

Sec A MODEL ANSWERS

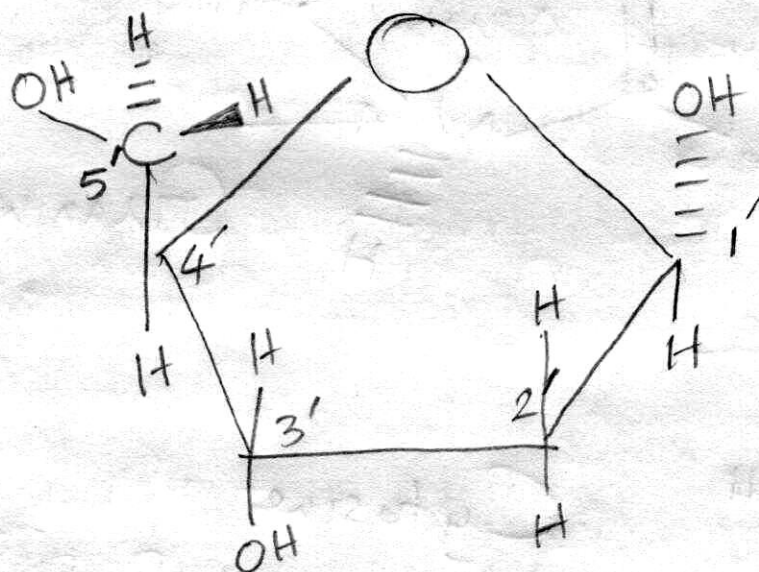
1 a) Backbone notations

$\alpha, \beta, \gamma, \delta, \epsilon, \zeta$

b) Sugar ring torsion

$\tau_1, \tau_2, \tau_3, \tau_4$

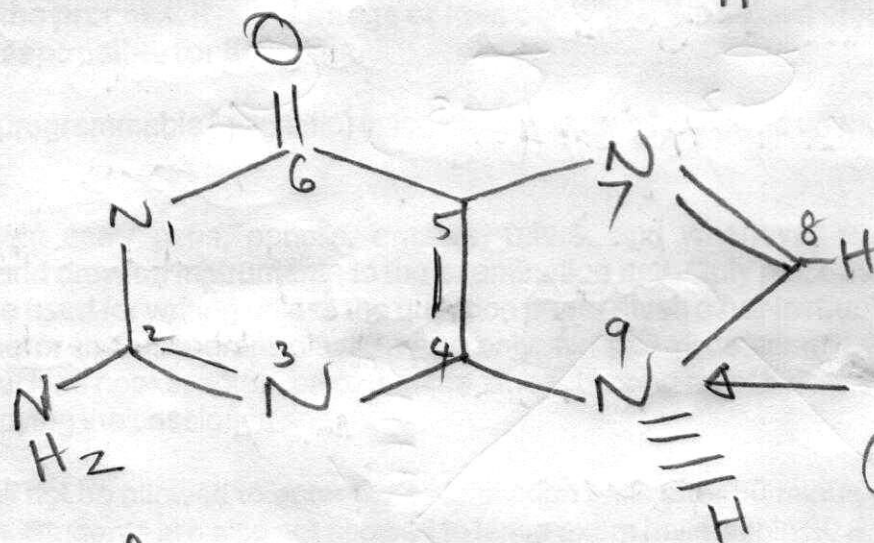
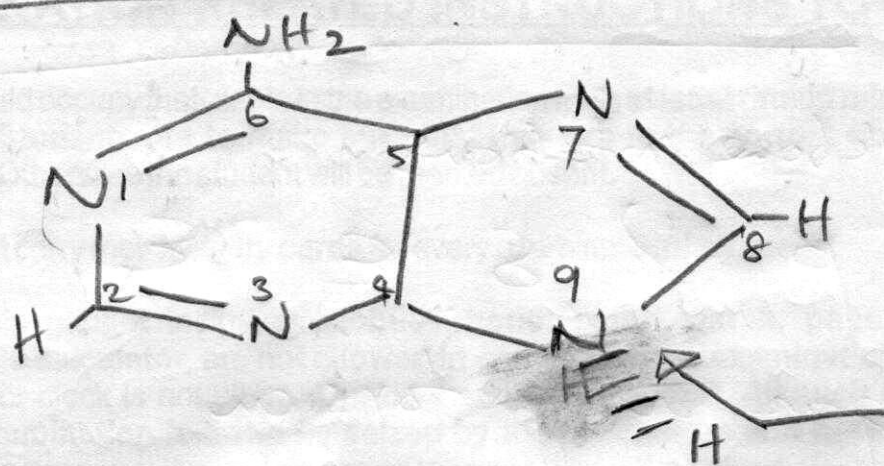
2.



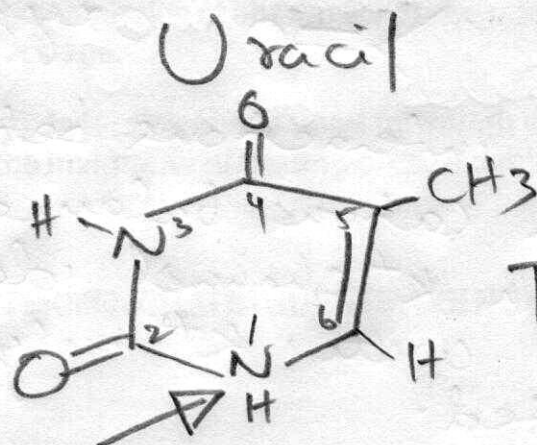
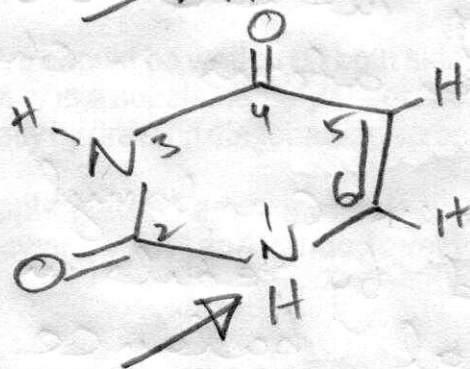
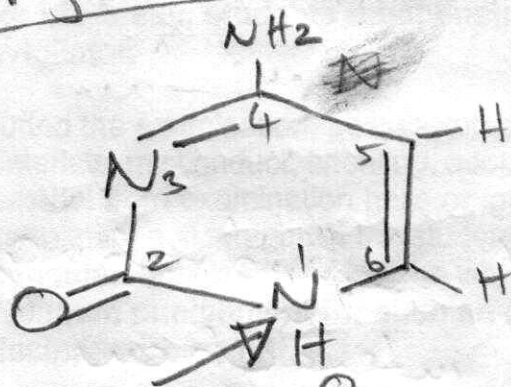
3. Free energy cost of dehydrating Na^+ not recovered by interaction with >=O oxygen atoms in channel

Favourable interactions between carbonyl O atoms with cation balanced by repulsion of O atoms. In K^+ channel ideal balance achieved with K^+ only, not Na^+ , so Na^+ is rejected.

4. Purines



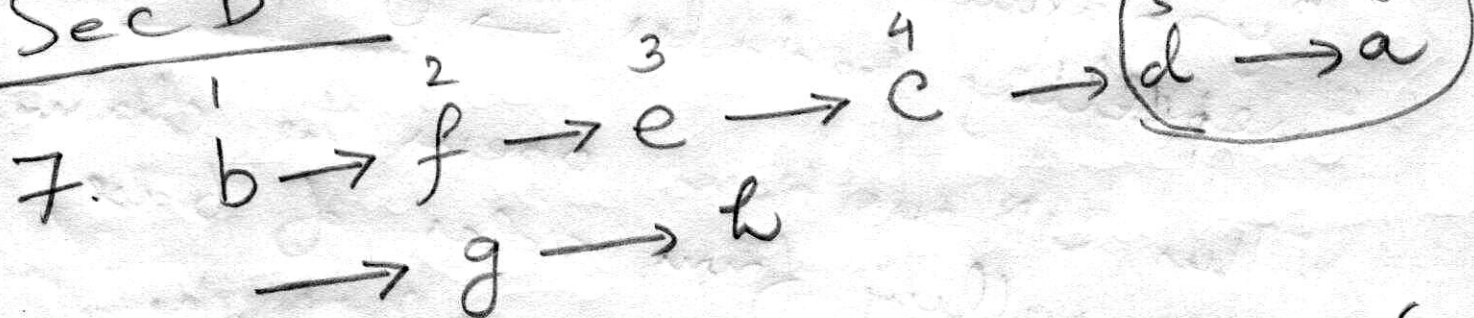
Pyrimidines



5. Bacteria control membrane fluidity by :-
- * Introducing unsaturation in lipid acyl chains
 - * Controlling length of acyl chains synthesised

- 6.
- N \longrightarrow binds ATP
 - P \longrightarrow Accepts phosphoryl group from Asp residue
 - A \longrightarrow Activator, links changes in N and P domains to transmembrane part of enzyme
 - TM \longrightarrow Calcium ion binding sites

Sec B



8. Rapid transport of K^+ favoured by REPULSION between K^+ ions in adjacent binding sites in channel.
Each new ion entering the pore

with +ve charge will REPEL
K⁺ ion in nearest site favouring
its release from other side.

Voltage gating requires major
Conformational changes in specific
ion channel domains

S1 → S4 paddles

S4 - Voltage sensor has helix
with +vely charged residues

Closed state → Paddles down

On membrane depolarization
Cytoplasmic side more +vely charged
repelling paddles → UP position

This UP position opens the channel
by pulling from sides of base,
increasing access to selectivity
filter

A DNA

9.

bp center shifted from
global helical axis

$$dx \sim 4 \text{ \AA} \quad dy \sim 0$$

Prominent inclination
in bp planes as
large as 20°

Mean helical twist

$$-\Omega = 34-36^\circ$$

10-10.5 bp/turn

Deoxyribose favours

C2' endo sugar
config.

Minor groove not
deep

~~Top view \rightarrow No hole
in helix cylinder~~

Top view \rightarrow reveals
hole in centre.

B DNA

Helix axis runs
thru' center of each
bp $dx, dy \approx 0$

BPs stack \perp to
helix axis.

$$-\Omega \approx 33^\circ$$

11 bp/turn

Sugar favours

C3' endo pucker

Minor groove
deep

Top view \rightarrow
No hole in helix
cylinder

10. Pumps: - Energy transducers, convert one form of energy to another like ATP driven pumps

↙
P-type ATPases

↓
ATP binding cassette
(ABC transporters)

Free energy of ATP hydrolysis drives movement of ions against concn. gradient
(Primary ACTIVE Transport)

Carriers: Utilize gradient of one ion to drive transport of another molecule against its concn. gradient
(Secondary ACTIVE transport)

E.g. E. Coli Lactose Transporter

11. * Patch Clamp Technique reveals single chan. ion conductance

* Single steps reveal single ion channel present in that membrane patch.

* Max. current of 2 pA says (steps)²
 a maximum of 2 ion channels simultaneously open to passage of ions across membrane

* It also reveals the temporal (time-dependent) opening and closing of channels in the millisecond time scale.

12 A) No. of Na^+ ions flowing into cell $= 10^4 \times 10^5 = 10^9$

$$\begin{aligned} \text{Amount of } \text{Na}^+ \text{ inside cell} &= 14 \times 10^{-3} \times 6.023 \times 10^{23} \times 12000 \times 10^{-18} \\ &= 14 \times 6.022 \times 12000 \times 10^{-3} \times 10^{23} \times 10^{-18} \\ &= 1.0117 \times 10^{11} \end{aligned}$$

Fraction of Na^+ entering cell relative to intracellular $[\text{Na}^+]$

$$= \frac{10^9}{1.0117 \times 10^{11}} \times 100$$

$$= 0.988\%$$

$$\approx 1\%$$

12.B) $V_{eq} = -\left(\frac{RT}{ZF}\right) \ln\left(\frac{[X]_{in}}{[X]_{out}}\right)$

For Na^+

$$V_{eq} = -\left(\frac{8.314 \times \cancel{310} 310}{1 \times 96500}\right) \ln\left(\frac{14}{143}\right)$$

$$= (+62 \text{ mV})$$

For K^+

$$V_{eq} = -\left(\frac{8.314 \times 310}{96500}\right) \ln\left(\frac{157}{4}\right)$$

$$= (-98) \text{ mV}$$