

Question 2: a) (1) DCC is used for as the activator for peptide bond coupling

2pts each
4pts total.

(2) HF is used in the final deprotection step to ~~to~~ step i) cleave the peptide from the support; ii) deprotected side chains.

(3) TFA is for deprotecting $-NH_2$

(4) tBoc is used as protecting groups for $-NH_2$ of the a.a.

(b) homo polymer of alanine is more likely to form α -helix in a lipid bilayer. (3pts)

6pts total

~~because~~ the lipid bilayer interior is hydrophobic, by forming an α -helix. H-bonds between the intrachain amide proton & carbonyl oxygen would stabilize the α -helix; in water, H-bonding is competing w/ intra-chain

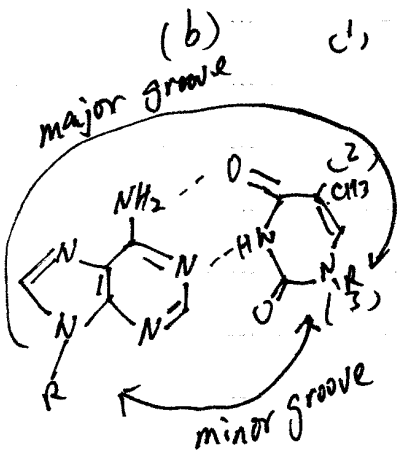
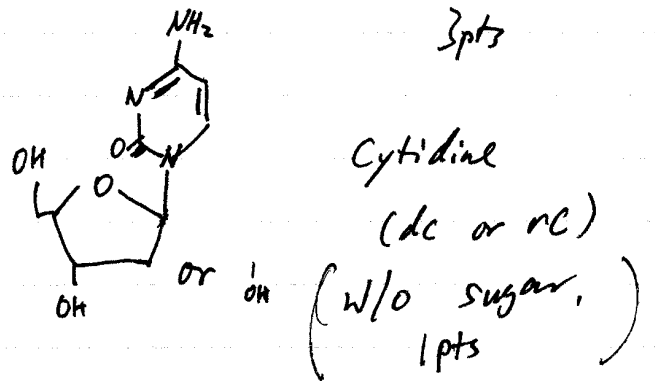
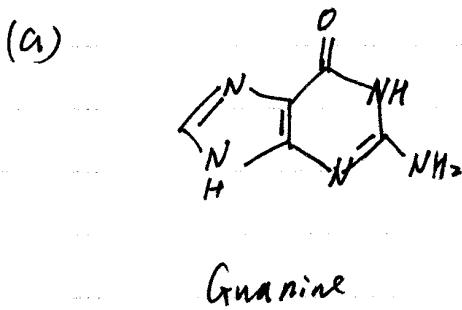
(3pts)

the solvent, and there is no energetic reason to favor an α -helix

(c) The column should be an anion exchange one, which separate the molecules based on the amount of "-" charges. (3pts)
 6pts total

The two peptides diff primary in the (3pts) presence of E, which incur a "-" charge for one.

Question 4: 6pts each. 30pts total



(c) Yes ; C β -NH $_2$ of A 2pts

~~Yes ; No 20 of 1 2pts 1pts~~

any one w/ H-bond ~~acceptor~~ donor such as Arg 3pts.

(c) There are two major factors for duplex
bpts total. stability: H-bonds & stacking.

The 2 duplexes have the same # of total
H bonds, or the same total # of A/T vs G/C
pairs (6/4).

The difference is in stacking. duplex 1 has
consecutive G/C pairs, which stacks better than



therefore, better stacking in duplex 1, ~~high~~ better
stability, higher T_m .

(d) i) a primer should be $\sim 15-20$ bp. ends w/
bpts: G/C.

forward: 5' GTACC GTAC, CAT, TGC 3' (pair to #1-#15)
could extend to #18
or #19)

backward: 5' GAAACC, CTG, ATT, GAG 3'

pair to 923 ~ 937

(d) (2) $N = N_0 (1 + \gamma)^x$

6 pts.
 $N = 1 \times 10^9$
 $N_0 = 1$
 $\gamma = 0.9$

$(1 + \gamma)^x = N_0 / N$

$x \log_{10}(1 + \gamma) = \log_{10}(N_0 / N)$

$x = \frac{\log_{10}(N_0 / N)}{\log_{10}(1 + \gamma)} = \frac{\log_{10}(1 \times 10^9)}{\log_{10}(1.9)}$

$x = \frac{9}{0.2787} = 32.3 \approx 33$

need 33 cycles.

Question 5:

$\Delta G = G_{in} - G_{out}$ 3 pt

$G_{in} = \mu_0 + RT \ln [H^+]_{in} + ZF\phi_{in}$ 3 pt

$G_{out} = \mu_0 + RT \ln [H^+]_{out} + ZF\phi_{out}$ 3 pt

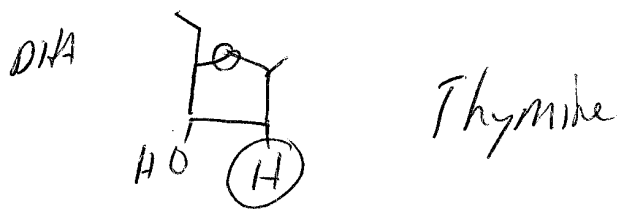
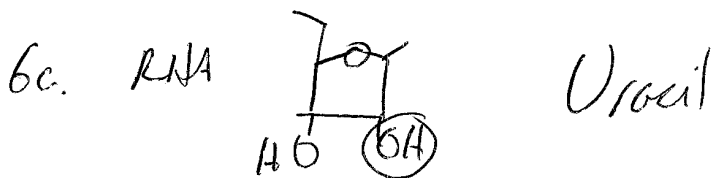
$\Delta G = (\mu_0 + RT \ln [H^+]_{in} + ZF\phi_{in}) - (\mu_0 + RT \ln [H^+]_{out} + ZF\phi_{out})$

$= RT \ln \frac{[H^+]_{in}}{[H^+]_{out}} + ZF(\phi_{in} - \phi_{out})$ 3 pt

$= 0.001987 \times (273 + 37) \times \ln \frac{10^{-8.4}}{10^{-7.0}} +$

$23.1 \times 1 \times (-0.14 - 0)$ 3 pt.

$= -5.2 \text{ kcal/mol}$



b. 1) Synthesize mRNA with any sequence but
lets say

5' AAA AAA AAA AAA 3'

2) transcribe into peptide

3) analyze peptide by any of three methods

a) edman degradation / peptide sequencing

b) mass spec

c) NMR

KEY for these experiments you don't need
to know it is a 3 letter code

although $6^3 = 216$