MID-TERM EXAM 3 - 11/5/01
C484, Fall 2001

You will have 1 hour to complete this exam. There are **14** pages containing 5 questions worth 100 points and a bonus question worth 15 points. A page of reference material is provided at the end of the exam. Please answer the questions in the space provided. There is a blank page at the back in case you need additional space. Be sure to indicate that you have completed a problem on this page to insure that you receive credit for the work. Please show all of your work, including units, in order to receive full credit. You may use a calculator but you may NOT share a calculator with your neighbor.

READ THE QUESTIONS CAREFULLY! In several cases, you have the choice of which question you want to answer.

Pace yourself. Many of the questions have multiple parts, so do what you can on one question and then move to the next. The exam will most likely take you the full hour to complete.

Please try to be neat. If we cannot read your writing, we cannot award you credit for your answer.

Question 1	12.5 /15
Question 2	11 /20
Question 3	20 /25
Question 4	17 /20
Question 5	10.5 /20
Bonus	10 /15
TOTAL:	81 /100

1) Define **any 5** the following terms: **(3pts. each/15 pts. total)**

a) cloning vector

b) palindrome - a sequence of nucleotides that can be read the same forwards or backwards

+3

c) restriction endonuclease - an enzyme that cleaves DNA specifically; cleaves at specific sites

+3

d) intercalation

e) propeller twist - a twist in a base pair that makes the bases closer together. Brings the hydrophobic regions closer together. A twist in the H-bonding.

+3

f) writhe – when DNA crosses over itself.
occurs in supercoiling and in circular DNA.

8 ← this is a writhe.

+2

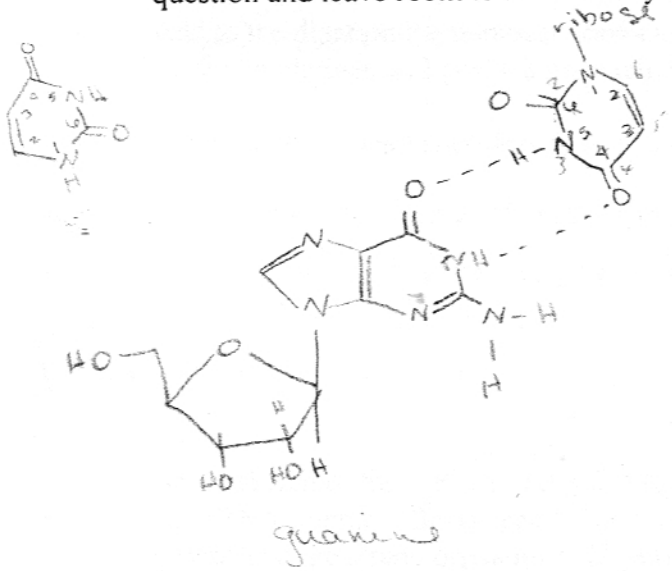
g) hyperchromism

h) nucleosome core particle – this contains 8 histones that attaches to the anionic phosphate groups & arginine, lysine rich DNA. DNA wraps around the histones and the whole unit is a nucleosome.

+1½

2) Nucleobases, nucleosides and nucleotides. **(20pts)**

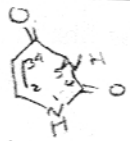
a) In RNA, G•U base pairs are quite common and often highly conserved. Draw a G•U base pair. You must indicate the position of the ribose attachment, but you do not need to draw its entire structure (i.e. "---Ribose"). Before you start drawing, read part c of this question and leave room to add this to your sketch. **(6 pts)**



guanine

6

b) Number the positions on the pyrimidine ring. **(2 pts)**



correct ring, wrong # ing -1

c) Select an amino acid that can specifically recognize (discriminate the face of the G•U base pair in part a. Add this amino acid side chain (show the complete side chain) to the drawing above and show the hydrogen bonding interaction(s) it would make. Please provide the 1- and 3-letter codes for this amino acid. **(6 pts)**

? ?

0

d) Briefly explain why G•U base pairs are acceptable in RNA biochemistry but the equivalent G•T base pair is never observed in genomic or plasmid DNA. **(6 pts)**

G·U base pairs are accepted in RNA biochemistry because U is the hydrolyzed form of cytosine. In DNA, T must be present in order to pair with adenine. If U was present, A would bind with U and nothing would bind with G because U is closely related to C and U would be mistaken for C causing mutation

4

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