

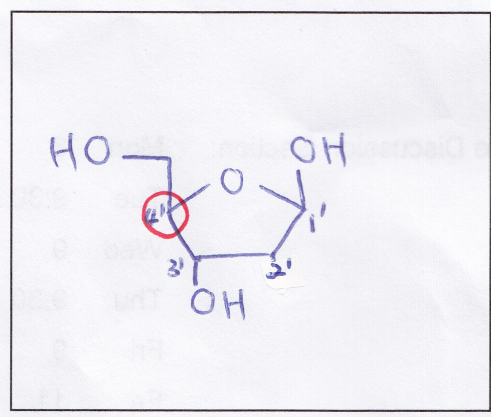
- Q: Quiz
- S: Sample exam
- P: Suggested p.
- L: Lecture note

2 L 1. (1) DNA are polymers composed of monomer units called deoxynucleotides nucleotides linked by phosphodiester bonds.

2 L (2) Proteins are polymers composed of monomer units called amino acids linked by peptide/amide bonds.

4 L 2. (1) The sugar found in DNA is (  $\alpha$   $\beta$  -circle one) - 2' -deoxy- ( D ) L -circle one) ribose.

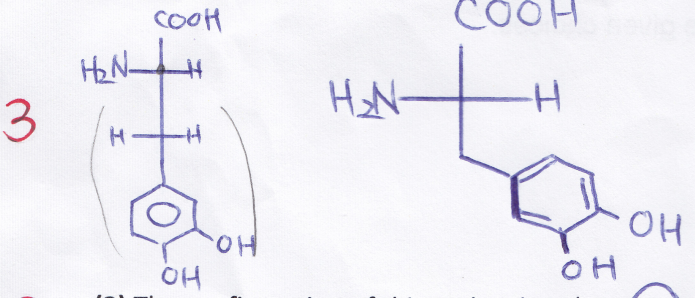
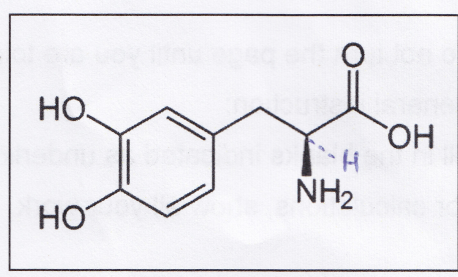
3 L (2) Draw the Haworth perspective of this sugar in the box on the right.  
S1.2 (fig)



2 (3) Circle the atom that is responsible for the D- or L- configuration.  
S.7 (fig)

2 L (4) Show the numbering of the carbons on the Haworth perspective drawn in (2). The number on the carbon is responsible for the  $\alpha$  or  $\beta$  configuration is 1'.

L 3. (1) Draw the Fisher projection of the molecule shown on the right.  
Q \*Hint: First identify the functional groups and see if it resembles something you already know!



\* correct permutation on the same scaffold is OK

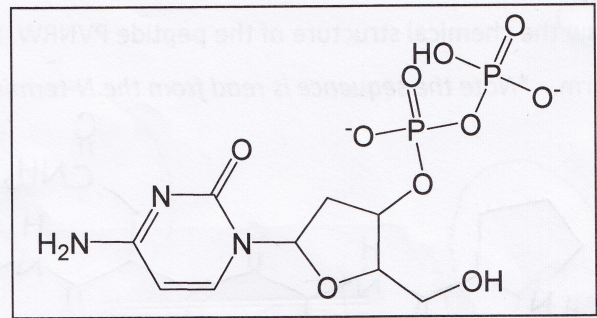
2 (2) The configuration of this molecule is ( D ) L cannot be determined -circle one).

2 (3) Therefore, it has the ( same ), opposite , cannot be determined -circle one) configuration as the amino acids found in naturally made proteins.

21 + 1

4. (1) The molecule shown on the right is called

SI.1.7 <sup>2</sup> deoxycytidine <sup>2</sup> 3'-diphosphate

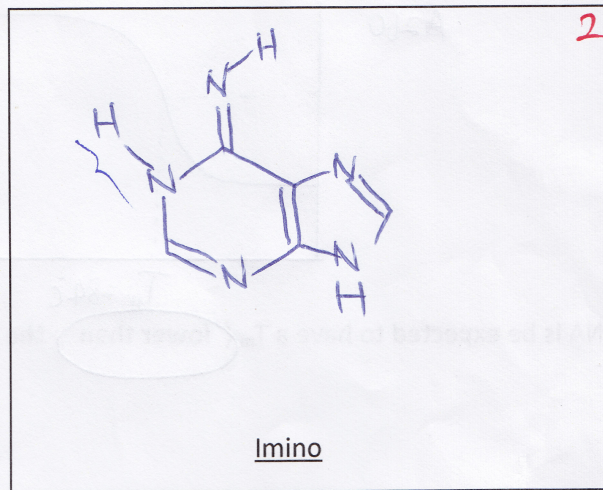
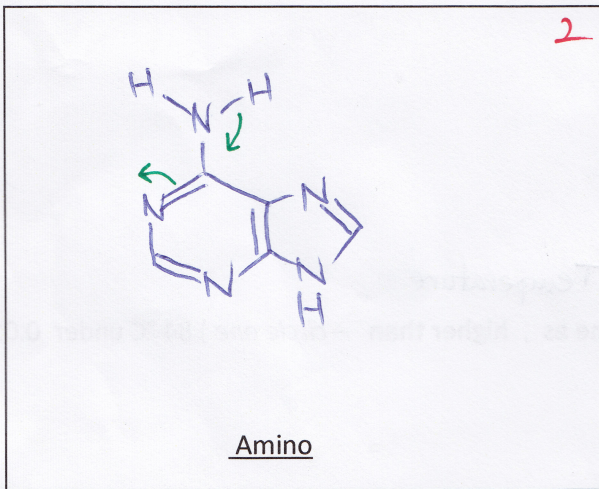


\*Do not abbreviate.

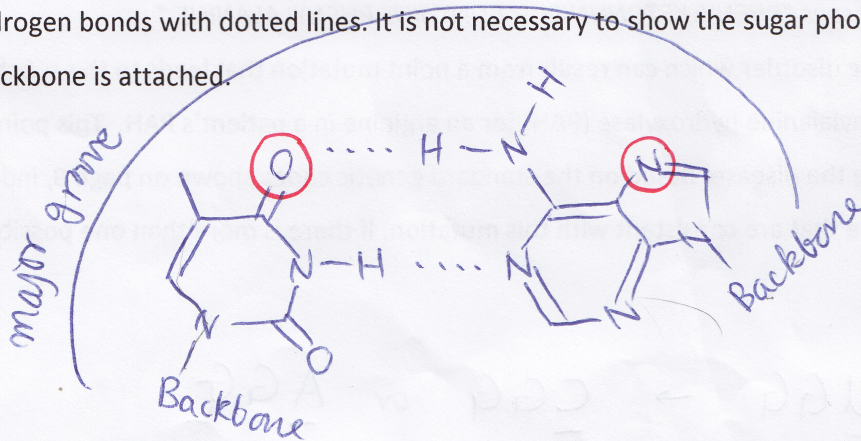
\*Don't forget to denote the location of phosphates.

(2) The base in (1) is called Cytosine, which pairs with Guanine (base name) in DNA. \*Do not abbreviate.

5. (1) Draw the amino- and imino- tautomers of adenine in the given squares below.



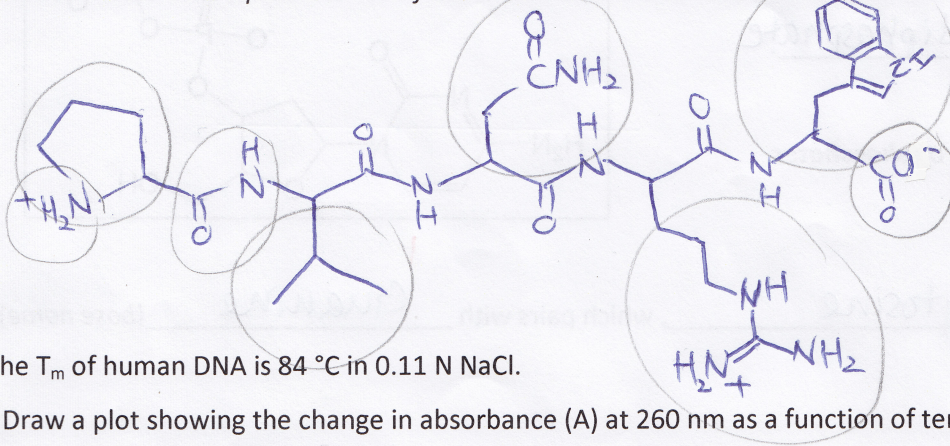
SI.6 (2) Draw the complete structure of the base pair involving the major tautomeric form of adenine found in DNA double helix. Indicate the hydrogen bonds with dotted lines. It is not necessary to show the sugar phosphate backbone, but indicate where the backbone is attached.



(3) Circle the atoms that can accept a hydrogen bond in the major groove side of the base pair drawn in (2).

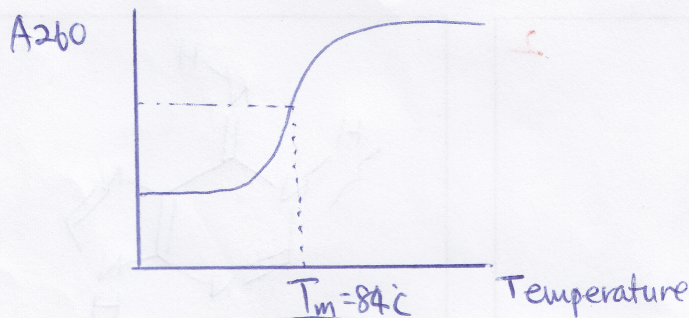
"Homework"

6. Draw the chemical structure of the peptide PVNRW. For amino acids that are charged, draw them in the charged form. \*Note the sequence is read from the N-terminus to C-terminus - ALWAYS!



7. The  $T_m$  of human DNA is  $84^\circ\text{C}$  in  $0.11\text{ N NaCl}$ .

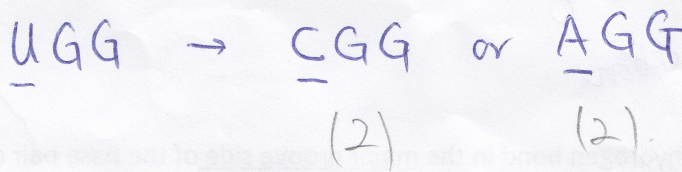
(1) Draw a plot showing the change in absorbance (A) at  $260\text{ nm}$  as a function of temperature for melting of human DNA under  $0.11\text{ N NaCl}$ . Label the axes and indicate  $T_m$  on the plot.



(2) Human DNA is be expected to have a  $T_m$  (lower than, the same as, higher than - circle one)  $84^\circ\text{C}$  under  $0.01\text{ N NaCl}$ .

8. The label on a Diet Coke says "PHENYLKETONUNIRCS: CONTAINS PHENYLALANINE."

Phenylketourea is a genetic disorder which can result from a point mutation that leads to the substitution of a tryptophan in normal phenylalanine hydroxylase (PAH) for an arginine in a patient's PAH. This point mutation makes the enzyme inactive and hence the disease. Based on the standard genetic codes shown on page 9, indicate changes in mRNA (not DNA!) sequence that are consistent with this mutation. If there is more than one possibility, write all the possible cases.



9. One strand of a double-helical DNA has the sequence 5'-GCATCTCATGC-3'.

(1) Write the base sequence of the complementary strand.

P.  
(Ch 8.2)

3'-CGTAGAG TACG-5'

2

5'-GCATGAGATGC-3'

(2) Does the DNA have the potential to form any alternative structures?

Yes.



2

10. The following DNA fragment was sequenced by the Sanger method. The asterisk indicates a fluorescent label primer with a sequence of 5'-GCCG-3'.

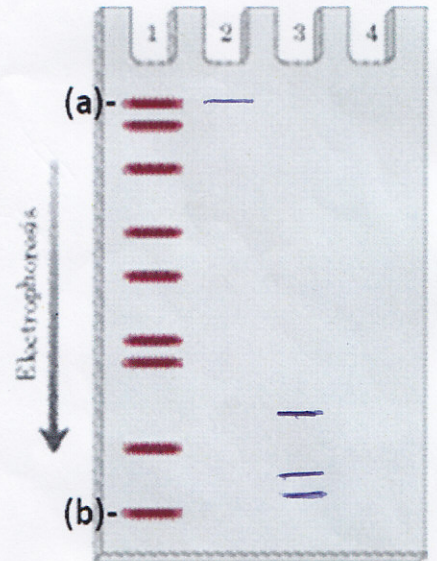
P.  
(Ch 8.2)

\*5'-GCCG-3'-OH  
3'-ATTACGCAAGGACATTAGAC-5'

A sample of the DNA was reacted with DNA polymerase and each of the nucleotide mixtures (in an appropriate buffer) listed below. Dideoxynucleotides (ddNTPs) were added in relatively small amounts.

- 1. dATP, dTTP, dCTP, dGTP, ddTTP
- 2. dATP, dTTP, dCTP, dGTP, ddTDP
- 3. dATP, dTTP, , dGTP, ddATP

The resulting DNA was separated by electrophoresis on an agarose gel, and the fluorescent bands on the gel were located. The band pattern resulting from nucleotide mixture 1 is shown on the right.



(1) What is the sequence of the DNA of the following bands in lane 1? \*Pay attention that there are 9 bands (not 8!). Assume the template DNA was in excess of the primer and again, note that the fluorescent label is on the primer.

Band (a) GCCG TAA TGCG TTCCT, G TAA TC, TG

2

Band (b) GCCGT

2

(2) Assuming that all mixtures were run on the same gel, what would the lane 2 of the gel look like? Draw directly on the gel picture.

(gel)

3

(3) shown on gel (gel)

3

14

MW.

g/mole

11. Bacteriophage T2 has a DNA of molecular weight  $120 \times 10^6$  Da contained in a head about 200 nm long.

(1) Calculate the length of the DNA (assume the molecular weight of a nucleotide pair is 600 Da). Assume that the DNA is in B-form and that there is 10 bp per turn. 3

$$\frac{120 \times 10^6 \text{ Da}}{600 \text{ Da}} = 2 \times 10^5 \text{ bp} \sim 2 \times 10^4 \text{ turns} \times 3.4 \text{ nm/turn}$$

$$\therefore \text{Total length} = \underline{\underline{6.8 \times 10^4 \text{ nm}}}$$

(2) Compared with the length of the T2 head, the total length of the DNA is 340 times (longer, ~~shorter~~) 2  
~~circle one~~.

$$\frac{6.8 \times 10^4}{2 \times 10^2} = 3.4 \times 10^2$$

12. Bacteriophage  $\lambda$  infects E. coli by integrating its double-stranded DNA into the bacterial chromosome. The success of this recombination depends on the topology of the E. coli DNA. When the superhelical density ( $\sigma$ ) of the E. coli DNA is greater than -0.045, the probability of integration is <20%; when  $\sigma$  is less than -0.06, the probability is >70%. Plasmid DNA isolated from an E. coli culture is found to have a length of 13,800 bp and an Linking number (L) of 1,200.

Assume that the DNA is in B-form and that there is 10 bp per turn.

(1) Calculate W for this DNA when the DNA is allowed to supercoil. 3

$$L_0 = T_0 = \frac{13800}{10} = 1380 = T \text{ when supercoil}$$

$$W = L - T = 1200 - 1380 = \ominus 180$$

(2) The likelihood that bacteriophage  $\lambda$  will be able to infect this culture is

( <20% , 20-70% , >70% , cannot be determined -circle one) . 2

\* Hint: Superhelical density  $\sigma = W/L_0$  and  $L_0 = T$  when DNA is linearized)

$$\sigma = \frac{\ominus 180}{1380} = \ominus 0.13 < -0.06 \quad \therefore \text{Probability} > 70\%$$

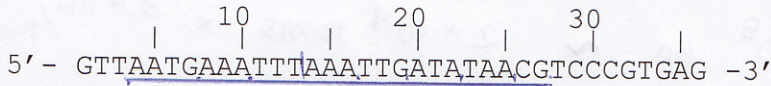
(3) The plasmid DNA obtained above has (right-handed), left-handed -circle one) supercoils. 2

\* Negative SC for RH DNA

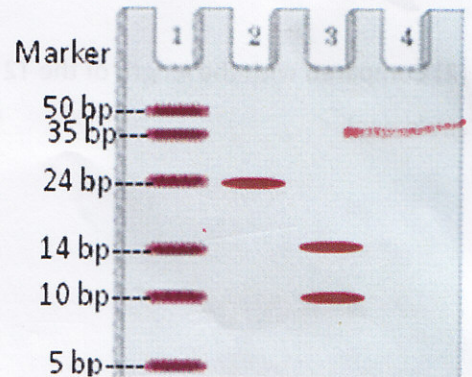
\* PCR\*

13. Your supervisor asks you to perform PCR on the following piece of double stranded DNA (X)

\*By convention, only one strand of the two is shown :



Each primer is 6 nucleotide-long and pairs with the template DNA without any mismatch. However, the sequences of the primers are lost because the computer crashed (duh!). Luckily, the PCR reactions worked. In order to identify the primers used in the successful PCR, you treated the PCR product with DraI restriction enzyme of which the restriction site is TTT ↓ AAA. The picture on the right shows the polyacrylamide gel of the following samples: a size marker (Lane 1), the PCR product before DraI treatment (Lane 2), and the PCR product after DraI treatment (Lane 3).



\* stressed .

3 (1) PCR stands for Polymerase Chain Reaction

(2) Deduce the sequences of the two primers were used in the PCR reaction.

2 Primer 1 5'- A A T G A A -3'

2 Primer 2 5'- C G T T A T -3'

7

1 for 1 misspelled alphabet

14. The  $pK_a$ 's of the amino-, carboxy- and the imidazole groups in amino acid X are 9.0, 2.0 and 6.0, respectively.

(1) Amino acid X is Histidine (full name). \*Do not abbreviate.

(2) What is the ratio of the base to conjugate acid forms (i.e., [base]/[acid]) of the following groups in X at pH 7.0?

(1) - Amino-  $10^{7-9} = \frac{1}{100}$   $pH - pK_a = \log \frac{[A]}{[HA]}$   $\frac{[A]}{[HA]} = 10^{pH - pK_a}$

(1) - Carboxy-  $10^{7-2} = 10^5$

(1) - Side chain  $10^{7-6} = 10$

calculate or

Round

(3) Based on the ratios obtained above, calculate the average charge on each functional group. Calculate to the first decimal place.

(1) - Amino-  $\frac{NH_2}{NH_3^+} = \frac{1}{100}$  Net charge =  $\frac{(+1 \times 100) + (0 \times 1)}{101} = 1.0$  or 0.99

(1) - Carboxy-  $\frac{COO^-}{COOH} = 10^5$  " =  $\frac{(-1 \times 10^5) + (0 \times 1)}{10^5 + 1} = -1.0$

(1) - Side chain  $\frac{Im}{Im^+} = \frac{10}{1}$  " =  $\frac{(+1 \times 1) + (0 \times 10)}{10 + 1} = \frac{1}{11} = 0.091$

(4) What is the net charge on this amino acid at pH 7.0?

\*Hint: Sum up the three average charges obtained in (2).

$1 - 1 + 0.1 = +0.1$   
or

$0.99 - 1 + 0.091 = 0.081$   
 $\frac{100}{101} - 1 + \frac{1}{11} = 0.081$

(5) Calculate the pI of this amino acid X.

\* Note: A molecule is expected to have a net negative charge when  $pH > pI$  and a net positive charge when  $pH < pI$ . Does your answer in (4) make sense?

$pI = \frac{9.0 + 6.0}{2} = 7.5$

$\therefore pH = 7 < pI$ , H should be positively charged, +0.1

14 - 2 = 12