

CHEM-527 Introductory Biochemistry  
Final Examination  
3:30 -6:30 PM, Friday, December 13, 2013  
Dr. White Instructor

Name \_\_\_\_\_

If you feel any question is unclear or ambiguous, clearly explain your answer or interpretation.

Do not expose your answers to the scrutiny of your neighbors. Please fold under each page before you go on to the next.

- Write your name on every page.
- A maximum score on this examination is 136 points.
- There are 11 pages to this examination including this page and a tear off genetic code at the back.
- A copy of the metabolic pathway sheet for glycolysis, gluconeogenesis, the pentose phosphate pathway, the citric acid cycle, and beta oxidation of fatty acids will be distributed separately.
- This examination will assess your learning, problem-solving skills, and ability to communicate clearly. Parts are intended to be challenging even to the best students in the class. Remember, ***Problem-solving is what you do when you don't know the answer. If you know the answer, it is not a problem.***
- Writing reflects how you think. Better quality answers will receive higher marks. Therefore organize your thoughts before you write and draw. Among the "right answers" I will read, some will be better than others because they:
  - show greater depth of understanding,
  - provide a more logical structure,
  - use appropriate examples,
  - include appropriate illustrations,
  - avoid extraneous or inaccurate information, and
  - choose words with precision.
- Strive to write not that you may be understood, but rather that you cannot possibly be misunderstood. Stream of consciousness answers are rarely well organized or clearly presented.

Breakdown of the Exam by sections:

I.	Short Answer	20 Points
II.	Multiple Choice	26 Points
III.	<u>Problems and Short Essay</u>	<u>90 Points</u>
	Total	136 Points

**Have a Safe and Happy Holiday!**

**Part I. Short Answer “Bloom’s Basement” (20 points, 1 point each)**

- \_\_\_\_\_ 1. Process in the maturation of mRNA that modifies the 5' end of the RNA.
- \_\_\_\_\_ 2. Process in the maturation of eukaryotic mRNA in which segments of RNA are removed and others joined.
- \_\_\_\_\_ 3. Process in the maturation of mRNA in which the 3' end of the RNA is modified.
- \_\_\_\_\_ 4. The regions of RNA that are excised are called.
- \_\_\_\_\_ 5. The regions of RNA that are joined and retained and typically code for protein are called.
- \_\_\_\_\_ 6. Replication is catalyzed by this enzyme.
- \_\_\_\_\_ 7. Transcription is catalyzed by this enzyme.
- \_\_\_\_\_ 8. Translation is catalyzed by this ribonucleoprotein complex.
- \_\_\_\_\_ 9. Ratio of nitrogen to phosphorus in ATP.
- \_\_\_\_\_ 10. Name of five membered ring embedded in the bicyclic purine structure.
- \_\_\_\_\_ 11. Name of six-membered ring embedded in the bicyclic purine structure.
- \_\_\_\_\_ 12. In a cell, the primer for DNA synthesis is a small piece of \_\_\_\_\_.
- \_\_\_\_\_ 13. During starvation, the human brain adapts to metabolize these four-carbon metabolites.
- \_\_\_\_\_ 14. If  $[S] = K_m$ ,  $v = \text{_____} V_{\max}$ ?
- \_\_\_\_\_ 15. Vitamin precursor for FMN and FAD
- \_\_\_\_\_ 16. Enzymes that use ATP are called \_\_\_\_\_ .
- \_\_\_\_\_ 17. Compound that accumulates in gout.

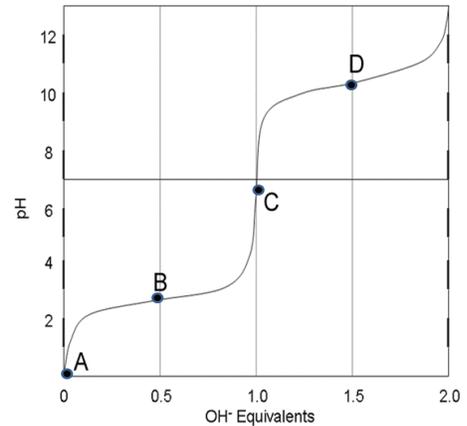
The next cryptic clues refer to Famous Nobel Prize Winners.

- \_\_\_\_\_ 18. Two who unraveled DNA; the second a “pain in the neck”.
- \_\_\_\_\_ 19. One with two cycles named for him, but not a bicycle.
- \_\_\_\_\_ 20. A “musical” sequencer with two, one ditty with dideoxy in the land of Di.

**Part II. Multiple Choice Questions (26 points, 3 points each correct answer, 2 points for a brief correct explanation of your answer on 3-6.)**

- \_\_\_\_ 1. (3 Pts) If glycine,  $\text{NH}_2\text{CH}_2\text{COOH}$ , were dissolved in distilled water, what would the predominant form be in solution?
- $\text{NH}_2\text{CH}_2\text{COOH}$
  - $+\text{NH}_3\text{CH}_2\text{COO}^-$
  - $+\text{NH}_3\text{CH}_2\text{COOH}$
  - $\text{NH}_2\text{CH}_2\text{COO}^-$

- \_\_\_\_ 2. (3 Pts) Which point on the titration graph (A, B, C, or D) corresponds to glycine at its isoelectric point?

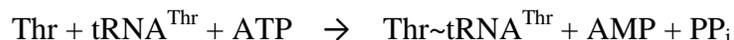


- \_\_\_\_ 3. (3 Pts) Consider a protein composed of  $n$  amino acid residues. How many mass units more or less is the mass of the protein compared to the mass of the separate amino acids needed to make it?

- $(n-1)18$  less
- $18n$  less
- no difference
- $(n+1)18$  more

Explanation (2 Pts):

- \_\_\_\_ 4. (3 Pts) Threonine aminoacyl tRNA synthetase catalyzes the ATP-dependent activation of threonine which becomes covalently bonded to the 3' end of its cognate  $\text{tRNA}^{\text{Thr}}$  as depicted below.



The chemical nature of the covalent bond between threonine and its tRNA is:

- Phosphoanhydride between the  $\alpha$ -carboxyl group of threonine and a  $\text{tRNA}^{\text{Thr}}$  phosphoryl group
- Amide between the  $\alpha$ -amino group of threonine and a  $\text{tRNA}^{\text{Thr}}$  carboxyl group.
- Thioester between the  $\alpha$ -carboxyl group of threonine and a sulfur modified base at the 3' terminus of  $\text{tRNA}^{\text{Thr}}$ .
- Ester between the  $\alpha$ -carboxyl group of threonine and a  $\text{tRNA}^{\text{Thr}}$  hydroxyl group.

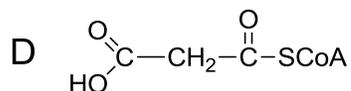
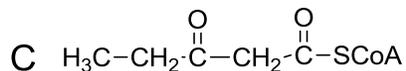
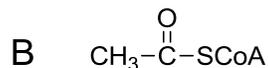
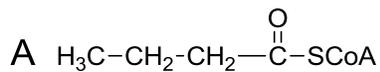
Explanation (2 Pts):

\_\_\_\_ 5. (3 Pts) When used as an artificial message, a synthetic RNA with a repeating nucleotide sequence encoded an alternating polypeptide containing a basic and an acidic amino acid. What is the sequence of the synthetic mRNA?

- A. (GAA)<sub>n</sub>      B. (CGC)<sub>n</sub>      C. (AG)<sub>n</sub>      D. (CG)<sub>n</sub>      E. (AC)<sub>n</sub>

Explanation (2 Pts)

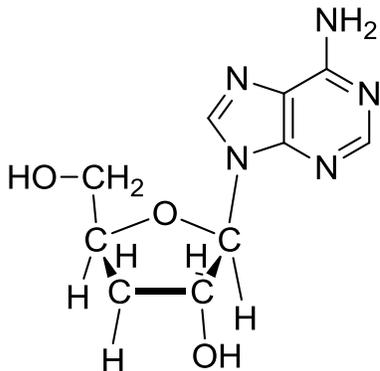
\_\_\_\_ 6. (3 Pts) Which of the following compounds would be an intermediate in the **complete** oxidation of odd **and** even chain-length fatty acids?



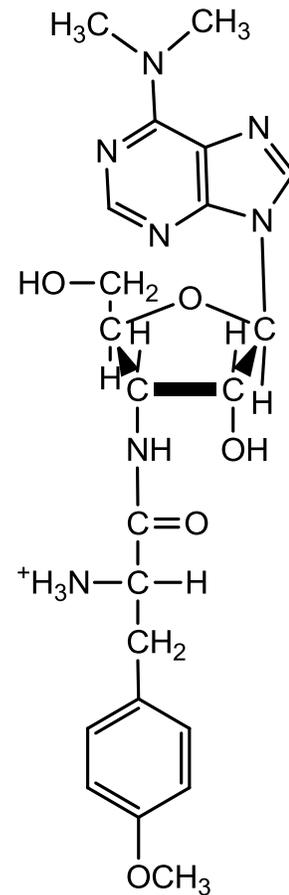
Explanation (2 Pts)

### Part III (90 Points) Thought Questions and Short Essays

1. (5 Points) Explain why Cordycepin (below) inhibits RNA Synthesis.



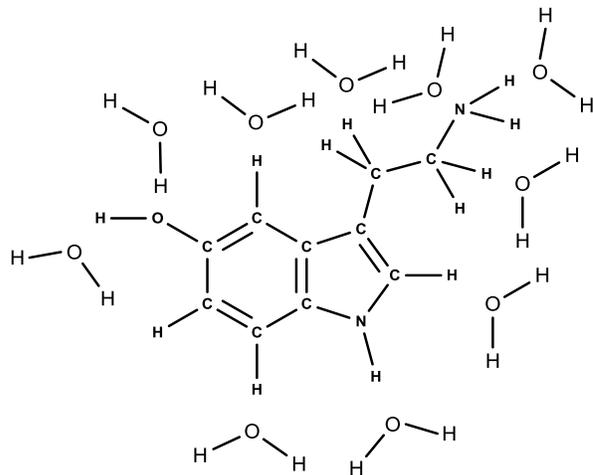
2. (13 Points Total) Puromycin (right) inhibits protein synthesis by mimicking the 3' end of an amino acyl-tRNA and binding to the ribosomal A-site where it terminates translation by reacting with the peptidyl-tRNA in the P-site.



- (2 Pts) The aminoacyl portion of puromycin most closely resembles what amino acid?
- (4 Pts) The top part of puromycin mimics adenosine. Circle those parts of the structure that make it different from adenosine.
- (2 Pts) What type of bond links the amino acyl group to the adenosyl-like portion of puromycin?
- (2 Pts) In an aminoacyl-tRNA, how would this bond be different?
- (3 Pts) Put an X on the atom that will be covalently linked to a peptide after puromycin reacts with the peptidyl tRNA.

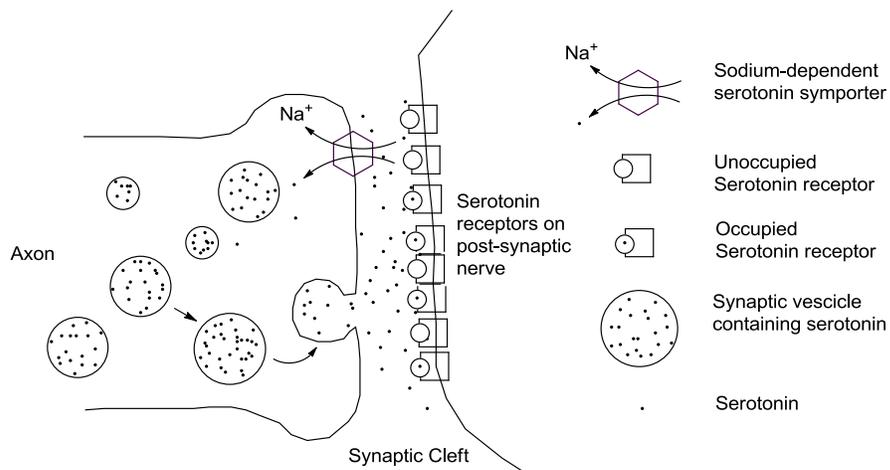
3. (24 Points total) Serotonin shown below is a neurotransmitter associated with feelings of well-being and happiness.

- (5 Points) The structure of serotonin is shown to the right surrounded by 10 water molecules arranged as if ready to make hydrogen bonds with serotonin. However some can and others can't. **Put an "X" through all water molecules that cannot make a H-bond to serotonin. Indicate with a dark line between atoms those H-bonds that can form between water molecules and serotonin. (Minus 2 points for incorrect answers. No credit for 3 or more incorrect answers.)**



- b. (5 Points) Examine the structure of serotonin with respect to similarities to the 20 protein amino acids. **Identify** and **draw the structure** of the amino acid most closely similar in structure to serotonin.

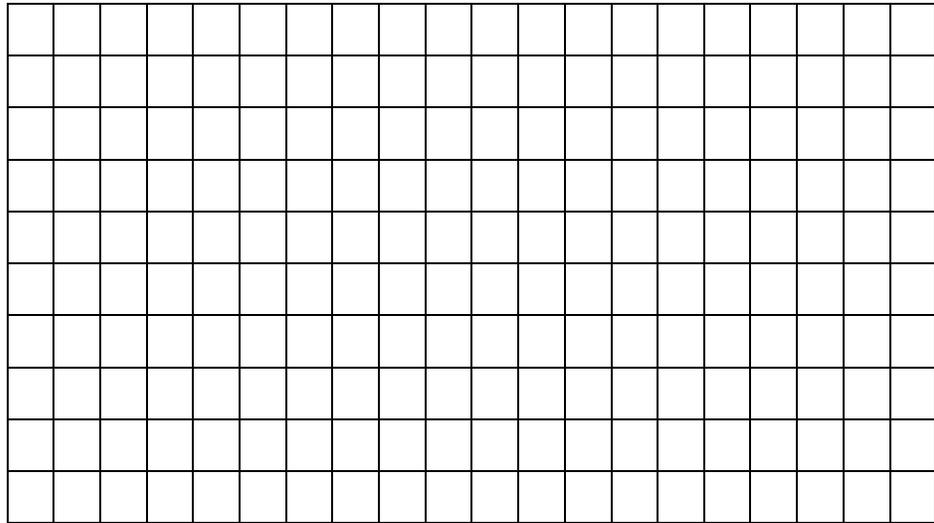
- c. (4 Points) Like acetylcholine, serotonin is released at a synapse in response to a signal and diffuses across the synaptic cleft to the post synaptic nerve where it binds to serotonin receptors that in turn transmit the signal to that cell. Unlike acetylcholine, which is destroyed by hydrolysis, serotonin is recycled back to the axon by a specific sodium-serotonin symport system as shown in the diagram below. Prozac (fluoxetine) is an antidepressant drug that inhibits the sodium-serotonin symport system. The illicit drug Ecstasy also interferes with this process and can cause irreversible changes to the brain.



The uptake system does not require ATP. What contributor to the membrane potential would favor the removal of serotonin from the synaptic cleft? (Answer in a complete sentence.)

- d. (6 Points) Membrane transport proteins are effectively enzymes catalyzing the movement of specific molecules and ions across membranes and can be described in similar terms of binding affinity and rates of transport. Prozac for example, binds to the sodium-serotonin symport system with a dissociation constant ( $= K_i$ ) of about 200nM. People with severe depression often have lower than normal concentrations of serotonin. Prozac often restores mood and a sense of well-being for these people.

On the graph below **label the axes** and **draw a line** that would represent the **rate of serotonin uptake** from the synaptic cleft **as a function of Prozac dose** (concentration). **Indicate the location** of  $K_i$  on your graph.



- e. (4 Points) What would be the effect of Prozac that would make it an antidepressant?

4. (12 Points) A major breakthrough occurred with a method to sequence DNA. The basic idea was to have DNA polymerase extend a radioactive primer in the presence of small amounts of a dideoxynucleotide triphosphate resulting in termination whenever the ddNTP was incorporated into the chain. The products of the reaction were separated by electrophoresis which separated the oligonucleotide in order of their decreasing molecular weight.

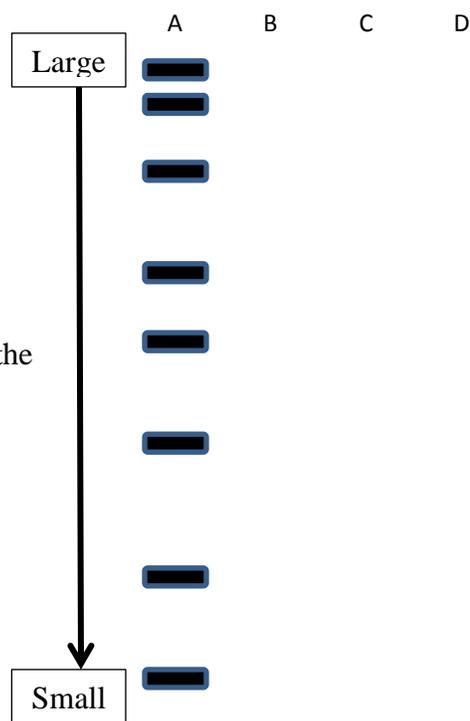
DNA shown below is to be sequenced with this method. In the electrophoretic gel diagram below the results for mixture A are given. **Draw in the bands** that will appear if DNA polymerase is added to the reaction along with the nucleotide mixtures indicated in B, C, and D. Dideoxynucleotides (ddNTPs) are added in relatively small amounts. The asterisk\* represents a radioactive label. (Question provided by Michael Cox.)

\*5'--3'OH  
3'----ACGACGTAGGACATTAGAC-5'

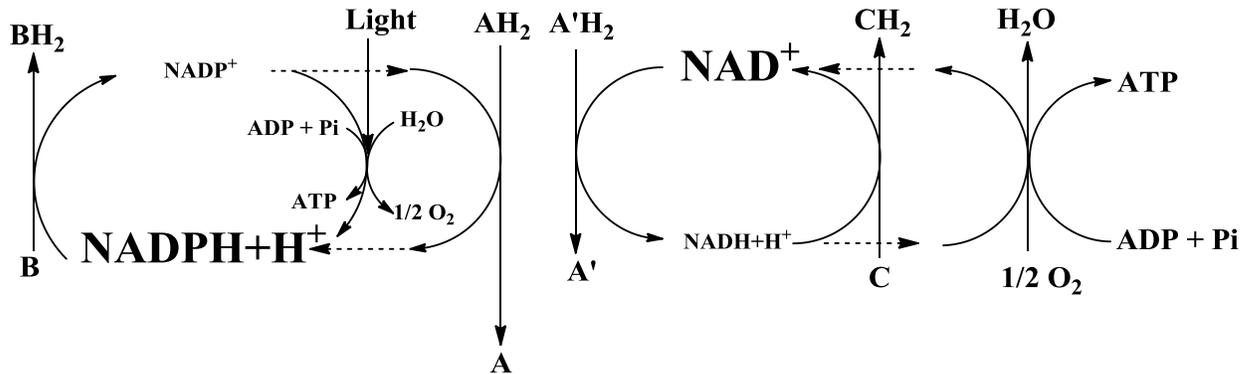
Nucleotide mixtures:

- A. dATP, dTTP, dCTP, dGTP, ddTTP (given)
- B. dATP, dTTP, dCTP, dGTP, ddATP
- C. dTTP, dGTP, dCTP, ddGTP, ddCTP
- D. dATP, dTTP, dCTP, ddGTP

Electrophoretic migration is from top to bottom with the smaller oligonucleotide moving farthest.



5. (19 Points Total) The following is a figure used in the class with some text elements removed. Please **provide a title** for this figure **and a legend** that explains what the figure is intended to convey.



- a. (3 Points) A title for the figure:
- b. (8 Points) **Explanatory Figure Legend.** You may add back text to the figure to supplement your description. You may use bullet points to deal with different aspects of the figure. Use the back of this page, if you need more room.
- c. (8 Points) Give one specific example for each of the four general reactions shown.
- i.  $AH_2 \rightarrow A$
  - ii.  $A'H_2 \rightarrow A'$
  - iii.  $B \rightarrow BH_2$
  - iv.  $C \rightarrow CH_2$

6. (17 Points Total) The  $\alpha$ -chain of human hemoglobin is normally 141 amino acid residues long. Three unusual variants have been discovered in which the  $\alpha$ -chain is longer than normal. Hb-Constant Spring and Hb-Icaria both have  $\alpha$ -chains 172 residues long and differ from each other only by one amino acid at position 142. The first 141 residues are identical with the entire normal  $\alpha$ -chain. The  $\alpha$ -chain of Hb-Wayne is 146 residues long. The last 8 residues differ from both normal and Hb-Constant Spring  $\alpha$ -chains. The amino acid sequences from residue 138 to 148 are presented below. Each of these inherited defects can be explained by single base mutational events either a base substitution or a nucleotide deletion-insertion.

Residue No.	138	139	140	141	142	143	144	145	146	147	148..
Normal	Ser	Lys	Tyr	Arg	-						
Constant Spring	Ser	Lys	Tyr	Arg	Gln	Ala	Gly	Ala	Ser	Val	Ala
Icaria	Ser	Lys	Tyr	Arg	Lys	Ala	Gly	Ala	Ser	Val	Ala
Wayne	Ser	Asn	Thr	Val	Lys	Leu	Glu	Pro	Arg	-	

- (3 Pts) What is the termination codon for normal  $\alpha$ -chain? **Be specific** as possible and explain your deduction.
- (6 Pts) From the above sequences it is possible to unambiguously deduce a 26-base sequence of normal  $\alpha$ -chain mRNA. **Write out** 15 bases of this sequence extending 6 bases on either side of the normal termination codon. **Indicate** the 5' and 3' ends.
- (4 Pts) **Write out** the base sequence strand of DNA coding for the mRNA in part b. **Indicate** the 5' and 3' ends.
- (4 Pts) Specifically **what are the base changes** that can explain each of the three hemoglobin variants? Can this be ascertained unambiguously?

## Genetic Code Chart

UUU	PHE	UCU	SER	UAU	TYR	UGU	CYS
UUC		UCC		UAC		UGC	
UUA	LEU	UCA	PRO	UAA	End	UGA	End
UUG		UCG		UAG		UGG	TRP
CUU		CCU		CAU	HIS	CGU	ARG
CUC		CCC		CAC		CGC	
CUA	CCA	CAA	GLN	CGA			
CUG	CCG	CAG		CGG			
AUU	ILE	ACU	THR	AAU	ASN	AGU	SER
AUC		ACC		AAC		AGC	
AUA		ACA		AAA	LYS	AGA	ARG
AUG	MET	ACG	AAG	AGG			
GUU	VAL	GCU	ALA	GAU	ASP	GGU	GLY
GUC		GCC		GAC		GGC	
GUA		GCA		GAA	GLU	GGA	
GUG		GCG		GAG		GGG	