphate groups from the phosphorylated form of the transcription factor NFAT2, which is typically found in the cytoplasm. Once dephosphorylated, NFAT2 moves into the nucleus, where it blocks the transcription of another protein, ATF3. ATF3, when active, prevents the cell cycle regulatory protein pGoG from inducing apoptosis and blocking cell division (see figure). Low extracellular pH activates TRPV1 through the binding of H^+ ions to TRPV1.



71. (1.00 pts) Based on the information and figure above: **Describe the properties, including the location, of the site of TRPV1 that allow H^+ ions to bind.**

Expected Answer: The site of TRPV1 that allows H^+ ions to bind will have to be negatively charged and will be part of TRPV1's extracellular domain.

72. (1.00 pts) **Describe the specific location in the cell where ATF3 protein is produced.**

Expected Answer: A description that ATF3 is produced on cytoplasmic ribosomes/on free ribosomes

73. (1.00 pts) **Researchers claim that many cancers include a mutation in the gene encoding pGoG. Support the researchers' claim.**

Expected Answer: The response includes support for the claim by stating that a mutation resulting in a nonfunctional pGoG will result in the inability of pGoG to stop cells from dividing/induce apoptosis, and cancer is characterized by excessive cell division.

Great job and good luck! I will get these scores back to you as soon as possible.