NAME: For GradeScope, please write your FIRST and LAST name in CAPITAL letters WITHIN the box:

Exam IV
November 20, 2023
Biochemistry I
BI/CH 421/621

I. _____/45
II. _____/10
III. _____/13
IV. _____/32

TOTAL _____/100

I. MULTIPLE CHOICE. (45 points; 3 points each)
Choose the BEST answer to the question and write the letter in the appropriate box.

[ ] 1. Topoisomerases:

A. are important for generating positive supercoils that help in replication and transcription to open up double-stranded DNA.
B. can sometimes use NAD^+ to seal nicks in DNA.
C. such as DNA gyrase (*E. coli* topoisomerase II), in the presence of ATP, will decrease the linking number of a covalently closed, circular DNA molecule.
D. always change the linking number in steps of one.
E. occur in all bacteria, but not in eukaryotes.

[ ] 2. The compound that consists of ribose linked by an *N*-glycosidic bond to N-9 of adenine is:

A. a purine nucleotide.
B. a pyrimidine nucleotide.
C. adenosine.
D. AMP.
E. a deoxyribonucleoside.

[ ] 3. Which of the following is true about a circular double-stranded DNA genome that is determined by chemical means to be 21% adenosine?

A. The genome is 10.5% guanosine.
B. The genome is 21% guanosine.
C. The genome is 29% guanosine.
D. The genome is 58% guanosine.
E. The base percent composition of guanosine in the genome cannot be determined from the information given.

[ ] 4. Which of the following is *not* a reducing sugar?

A. ribose
B. glucose
C. fucose
D. glyceraldehyde
E. sucrose

[ ] 5. Stereoisomers that are non-superimposable, complete, mirror images of each other are known as:

A. enantiomers.
B. diastereoisomers.
C. chiral compounds.
D. anomers.
E. cis-trans isomers.

6. Which of these statements about alternate forms of DNA is *false*?

   A. B-form DNA predominates in aqueous solution; dehydration favors the A-form.
   B. Z-form DNA has a helical sense (left-handed) that is opposite that for A-form DNA.
   C. B-form DNA has 3.6 base pairs per turn
   D. A major difference between the A-form and the B-form is in the "pucker" of the ribose ring.
   E. Nucleotide sequence affects whether DNA takes the Z-form.

7. At pH 7.0, the rare protonation of adenine at N1 (pK_a=3.8) can lead to:

   A. deprotonation of N7
   B. base pairing with thymidine
   C. A:T □ G:C mutations
   D. A:T □ A:G mutations
   E. A:T □ T:A mutations

8. The allosteric binding sites for the three heterotropic negative effector molecules for hemoglobin, CO_2, H^+, and BPG are located at the _____, respectively.

   A. N-term of the □-subunits, C-term His of the □-subunits, and in the cleft between the two □-subunits
   B. the cleft between the two □-subunits, N-term of the □-subunits, and the C-term His of the □-subunits
   C. the heme, C-term His of the □-subunits, and in the cleft between the two □-subunits
   D. the C-term His of the □-subunits, the heme, and in the cleft between the two □-subunits
   E. C-term His of the □-subunits, N-term of the □-subunits, and in the cleft between the two □-subunits

9. Which one of the following enzymes is *not* useful for protein folding in the cell?

   A. peptide prolyl isomerase
   B. carbonic anhydrase
   C. protein disulfide isomerase
   D. GroEL
   E. Hsp70

10. Which of the following statements about heme structure is true?

   A. Heme contains a tetrapyrrole ring with four methyl, four vinyl, and four propionate side chains.
   B. The iron atom in the heme may be present in the ferrous or the ferric state.
   C. The iron in free heme has six ligands.
   D. In deoxyhemoglobin, the iron atom is absolutely coplanar with the tetrapyrrole ring (porphorin)
   E. The axial coordination positions of heme are occupied by tyrosine residues in hemoglobin.

11. The notation: Glc α(1-->4) Glc best describes which polysaccharide?

   A. Glycogen
   B. Starch
   C. Hyaluronic acid
   D. Amylose
   E. Amylopectin

12. Which sugar would give a negative Benedict's or Nelson test (reducing sugar test)?

A. maltose
B. lactose
C. □-methylglucoside
D. sucrose
E. galactose
F. all of the above
G. both C and D
H. both B and E

13. Which of the following statements about protein structure is *true*?

A. Three-dimensional protein structure is principally stabilized by hydrogen bonds.
B. Hydrophobic interactions are responsible for the greatest amount of stabilizing energy, while hydrogen bonding and polar interactions are responsible for specificity in protein-protein interactions, as well as enzyme-substrate interactions.
C. Because proteins are compact, detergents are unable to disrupt protein stability.
D. All salts denature proteins by neutralizing the charged amino-acid side chains.
E. By studying protein-protein interactions we have learned that the most optimal binding interactions occur when two proteins rely upon extensive intermolecular hydrogen bonding, and very little on hydrophobic interactions between the two molecules.

14. The ribose-sugar pucker affects DNA structure in drastic ways. Which explanation below best describes how this occurs?

A. The 3'-endo pucker leads to a conformational change from anti to syn for the purine and pyrimidine bases.
B. The 5'-exo pucker leads to a decrease in the distance between phosphates in attached to the 5' and 3' hydroxyl groups in the DNA polymer.
C. The 3'-endo pucker leads to a decrease in the distance between phosphates in attached to the 5' and 3' hydroxyl groups in the DNA polymer.
D. The 2'-exo pucker leads to a decrease in the distance between phosphates in attached to the 5' and 3' hydroxyl groups in the DNA polymer.
E. The 2'-endo pucker leads to a decrease in the distance between phosphates in attached to the 5' and 3' hydroxyl groups in the DNA polymer.

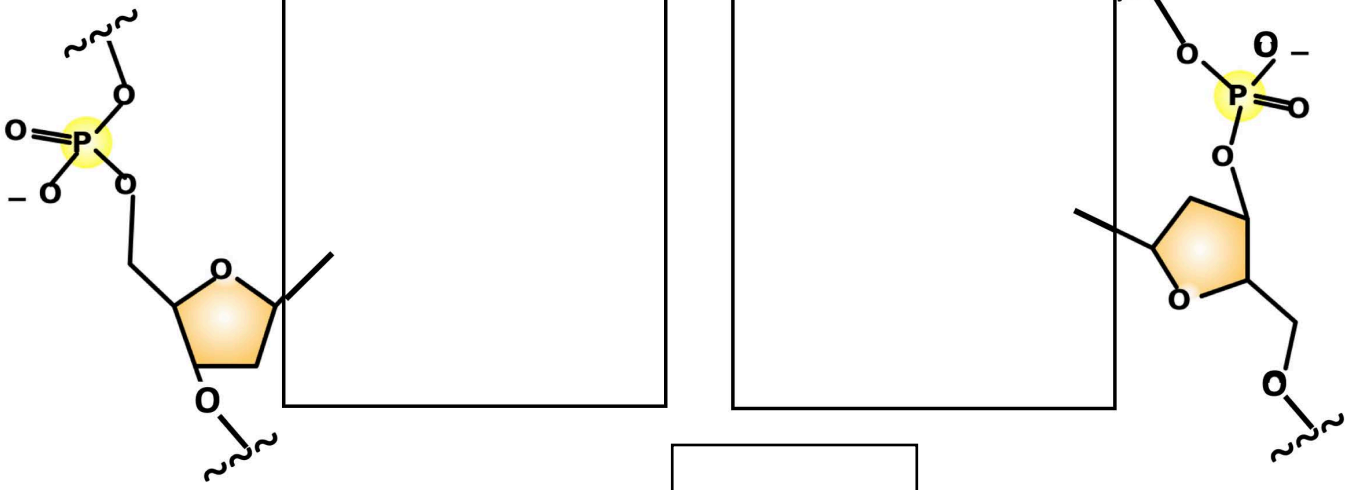
15. DNA rich in G/C base pairs has a higher T_m than DNA that is rich in A/T base pairs because _____

A. G/C base pairs have 3 hydrogen bonds, whereas A/T base pairs have only 2 hydrogen bonds.
B. G/C base pairs have 2 hydrogen bonds, whereas A/T base pairs have 3 hydrogen bonds.
C. G/C base pairs can form very strong Hoogsteen base pairs, whereas A/T base pairs cannot.
D. G/C base pairs have much more van der Waals interactions in B-DNA than do A/T base pairs.
E. The stacking energy for A/T base pairs is lower (larger negative ΔH) than for G/C base pairs, which results in strand repulsion.

II. STRUCTURE. (10 points)

16. Draw the structure of a C:G base pair, including dashed lines for the H-bonds between the two bases (4 pts).

C G



This is a base-pair found in DNA or RNA

17. Carbohydrate structures (6 pts):

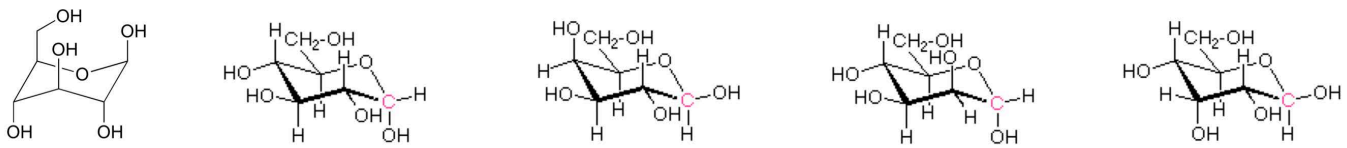
a.. DRAW the structure of Gal in a Fisher projection.

b. DRAW the structure of β-D-GlcNAc in the Haworth projection.

c. Gal is the C__ epimer of Glc

d. Man is the C__ epimer of Glc

e. Circle the correct structure of α-D-glucose



III. SHORT ANSWER. (13 points)

18. Complete this protein purification table from the data provided from measurements AFTER each step, *including any missing units*. (4 pts)

		Activity (units)	Total protein (mg)	Specific activity ( )	Extent of purificat. (fold from start)	Overall yield (%)
1.	Crude homogenate	100	1000		(1.0)	100
2.	Ammonium sulfate precipitation	90	300			
3.	Affi-gel Blue chromatography	75	7.5			

19. In the molecular-modeling laboratory, the program used to visualize protein structures was [ ]

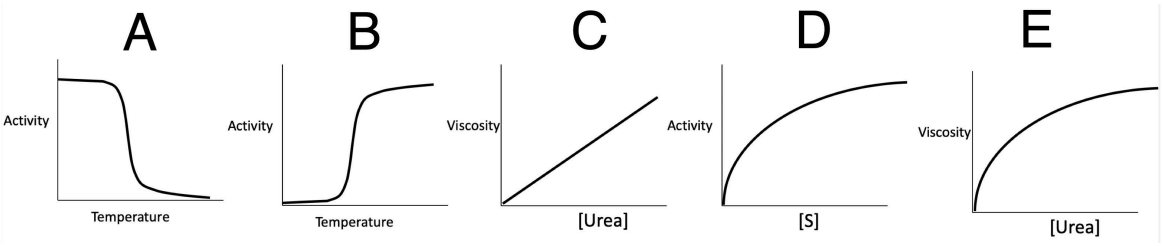
The [•] files used for this contain the x.y.z. coordinates of each atom in the protein structure (2 pts).

20. Place the events in the proper order for dioxygen binding to hemoglobin that results in a T-state to R-sate transition (3 pts)

[– – – – – –]

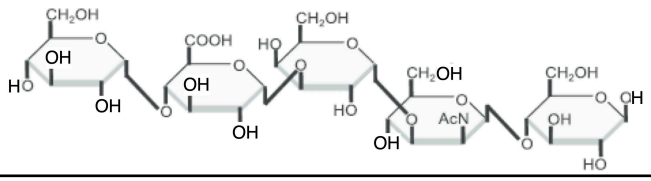
1. Salt bridges with the C-term residue of one α/β-subunit and other residues on the other α/β dimer are destablized.
2. the H-bond between Val on helix F and Tyr near the C-term of either subunit breaks
3. Helix F moves
4. the two α/β dimers shift by 15°
5. the proximal His residue, which is bound to the Fe^{2+}, moves 0.6 Å
6. BPG is released
7. dioxygen binds to the Fe^{2+} in the heme

21. In the box, place the letter corresponding to a graph that shows the correct process of protein unfolding (2 pts).



[ ]

22. Write out the proper name of this oligo-saccharide in the box below (2 pts).



[ ]

IV. **MATCHING** (32 points)

23. Match each item on the left with the best answer on the right. Only one choice per blank and choices on the right are only used once or not at all. (6 points)

☐ 1.	transition between native and dentured states	A. Anfinsen
☐ 2.	prevents protein aggregation in the cell	B. GroEL/GroES
☐ 3.	catalyzes proper disulfide bond formation	C. PDI
☐ 4.	small molecule that stabilizes the native state	D. Crick
☐ 5.	small molecule that stabilizes the stabilizes denatured state	E. 2-mercaptoethanol
☐ 6.	Scientist that showed the primary structure of proteins dictates its teriary structure	F. proteosome
		G. $(NH_4)_2SO_4$
		H. urea
		I. linear
		J. sigmoidal
		K. PPI

24. DNA structure. Write the DNA structure type (A, B, or Z) in the blanks to the left of the descriptions. (6 points)

☐ 1. 10 base pairs (bp) per turn

☐ 2. 11 base pairs (bp) per turn

☐ 3. rise of 3.4 Å per bp

☐ 4. relatively de-hydrated

☐ 5. C2'-endo sugar pucker

☐ 6. C3'-endo sugar pucker

☐ 7. left-handed helix

☐ 8. propeller twist of 20°

☐ 9. Diameter of 26 Å

☐ 10. Diameter of 20 Å

☐ 11. Diameter of 18 Å

☐ 12. major <u>and</u> minor grooves are deep

25. Place an "X" in the box next to the condition wherein a DNA duplex would have the *higher* T_m. Unless stated, all other conditions are identical. (5 pts)

☐ 1.	GC content of 50%	OR	AT content of 60%	☐
☐ 2.	1X SSC	OR	0.1X SSC	☐
☐ 3.	50% formamide	OR	no formamide	☐
☐ 4.	5X SSC, pH 12	OR	5X SSC, pH 7	☐
☐ 5.	1X SSC, pH 1	OR	1X SSC, pH 7	☐

26. The following phrases in the left-hand column best match an answer, feature, or completion in the right-hand column. Put the letter corresponding to the **best** answer in the box to the left of each phrase. An answer may be used once or not at all. (5 pts)

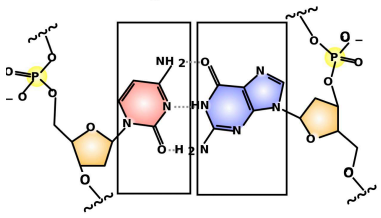
☐ 1. Hemoglobin is a tetrameric protein best described as a ____.	A. 2.8
☐ 2. oxygen binding to Hb eventually leads to the	B. $\square_2\square_2$ structure
☐ 3. Hill coefficient for hemoglobin with BPG bound.	C. $(\square\square)_2$ structure
☐ 4. Hill coefficient for hemoglobin without BPG bound.	D. 1.0
☐ 5. Sickle-cell anemia	E. Transition from the R-state to the T-state
	F. breaking of several hydrogen bonds and salt-bridges at the in helices A and C
	G. Transition from the T-state to the R-state
	H. Caused by mutation substituting Val, which finds a binding pocket in deoxy-Hb of another tetramer.
	I. Caused by mutation substituting Val, which finds a binding pocket in oxy-Hb of another tetramer.

27. The following phrases in the left-hand column are best matched with an answer, feature, or completion in the right-hand column. Put the letter corresponding to the **best** answer in the BOX to the left of each phrase. An answer may be used only once or not at all. (10 pts)

☐ 1. Hexoses, with four chiral carbons, have _____ possible stereoisomers (open-chain only).	A. disaccharide containing two glucoses
☐ 2. The smallest aldose is _____.	B. deoxy
☐ 3. The monosaccharides □-D-galactose and □-D-galactose are _____.	C. chondroitin sulfate
☐ 4. Bulky ring substituants preferentially occupy _____ positions in the chair conformation.	D. axial
☐ 5. The _____ sugars are monosaccharides in which a hydroxyl group is replaced with a hydrogen.	E. anomers
☐ 6. The disaccharide commonly found in dairy products is _____.	F. two
☐ 7. Both □(1□4) and □(1□6) bonds can be found in the plant product_____.	G. lactose
☐ 8. The main component of one proteoglycan is a _____.	H. glyceraldehyde
☐ 9. An example of a homopolysaccharide in liver and muscle is _____.	I. starch
☐ 10. The main component of a glycosaminoglycan is a _____.	J. epimers
	K. sixteen
	L. glycogen
	M. equatorial
	N. disaccharide containing a sugar acid
	O. eight

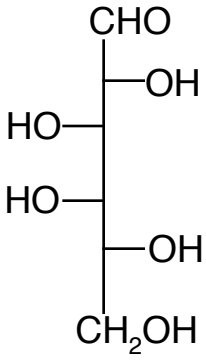
No. on Test	Correct Answer
1	C
2	C
3	C
4	E
5	A
6	C
7	C
8	A
9	B
10	A
11	D
12	G
13	B
14	C
15	D

16 a.

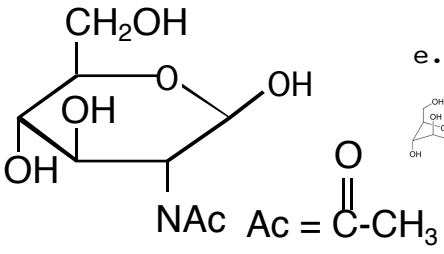


b. DNA

17 a.

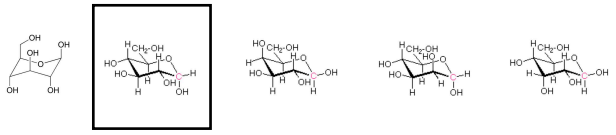


b.



c. 4 d. 2

e.



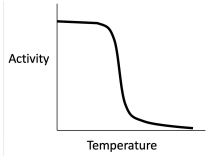
18

		Activity (units)	Total protein (mg)	Specific activity (U/mg)	Extent of purificat. (fold from start)	Overall yield (%)
1.	Crude homogenate	100	1000	0.1	(1.0)	100
2.	Ammonium sulfate precipitation	90	300	0.3	3	90
3.	Affi-gel Blue chromatography	75	7.5	10	100	75

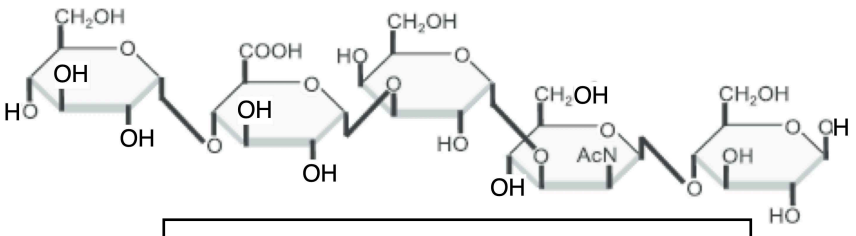
19 Pymole / .pdb

20 7-5-3-2-1-4-6

21 A



22



αGlc (1-4) αGlcUA(1-3) αGal (1-3) βManNAc (1-4) Glc (β)

23

1. J
2. B
3. C
4. G
5. H
6. A

24

1. B
2. A
3. B
4. A
5. B
6. A
7. Z
8. Z
9. A
10. B
11. Z
12. B

25. X
X
X
X
X

26.

1. C
2. G
3. A
4. D
5. H

27.

1. K
2. H
3. E
4. M
5. B
6. G
7. I
8. C
9. L
10. N