C483 Exam 1
Fall 2017

Name Key Seat Number _____

Student ID _____ AI _____

The last page of this exam contains pKa values and other information you might find useful.
This exam contains 110 points. The highest score you may earn on this exam is 100 points.

1 _____/20pts

2. _____/10pts

3. _____/20pts

4. _____/10pts

5. _____/10pts

6. _____/10pts

7. _____/10pts

8. _____/10pts

9. _____/10pts

Total:

1 pt bonus: Which problem contains a hidden pun? _____

Regrading: All requests for regrades must be submitted in writing within 48 hours of the return of the exam. You must explicitly state what has been misgraded and why it is an error. The entire exam will be regraded, which could result in points being added or deducted overall.

1. 20 pts. Fill in the blanks (2 points each.)

A. In the protein analysis technique called SDS PAGE, a detergent is used to denature a mixture of proteins, which are then separated based on their size using electrophoresis.

B. Nucleotide monomers are joined into a polymer through the phosphodiester linkage.

C. The exclusion of nonpolar molecules from aqueous solution is known as the hydrophobic effect.

D. At pH 5, the major species of histidine has a formal charge of +1.

E. Myoglobin has a lower (higher/lower) P_{50} than hemoglobin, which means myoglobin has higher (higher/lower) affinity for oxygen binding than hemoglobin.

F. The two strands of DNA in a double helix run antiparallel, with one having a 5'→3' directionality and the other running 3'→5'.

G. A domain is a unit of tertiary protein structure that may be either structural or functional.

H. If an anionic amino acid sidechain exists in the core of a protein, it must be paired as a salt bridge with a positively charged amino acid sidechain.

I. In deoxymyoglobin, the iron ligands include the heme group and the proximal histidine.

J. Collagen structure is disrupted if a glycine amino acid residue, which reoccurs every three residues in the primary sequence, is mutated.

2. 10 pts. True or false (1 points each)

A. False A process with a negative change in enthalpy and a negative change in entropy will always be a spontaneous process.

B. False The chemical nature of the peptide bond limits rotation around the carbonyl-C_α bond.

C. False Due to its steric bulk, a tryptophan residue is more likely to be located in an irregular loop on the surface of a protein than in an α helix in the protein core.

D. True Proline will destabilize an α-helix because it lacks a hydrogen bond donor in the polypeptide backbone.

E. True Binding of 2,3-bPG in the central cavity of hemoglobin causes an equilibrium shift away from the R-state conformation toward the T-state conformation.

F. True To separate the polypeptides KVCTRSV and AWYPPQD, ion exchange chromatography would be a better choice than gel filtration chromatography.

G. True NTP binding sites are found in the structural proteins actin and tubulin.

H. True Only about 1.5% of the human genome encodes for protein products.

I. False It is possible for a biological reaction to be both spontaneous and slow as long as it is an "uphill" reaction.

J. True The proximity effect allows enzymes to enhance the rate of reaction by limiting motion of substrates and bringing them into correct alignment for a productive reaction.

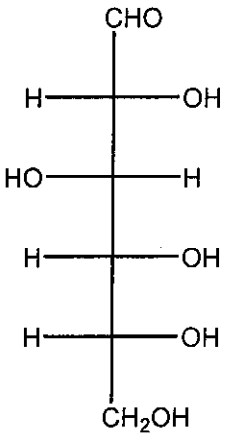
3. 20 pts. Short answer (5 points each)

A. Circle each of the following compounds that would be able to freely diffuse through a lipid bilayer:

A. CO_2

B. O_2

C.



D. Ca^{+2}

E. chymotrypsin

B. To which class of enzyme do each of the following enzymes belong?

Pyruvate decarboxylase lyase

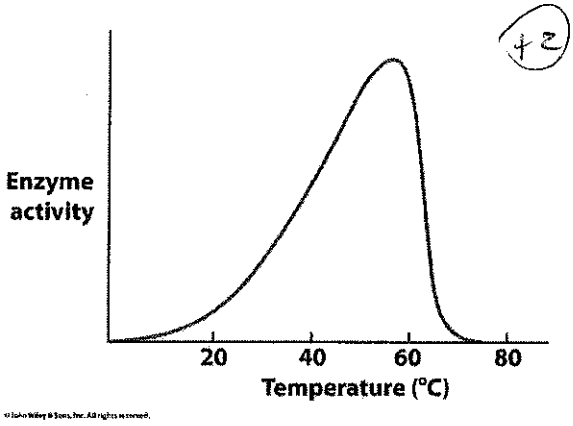
Hexokinase transferase

Alanine racemase isomerase

Malate dehydrogenase oxidoreductase

Alanine aminotransferase transferase

C. The rate of an enzyme-catalyzed reaction is measure at several temperatures, generating the curve shown below. Explain why enzyme activity increases with temperature and then drops off sharply.



(+2) Rate of rxns increase with temperature because more molecules have enough energy to overcome E_A.

(3) IF Temp is too high, the enzyme will denature, destroying the catalyst

D. Below is the coding strand for a small, but very important, gene. Draw the template strand sequence and the mRNA produced. What tripeptide is coded?

5'-GTAATCCCG-3'

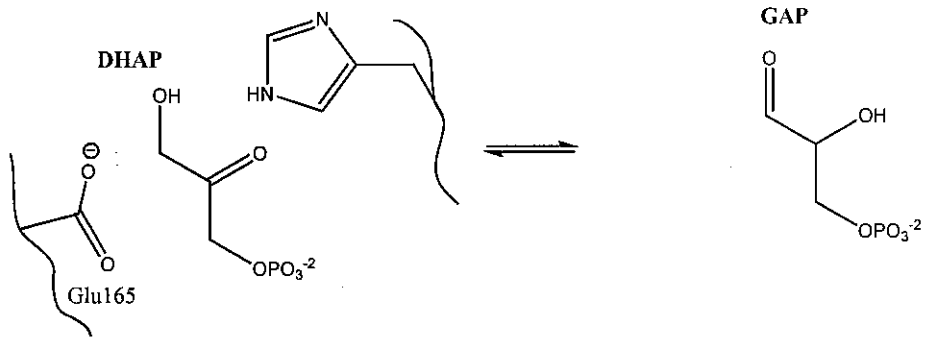
(+2) 3' CATTAGGGC 5' Template

(+2) 5' GUAAUCCCG 3' mRNA

(+1) V I P peptide

Section 2: Problems (10 points each)

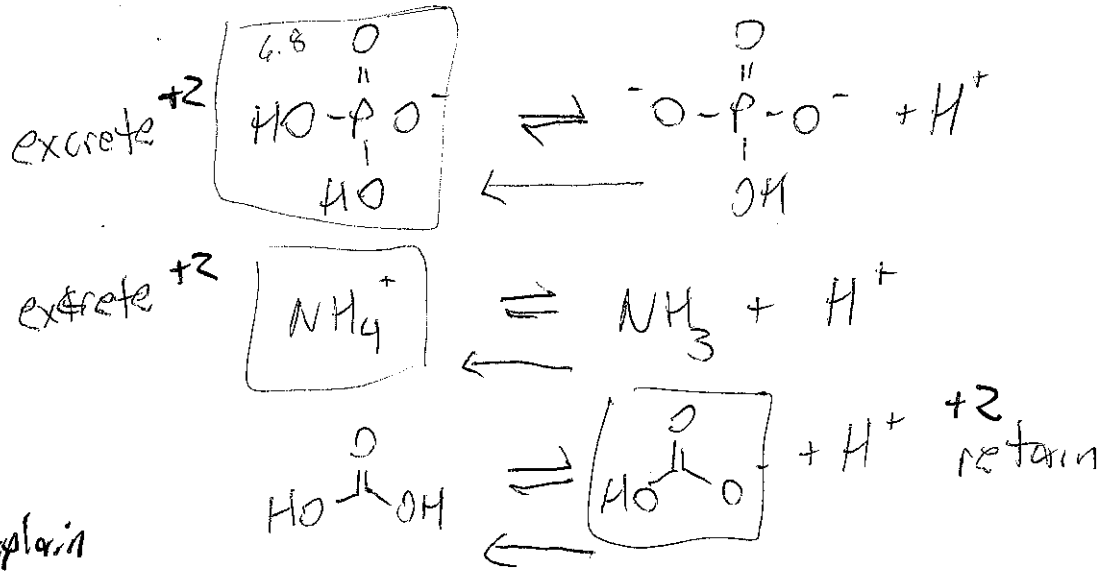
4. Draw an arrow mechanism for the isomerization of dihydroxyacetone phosphate (DHAP) to glyceraldehyde-3-phosphate (GAP) catalyzed by triose phosphate isomerase. The active site glutamate and histidine residues are given to help you get started.



see Lecture notes

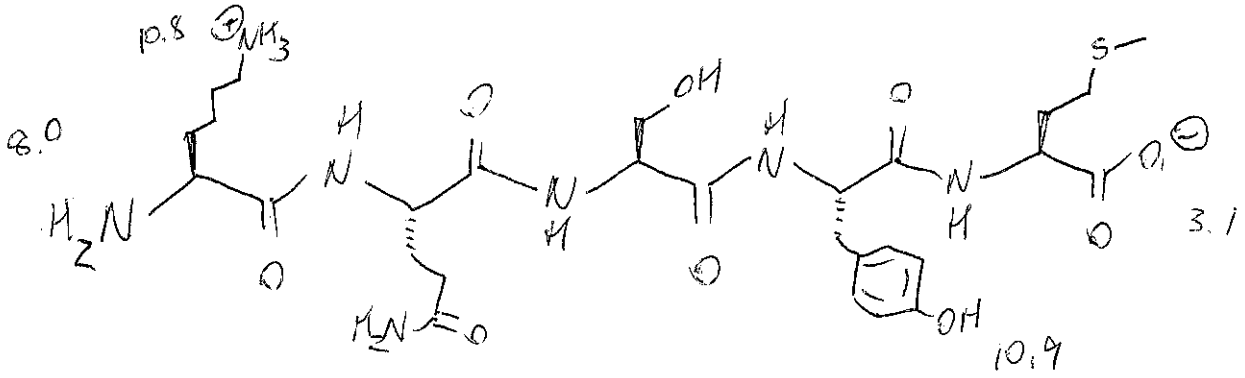
- can be 4 steps or 2 simultaneous protonation/deprotonation

(10) 5. Metabolic acidosis is a general term that describes a number of metabolic disorders in the body that result in a lowering of the blood pH from 7.4 to 7.35 or below. The kidney plays a vital role in regulating blood pH. The kidney can either excrete or reabsorb various ions such as $H_2PO_4^-$, NH_4^+, and HCO_3^-. Which ions will be excreted and which will be reabsorbed in metabolic acidosis? Explain using relevant chemical equations.



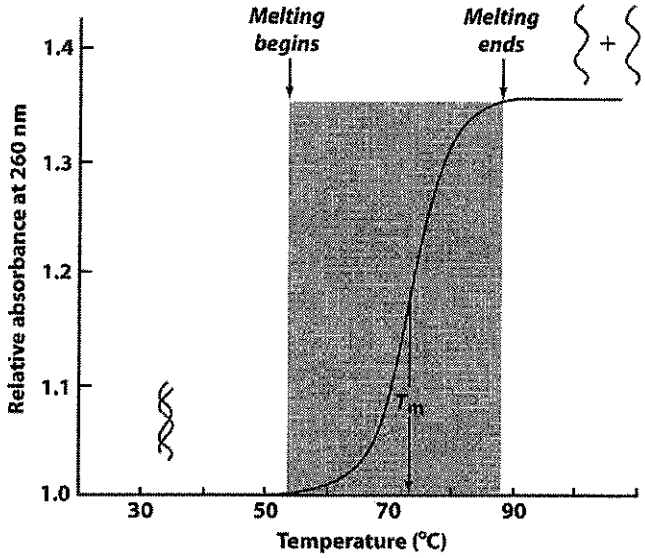
By LeChatlier's Principle: retain C.B; excrete C.A.
(2) eqn.s=2

(10) 6. Draw the peptide KQSYM in its major ionization state at its isoelectric point.



backbone +2
stereochem +1
sidechains +5
isoelectric point +2

7. Explain the shape of this DNA melting curve. Why is it not linear? Name one intermolecular force that plays a key role in the shape of this curve, and explain how it does so.

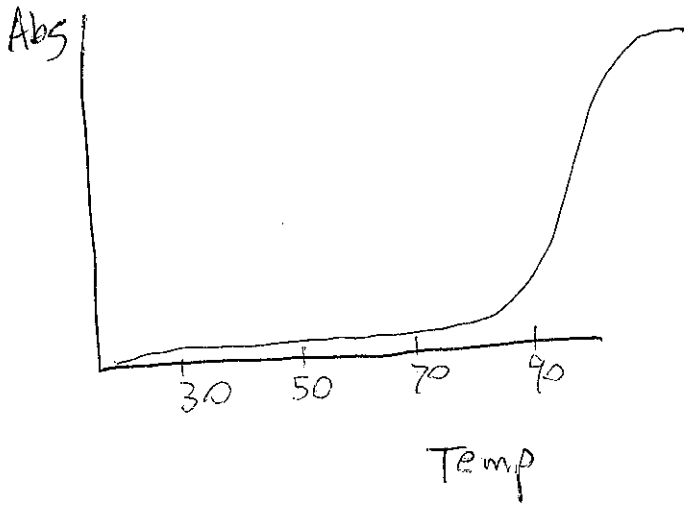


(+4) Explanation of cooperativity

(+4) Base stacking - London forces or π stacking

explanation hydrophobic effect

If the same analysis were performed on a GC-rich DNA segment, how would the melting curve change? Draw this curve to show how it is different than the curve above.



shifted right

(+2)

8. A buffer was made by dissolving 100 mmol of imidazolium chloride in water, adding 35 mmol of hydroxide, and bringing the final volume of the buffer to 500 mL.

A. What is the pH of this buffer?

$$pH = pK_a + \log \frac{[A^-]}{[HA]}$$

+4

$$= 7.0 + \log \frac{35}{65} = 6.7$$

B. Would this solution be able to effectively act as a buffer if 1.0 mL of 12 M HCl were added? Explain, showing your work.

$$0.001\ L \left(12 \frac{mol}{L}\right) = 0.012\ mol\ strong\ acid$$

+0 4

$$[A^-] = 35\ mmol - 12\ mmol = 23\ mmol$$

$$[HA] = 65\ mol + 12\ mmol = 77\ mol$$

$$pH = pK_a + \log \frac{A^-}{HA} = 7.0 + \log \frac{23}{77} = 6.5$$

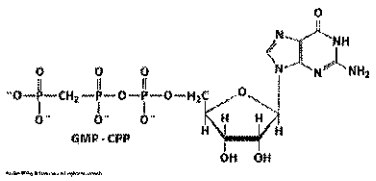
+0 2 based on above

This buffer is still effective - within the ±1 window of the pK_a

Section 3: Case study (10pts) The following data were obtained to study the mechanism of the Myosin V processive motor. On the figure below, propose a mechanism for this motor, and explain how each piece of data is consistent with your proposal.

A. When GMP·CPP (shown below) is added to a myosin/actin system, this nonhydrolyzable ATP analog can be shown to be attached to the trailing head of myosin V in a conformation in which only one head group is bound to actin.

B. Adenosine thiotriphosphate hydrolyzes in the motor slowly to produce ADP and thiophosphate. Thiophosphate stays tightly bound to the leading head group, locking the motor into having only one head bound to actin.



+2 explain A

+2 explain B

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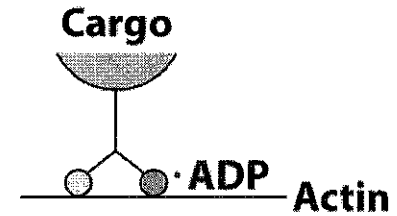
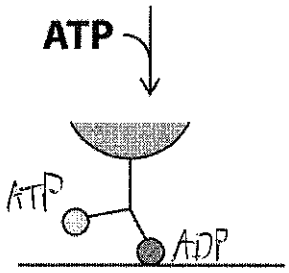
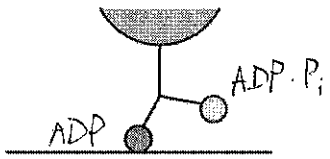
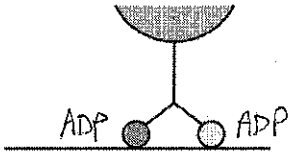




1) ATP binding causes the trailing foot to lift. When GMP·CPP is present, it binds in place of ATP, locking the motor at this step



2) Hydrolysis causes the trailing foot to swing forward. When the hydrolyzable analog is present, hydrolysis still swings this leg forward because the thiophosphate is in the leading foot.



3) P_i release allows the leading foot to bind actin. Thiophosphate can't be released, so this motor is stuck here.

4) The conformation with both feet down allows ADP release from lagging foot.

Data Tables

Amino acid pKa values

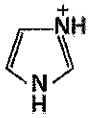
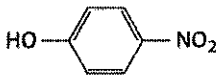
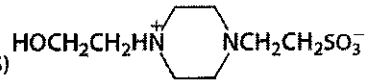
C-terminal	3.1
N-terminal	8.0
Aspartate, glutamate	4.1
Histidine	6.1
Cysteine	8.3
Tyrosine	10.9
Lysine	10.8
Arginine	12.5

TABLE 3-3 The Standard Genetic Code[a]

First Position (5′ end)	Second Position U		Second Position C		Second Position A		Second Position G		Third Position (3′ end)
U	UUU	Phe	UCU	Ser	UAU	Tyr	UGU	Cys	U
	UUC	Phe	UCC	Ser	UAC	Tyr	UGC	Cys	C
	UUA	Leu	UCA	Ser	UAA		UGA		A
	UUG	Leu	UCG	Ser	Stop		Stop		G
					UAG		UGG	Trp	
					Stop				
C	CUU	Leu	CCU	Pro	CAU	His	CGU	Arg	U
	CUC	Leu	CCC	Pro	CAC	His	CGC	Arg	C
	CUA	Leu	CCA	Pro	CAA	Gln	CGA	Arg	A
	CUG	Leu	CCG	Pro	CAG	Gln	CGG	Arg	G
A	AUU	Ile	ACU	Thr	AAU	Asn	AGU	Ser	U
	AUC	Ile	ACC	Thr	AAC	Asn	AGC	Ser	C
	AUA	Ile	ACA	Thr	AAA	Lys	AGA	Arg	A
	AUG		ACG	Thr	AAG	Lys	AGG	Arg	G
	Met								
G	GUU	Val	GCU	Ala	GAU	Asp	GGU	Gly	U
	GUC	Val	GCC	Ala	GAC	Asp	GGC	Gly	C
	GUA	Val	GCA	Ala	GAA	Glu	GGA	Gly	A
	GUG	Val	GCG	Ala	GAG	Glu	GGG	Gly	G

[a]The 20 amino acids are abbreviated: Ala, alanine; Arg, arginine; Asn, asparagine; Asp, aspartate; Cys, cysteine; Gly, glycine; Gln, glutamine; Glu, glutamate; His, histidine; Ile, isoleucine; Leu, leucine; Lys, lysine; Met, methionine; Phe, phenylalanine; Pro, proline; Ser, serine; Thr, threonine; Trp, tryptophan; Tyr, tyrosine; and Val, valine.

TABLE 2.4 p*K* Values of Some Acids

Name	Formula[a]	p*K*
Trifluoroacetic acid	CF_3COOH	0.18
Phosphoric acid	H_3PO_4	2.15[b]
Formic acid	$HCOOH$	3.75
Succinic acid	$HOOCCH_2CH_2COOH$	4.21[b]
Acetic acid	CH_3COOH	4.76
Succinate	$HOOCCH_2CH_2COO^-$	5.64[c]
Thiophenol	C_6H_5SH	6.60
Phosphate	$H_2PO_4^-$	6.82[c]
N-(2-acetamido)-2-amino-ethanesulfonic acid (ACES)	$H_2NCOCH_2\overset{+}{N}H_2CH_2CH_2SO_3^-$	6.90
Imidazole		7.00
p-Nitrophenol		7.24
N-2-hydroxyethylpiperazine-N′-2-ethanesulfonic acid (HEPES)		7.55
Glycinamide	$^+H_3NCH_2CONH_2$	8.20
Tris(hydroxymethyl)-aminomethane (Tris)	$(HOCH_2)_3C\overset{+}{N}H_3$	8.30
Boric acid	H_3BO_3	9.24
Ammonium ion	NH_4^+ 9.25	
Phenol	C_6H_5OH	9.90
Methylammonium ion	$CH_3NH_3^+$	10.60
Phosphate	HPO_4^{2-}	12.38[d]

[a]The acidic hydrogen is highlighted in red; [b]pK_1; [c]pK_2; [d]pK_3.