Chapter 7 HW Assignment

1. Compound A:

MW = 90.08 g/mol

Assume 100 g sample

40.00% C → $40.00\,g\,C \times \frac{mol\,C}{12.01\,g} = \frac{3.33\,mol}{3.33} = 1$

6.71% H → $6.71\,g\,H \times \frac{mol\,H}{1.008\,g} = \frac{6.66\,mol}{3.33} = 2$

53.29% O → $53.29\,g\,O \times \frac{mol\,O}{15.999\,g} = \frac{3.33\,mol}{3.33} = 1$

Elemental formula: CH_2O → Yes carbohydrate.

" " weight: 30.025 g/mol

n × elemental formula weight = molecular weight

$n = \frac{90.08\,g/mol}{30.025\,g/mol} = 3$

n × Elemental formula = molecular formula

$3 \times (CH_2O) = \cancel{C_2H_6O} \; C_3H_6O_3$

Compound B
MW 152.15 g/mol

100 g

$39.47\%\ C \Rightarrow 39.47\,g\,C \times \frac{1\,mol\,C}{12.01\,g} = \frac{3.29}{3.29}\,mol \div 1 \rightarrow 5$

$7.95\%\ H \Rightarrow 7.95\,g\,H \times \frac{1\,mol\,H}{1.008\,g} = \frac{7.87}{3.29}\,mol \div 2.4 \rightarrow 12$

$52.58\%\ O \Rightarrow 52.58\,g\,O \times \frac{1\,mol\,O}{15.999\,g} = \frac{3.29}{3.29}\,mol \div 1 \rightarrow 5$

Elemental formula: $C_5H_{12}O_5$ → Not a carbohydrate.
Elemental formula weight: 152.14 g/mol = Molecular weight

2. $C_6H_{12}O_6 + 6\,O_{2(g)} \rightarrow 6\,CO_{2(g)} + 6\,H_2O_{(g)}$

C 6	C ~~X~~ 6
H 12	H ~~X~~ 12
O ~~X~~ 18	O ~~X~~ ~~X~~ 18

$5.00\,\cancel{g}\ C_6H_{12}O_6 \times \frac{\cancel{mol\ C_6H_{12}O_6}}{180.15\,\cancel{g}} \times \frac{6\,mol\,CO_2}{1\,\cancel{mol\ C_6H_{12}O_6}} \times \frac{44.008\,g\,CO_2}{mol} = 7.33\,\cancel{g}\,CO_2$

$5.00\,g\,O_2 \times \frac{\cancel{mol\ O_2}}{31.998\,g} \times \frac{6\,mol\,CO_2}{6\,\cancel{mol\ O_2}} \times \frac{44.008\,g\,CO_2}{\cancel{mol}} = 6.88\,g\,CO_2$

O_2 is the limiting reagent

6.88g CO_2 is produced.

3. 7-carbon ketose

# of chiral centers: #C - 3

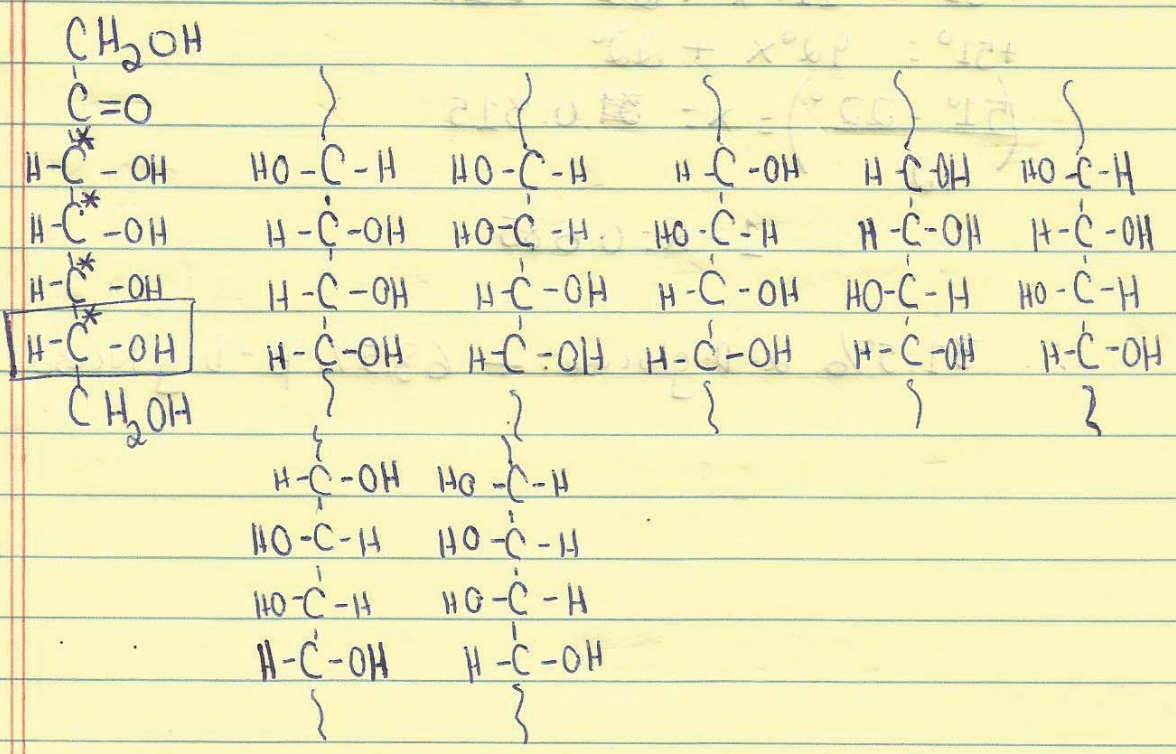
$7 - 3 = 4$

# of stereoisomers: $2^{\#C-3}$

$2^4 = 16$

∴ 8 D-stereoisomers + 8 L-stereoisomers

*: Chiral centers



4. The solution is composed of both α-D-glucose and β-D-glucose

α-D-glucose $[\alpha]_D^{25°C} = +114°$

β-D-glucose $[\beta]_D^{25°C} = +22°$

Solution $[\alpha]_D^{25°C} = +51°$

$+51° = x\,(+114°) + (1-x)\,(+22°)$

$+51° = 114°x + 22° - 22°x$

$+51° = 92°x + 22°$

$\left(\frac{51° - 22°}{92°}\right) = x = 0.315$

$1 - x = 0.685$

∴ 31.5% α-D-glucose + 68.5% β-D-glucose

5. $[\alpha]_D^{25°C} = \dfrac{\text{observed optical rotation (°)}}{\text{optical path length (dm)} \times \text{concentration } \left(\frac{g}{mL}\right)}$

$\underset{mL}{0.15g}$ sucrose $\xrightarrow{\text{invertase}}$ $\underset{mL}{0.075g}$ D-glucose + $\underset{mL}{0.075g}$ D-fructose

$[\alpha]_D^{25°C} = +51°$ $\quad [\alpha]_D^{25°C} = -95°$

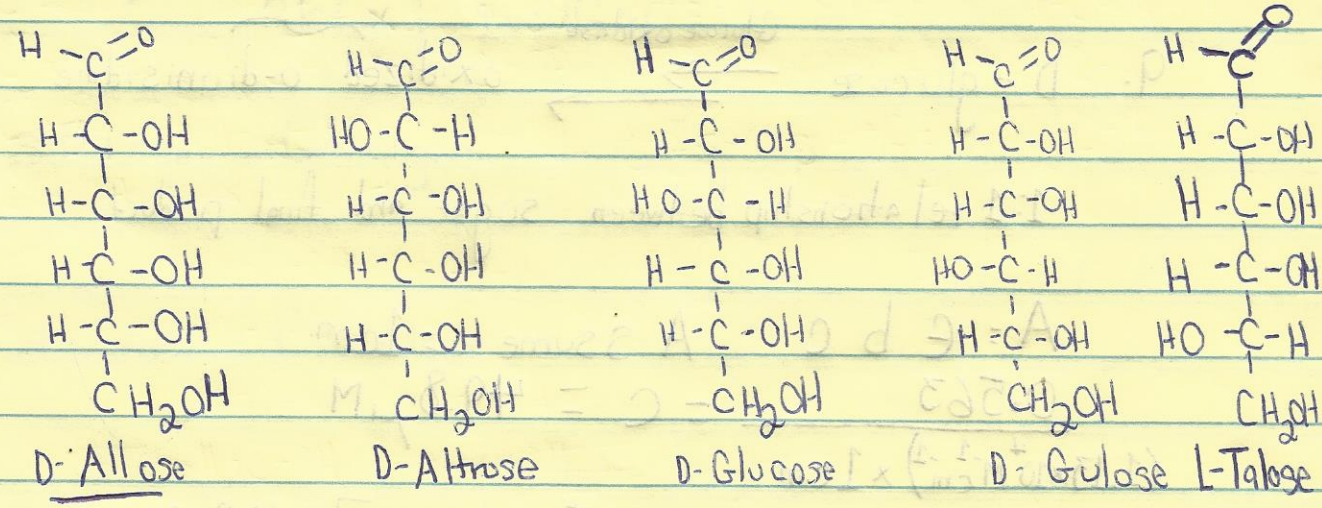
Optical path length = 1dm

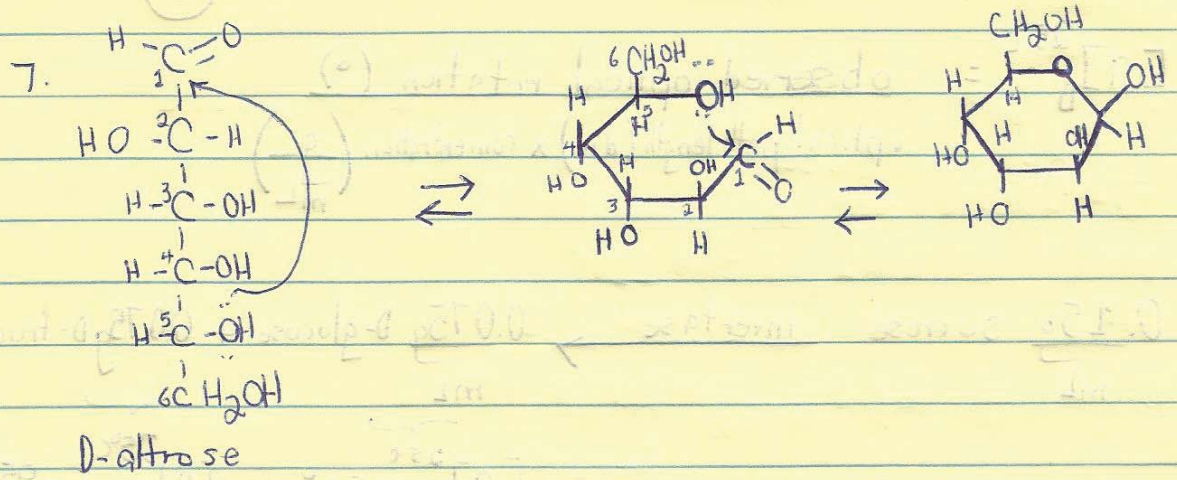
$[\alpha]_D^{25°C} \times$ optical path length $\times$ concentration = observed optical rotation (°)

$$\left(+51° \times 1dm \times 0.075\frac{g}{mL}\right) + \left(-95° \times 1dm \times \frac{0.075g}{mL}\right) =$$

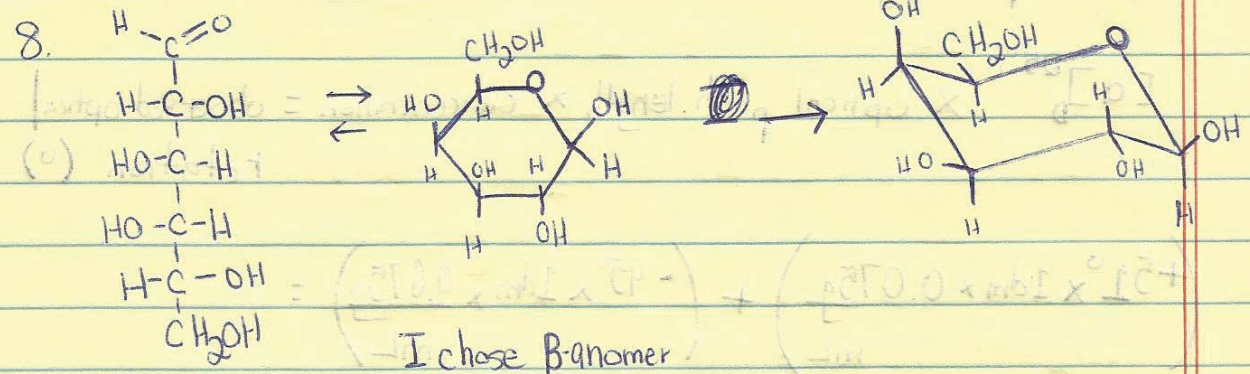
$$3.825° + -7.125° = -3.3$$

6.



7. 

D-altrose

8. 

I chose β-anomer

D-galactose

$\epsilon = 1.13 \times 10^{4}\ M^{-1} cm^{-1}$

9. D-glucose $\xrightarrow{\text{Glucose oxidase}}$ oxidized o-dianisidine

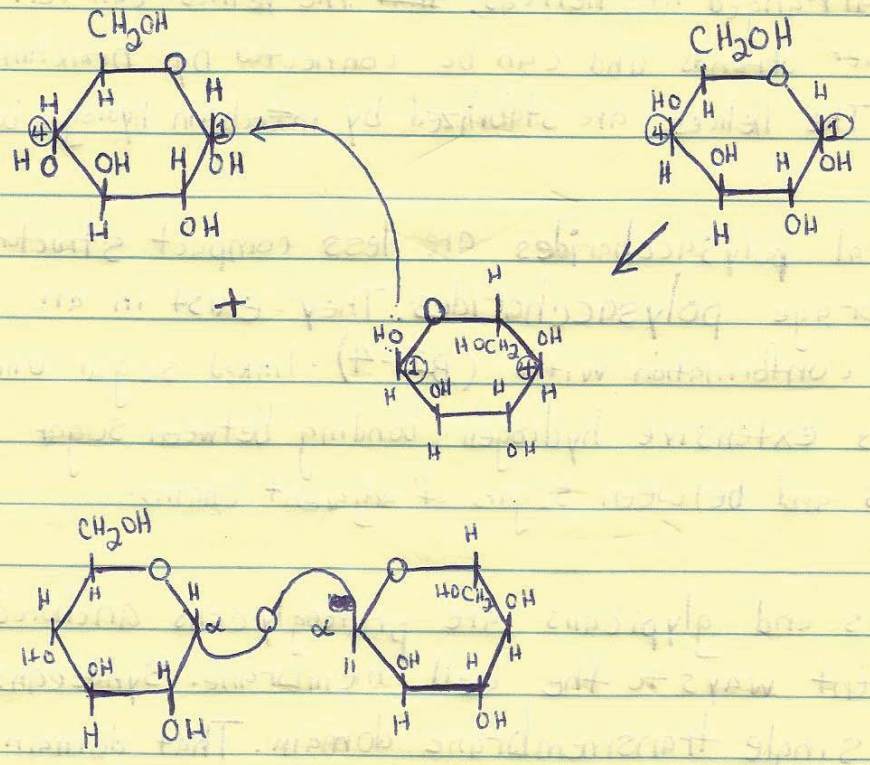
1:1 relationship between sugar and final product.

$A = \epsilon b c$ Assume $c = 1cm$

$$\frac{0.563}{(1.13 \times 10^{4}\ M^{-1} cm^{-1}) \times 1cm} = c = 49.8\ \mu M$$

$\therefore$ [D-glucose] = 49.8 μM

10. α-D-glucopyranose α-D-galactose



α-D-glucopyranosyl α-D-galactopyranoside
Glc(α1-1α)Gal

11. Storage: Glycogen

Structure: Cellulose

Information carrier: Hyaluronate

12. Storage polysaccharides have (α 1-4)-linked sugar units arranged in helices. ~~that~~ The helices can coil with other strands and can be connected by branching points. The helices are stabilized by interchain hydrogen bonds.

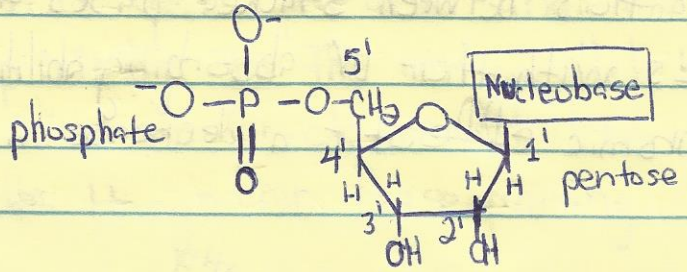
Structural polysaccharides are less compact structurally than storage polysaccharides. They exist in an extended conformation with (β1-4)-linked sugar units. There is extensive hydrogen bonding between sugar molecules and between sugars of adjacent chains.

13. Syndecans and glypicans are proteoglycans anchored in different ways to the cell membrane. Syndecans have a single transmembrane domain. That domain ~~is stabilized by hyd~~ consists of nonpolar amino acids which engage in stabilizing hydrophobic interactions with the plasma membrane lipids. Glypicans are anchored to a lipid membrane via a glycolipid such as glycophosphatidylinositol.

14. Lectin-carbohydrate interactions are very important for signaling praesses. However, these interactions can exist between partners from ~~the~~ different species. Viruses and bacteria have lectins that can recognize the carbohydrate ~~conjugates of~~ portion of glycoconjugates present on the extracellular portion of the cell membrane and by binding to the sugar they are able to enter foreign cells such as human cells and cause damage.

Chapter 8 HW Answer Key

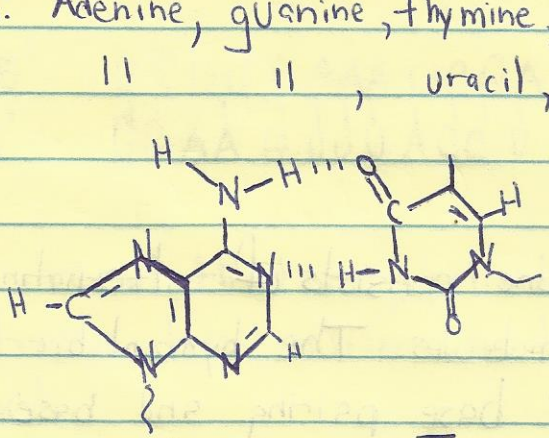
1) Nucleotides



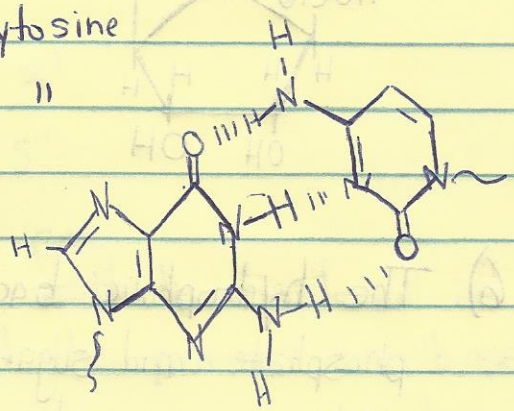
The nucleobase can be a pyrimidine or purine and is connected to the ribose via an N-glycosidic bond.

Nucleosides is a nucleotide with the phosphate group.

2) DNA: Adenine, guanine, thymine, cytosine
RNA: " " , uracil, "



A



T G C

Basically the same for U

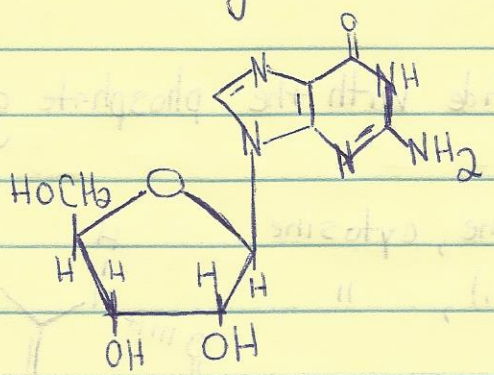
2 Hydrogen bonds

3 hydrogen bonds

3) The nucleobases absorb in the UV region and as a result DNA absorbs in the UV region. The absorbance of a DNA fragment can be used to quantify the mg/mL of DNA. The close interactions between stacked bases of stable DNA interferes with their UV absorbing abilities leading to a hypochromic effect - a decrease in their absorption.

4) RNA has a hydroxyl group @ position C2' of the ribose which serves as a nucleophile upon base deprotonation to break apart the phosphodiester bond linking the nucleotides.

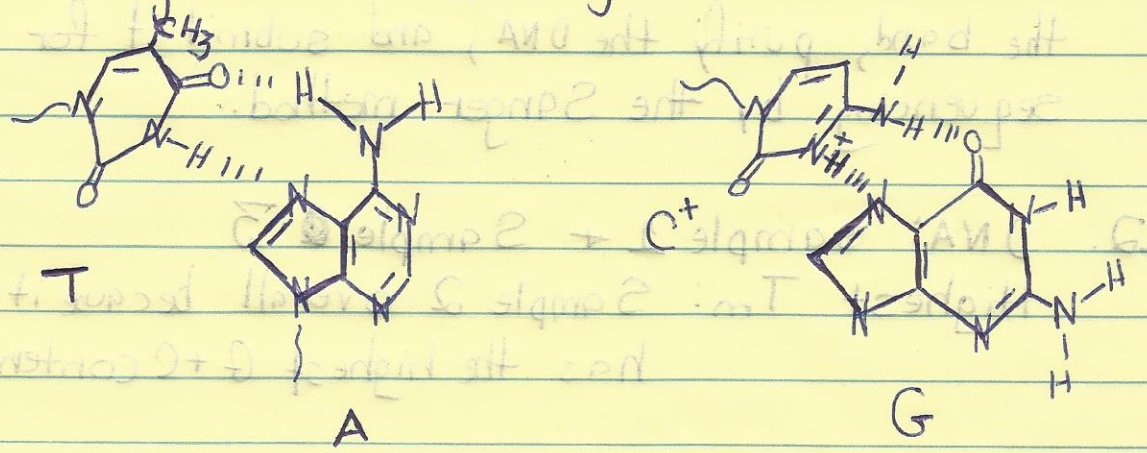
5)



6) The hydrophilic backbone consists of alternating phosphate and sugar molecules. The hydrophobic interior consists of base pairing and base stacking nucleobases. The purines in the Z form DNA can adopt a syn configuration resulting in a left-handed helix.

7) Mirror repeats do not have a self-complementary sequence.

8) You get parallel and antiparallel strand base pairing. ~~In~~ The antiparallel base pairing is of the Watson-Crick model. The parallel orientation follows ~~the~~ Hoogsteen base-pairing.



Two hydrogen bonds between T-A + C-G.

9) 5'... CCUU CAAA UGGA ... 3'
3'... GGAA GUUU ACCU ... 5'

But recall that a pyrimidine ~~will~~ can be displaced if between two purines so that the purines can base stack.

Bulge

5'... CCUUCAAA GGA ... 3'
3'... GGAAGUUU CCU ... 5'

The complementary strand would be different.

10. Supercoiling

11. You must use a specific restriction enzyme to linearize your DNA. You could then observe whether the one band corresponding to your cut DNA is of the approximate correct # of bp size. You could even then cut out the band, purify the DNA, and submit it for sequencing by the Sanger method.

12. DNA: sample 1 + Sample 3
Highest Tm: Sample 2 overall because it has the highest G+C content.

Sample 3 would have the higher Tm of the two DNA samples

13. Based on Tm (°C) then A + C have the greater degree of similarity because stronger interactions between them results in higher DNA stability. However, one has to be cautious about this conclusion because the higher Tm could also be due to higher G+C content so that must be taken of.

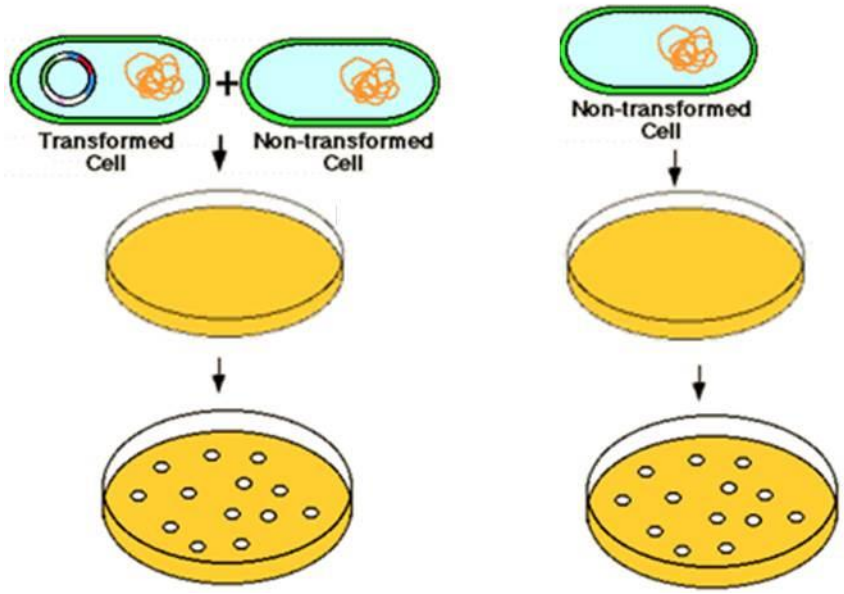
14. Radiation-induced mutagenesis

Chemistry 4055 (Spring 2013)
Biochemistry I- Introduction to the Chemistry of the Animal Cell
Chapter 9 HW Assignment

1. What is the difference between DNA sticky ends and blunt ends produced by restriction enzymes?

The restriction enzymes that produce sticky ends leave staggered cuts on the two DNA strands, leaving two to four nucleotides of one strand unpaired at each resulting end. The strands can base-pair with each other or with complementary sticky ends of other DNA fragments. These strands are far more efficient at ligating than blunt end strands. The blunt ends are formed by cleaving both strands of DNA at the opposing phosphodiester bonds, leaving no unpaired bases on the ends.

2. Say you have been diligently working on inserting a DNA fragment into a plasmid with a gene for ampicillin resistance and after transforming your cells you are ready to determine which cells contain the DNA fragment. You check the refrigerator to look for your agar plates containing ampicillin but notice you do not have any more left. You decide to see if Professor Tinoco has any and find that he has a stack of them but he made them when he was a grad student…many years ago! You decide "what the heck" and go ahead and use them. On one plate you load your cells that you transformed and on another plate you load cells that you did not transform. The next morning you find that both plates have cells on them as shown below. What does this data tell you?



The data indicate that the plates are way too old and that the ampicillin has expired.

What would have been the correct way to do this experiment? How would you determine whether a particular cell colony has your desired DNA fragment?

The correct approach would have been to make fresh agar plates containing fresh ampicillin. The colonies that would grow on these plates would certainly contain the plasmid but not necessarily the DNA fragment. One would then have to select representative members of different colonies and then culture them to produce a good amount of recombinant DNA. The recombinant DNA could then be digested with a restriction enzyme to separate the DNA fragment from the plasmid and run on an agarose gel. The DNA band that would correspond to the number of base pairs expected for the DNA fragment could then be cut out, purified, and sequenced by the Sanger method.

3. The following DNA duplex sequence is a modified form of a gene that you are interested in

5′-GATATCAGGAGGTATGXXXTAAGATATC-3′
3′-CTATAGTCCTCCATACxxxATTCTATAG-5′

where XXX is the 5′-3′ sequence of your gene and xxx is the complementary 3′-5′ strand.

a. What would be the mRNA sequence transcribed from the intact DNA duplex present in a bacterial expression vector?

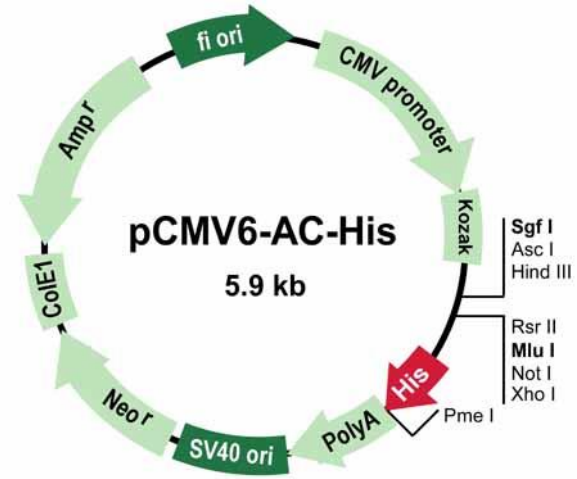
5′-GAUAUCAGGAGGUAUGXXXUAAGAUAUC-3′

b. If you obtained your gene from a commercially available plasmid, what forward and reverse primers should you use to obtain the modified gene presented above by PCR?

Forward primer: 5′-GATATCAGGAGGTATGX-3′
Reverse primer: 3′-xATTCTATAG-5′

Where X and x are 18 to 20 nucleotides from the sequence of your gene.

4. A gene is inserted into the pCMV6-AC-His expression vector (see below) using the NOT I restriction enzyme. What is the most efficient way to purify the protein that is expressed? What would happen if your insert contained a stop codon?



The pCMV6-AC-His expression vector contains a His-tag and so your protein will be His-tagged and you can use a Ni^{2+}-NTA column to affinity purify your protein. However, if your gene contains a stop codon then it would be expressed without the His tag and can not be affinity purified.